

Schreiber, David

153108

From: Angell, Jon E
Sent: Wednesday, May 04, 2005 4:58 PM
To: ~~Schreiber, David~~
Subject: SPDI Sequence Database Search Request 09/978,544 SPDI

SEARCH REQUEST FORM
Scientific and Technical Information Center

Examiner# : 78697
Art Unit : 1635
Phone Number: 571-272-0756
Date: 5/4/05
Serial Number: 09/978,544
Mailbox & Bldg/Room Location: REMSEN 2C18
Results Format Preferred (circle): Paper

This case is a SPDI Application

I would like to have a search performed (commercial and interference databases) using the following SEQ. ID NOS. from application : 09/978,544

SEQ ID NO: 58 (nucleic acid sequence ~ 2458 nucleotides long)
SEQ ID NO: 59 (amino acid ~ 373 amino acids long)

Please search the NUCLEIC ACID databases using SEQ ID NO: 58
Please search the PROTEIN databases using SEQ ID NO: 59

NOTE: The sequence of this application is also related to the sequences of 09/978,375 and 10/002,967 (search requests for these apps are also being submitted)

Please don't hesitate to call if you need clarification for any request

Thanks,
Eric

J. Eric Angell
Art Unit 1635
REMSSEN 2D20
571-272-0756

THIS PAGE BLANK (USPTO)

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number: 2- _____ Serial Number: _____
Location (Bldg/Room#): _____ (Mailbox #): _____ Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY

Searcher: D. Schreiber

Searcher Phone #: 272-2526

Searcher Location: Kensington E01 A61

Date Searcher Picked Up: _____

Date Completed: 5/11

Searcher Prep & Review Time: 15

Online Time: 19

Type of Search

1 NA Sequence (#)

1 AA Sequence (#)

_____ Structure (#)

_____ Bibliographic

_____ Litigation

_____ Fulltext

_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog

_____ Questel/Orbit _____ Lexis/Nexis

_____ Westlaw _____ WWW/Internet

☒ In-house sequence systems Compygen

☒ Commercial _____ Oligomer _____ Score/Length
☒ Interference ☒ SPDI _____ Encode/Transl

_____ Other (specify)

THIS PAGE BLANK (USPTO)

L1 148790 S ASHKENAZI-A?/AU OR BAKER?/AU OR BOTSTEIN-D?/AU OR DESNOYRES?/
L2 6496 S GERBER-H?/AU OR GERRITSEN-M?/AU OR GODDARD-A?/AU OR GODOWSKI-
L3 24118 S KUO-S?/AU OR NAPIER-M?/AU OR PAN-J?/AU OR PAONI-N?/AU OR ROY-
L4 178684 S L1 OR L2 OR L3
L5 2 S L4 AND PRO363 OR PRO-363
L6 2 DUP REM L5 (0 DUPLICATES REMOVED)
L7 16 S PRO363
L8 0 S L5 AND 209616
L9 0 S L4 AND 209616
L10 16 S PRO363
L11 1 S PRO-363
L12 17 S L10 OR L11
L13 0 S L11 AND ANTIBODY

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
OM protein - protein search, using sw model
Run on: May 6, 2005, 07:41:23 ; Search time 125 Seconds
(without alignments)
1154.093 Million cell updates/sec

Title: US-09-978-544A-59
Perfect score: 1908
Sequence: 1 MSLLLLLLLVYVGTGLTH.....TKAETTPSMIPQSGRAFQTV 373
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
SUMMARIES						
RESULT 1						
ID	AAY41692	standard; protein; 373 AA.				
DE	Human PRO 363	protein sequence.				
PN	WO9946281-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1908;	DB 2;	Length 373;		
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;				
RESULT 2						
ID	AAB33430	standard; protein; 373 AA.				
DE	Human PRO363 (UNQ318)	protein sequence.				
PN	WO200053758-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1908;	DB 3;	Length 373;		
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;				
RESULT 3						
ID	AAB44248	standard; protein; 373 AA.				
DE	Human PRO363 (UNQ318)	protein sequence.				
PN	WO200053756-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1908;	DB 3;	Length 373;		
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;				
RESULT 4						
ID	AAU12365	standard; protein; 373 AA.				
DE	Human PRO363	polypeptide sequence.				
PN	WO200140466-A2.					
PD	07-JUN-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1908;	DB 3;	Length 373;		
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;				
RESULT 5						
ID	AAB48108	standard; protein; 373 AA.				
DE	Human A236	polypeptide.				
PN	WO200069885-A2.					
PD	23-NOV-2000.					
PA	(MILL-) MILLENNIUM PHARM INC.					
Query Match	100.0%;	Score 1908;	DB 4;	Length 373;		
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;				
RESULT 6						
ID	AAB65293	standard; protein; 373 AA.				

us-09-978-544a-59.rag.spdi

DE Human PRO363 protein sequence SEQ ID NO:503.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 7
ID AAU83656 standard; protein; 373 AA.
DE Human PRO protein, Seq ID No 130.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 5; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 8
ID ABB84848 standard; protein; 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:64.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 5; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 9
ID AAE26448 standard; protein; 373 AA.
DE Human A236 protein.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 100.0%; Score 1908; DB 5; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 10
ID ABB95454 standard; protein; 373 AA.
DE Human angiogenesis related protein PRO363 SEQ ID NO: 64.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1908; DB 5; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 11
ID ABU58108 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 12
ID ABU59186 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO363.
PN US2002132252-A1.

PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 13
ID AB082698 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 14
ID ABO17809 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 15
ID AB060617 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 16
ID AB080803 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 17
ID ABO25194 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 18
ID ABO33769 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 19
ID AB013999 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 20
ID AB081063 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 21
ID AB072200 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 22
ID AB072584 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 23
ID AB066763 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 24
ID AB084880 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 25
ID AB059844 standard; protein; 373 AA.
DE Novel secreted and transmembrane protein PRO363.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 26
ID AB061078 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 27
ID AB059333 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 28
ID ABO26030 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 29
ID ABO25034 standard; protein; 373 AA.
DE Human secreted/transmembrane protein (PRO) #194.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 30
ID AB080347 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 31
ID ABU82112 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 32
ID ABU59039 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 33
ID ABU92417 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 34
ID ABU59482 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 35
ID ABU67039 standard; protein; 373 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 388.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 36
ID ABU92248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 37
ID ABU10954 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 38
ID ABU81706 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 39
ID ABU8645 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 40
ID ABO34159 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003017981-A1.

PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 41
ID ADA45907 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 42
ID ADA76338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 43
ID ABJ72292 standard; protein; 373 AA.
DE Human PRO363 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 44
ID ADA18988 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 45
ID ADA61611 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 46
ID ADB19396 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 47
ID ADB27937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 48
ID ADA86416 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 49
ID ADB15980 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 50
ID ADA38014 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 51
ID ADA47766 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 52
ID ADA21700 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 53
ID ADA10487 standard; protein; 373 AA.
DE Human secreted/transmembrane protein; PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 54
ID ADA67561 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 55
ID ADB30568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 56
ID ADA85864 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 57
ID ADA18031 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 58
ID ADA97076 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 59
ID ADA79380 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 60
ID ADA87519 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 61
ID ADB16721 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 62
ID ADA28139 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 63
ID ADA91813 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 64
ID ADB14876 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 65
ID ADA24598 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 66
ID ADB18837 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 67
ID ADA94052 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 6; Length 373;
RESULT 68
ID ADB19948 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082691-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 69
ID ADB13260 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 70
ID AB043342 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 71
ID AB019649 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 72
ID ADA12259 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 73
ID ADA94719 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 74
ID ADA74514 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 75
ID ADB24747 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 76
ID ADA82271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 77
ID ADA75234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 78				
ID ADA85312 standard; protein; 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2003082695-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 79				
ID ADA84760 standard; protein; 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2003082708-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 80				
ID ADB30016 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003073214-A1.				
PD 17-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 81				
ID ADA80544 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003082761-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 82				
ID ADA75786 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003082703-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 83				
ID ADA38944 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein PRO363.				
PN US2003059780-A1.				
PD 27-MAR-2003.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 84				
ID ADA47011 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003073210-A1.				
PD 17-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 85				
ID ADB25307 standard; protein; 373 AA.				
DE Human PRO polypeptide SEQ ID NO 388.				
PN US2003077715-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 86				
ID ADA93483 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003077721-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		
RESULT 87				
ID ADA93483 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003077721-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1908;	DB 6;	Length 373;
Best Local Similarity	100.0%;	Pred. No. 3.7e-145;		

RESULT 96
ID ADB26281 standard; protein; 373 AA.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 106
ID ADB29041 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 107
ID ABO53245 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
FN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 108
ID ADA76993 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003059509-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 109
ID ADA22626 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
FN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 110
ID ADA88623 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 111
ID ADA97628 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 112
ID ADB27385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003022239-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 113
ID ADB22318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003087344-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 114
ID ABO22615 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
FN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 115
ID ADA06792 standard; protein; 373 AA.

DE Human secreted/transmembrane PRO polypeptide #140.
FN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 116
ID ABJ72122 standard; protein; 373 AA.
DE Human membrane bound receptor/protein PRO363 amino acid sequence.
FN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 117
ID ADA39485 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
FN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 118
ID ADA67009 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 119
ID ADB22870 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 120
ID ADB23643 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
FN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 121
ID ADA92365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 122
ID ADBi5428 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 123
ID ADB83620 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 124
ID ADB80726 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US200308068-A1.
PD 08-MAY-2003.

RESULT 143
ID ADB76281 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
FN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 144
ID ADB77348 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 145
ID ADB34505 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
FN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 146
ID ADB35609 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
FN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 147
ID ADB33953 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
FN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 148
ID ADB35057 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
FN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 149
ID ADB36161 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
FN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 150
ID ADB46556 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 151
ID ADC43707 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 152

ID ADC57983 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
FN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 153
ID ADC55347 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
FN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 154
ID ADC12214 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
FN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 155
ID ADC61467 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 156
ID ADC63431 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 157
ID ADC66531 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 158
ID ADC56636 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
FN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 159
ID ADC68655 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 160
ID ADC62715 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 161
ID ADC67780 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 171

ID ADC59955 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 172

ID ADC49880 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 173

ID ADC49079 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 174

ID ADC49596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 175

ID ADC47457 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 176

ID ADC52962 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 177

ID ADC57316 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 178

ID ADC60507 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 179

ID ADC50982 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 180

ID ADC50982 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 180

ID ADC65509 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003087362-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 181

ID ADC54607 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
FN US2003087363-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 182

ID ADC53568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
FN US2003087364-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 183

ID ADC59091 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
FN US2003087359-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 184

ID ADC55969 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
FN US2003087360-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 185

ID ADC58539 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
FN US2003087346-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 186

ID ADC14803 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003082546-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 187

ID ADC47202 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003105288-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 188

ID AD08335 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003068623-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 189

ID ADD03213 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003092104-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 190
ID ADC90205 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 191
ID ADC82160 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
FN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 192
ID ADC69624 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 193
ID ADC48513 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 194
ID ADD10042 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 195
ID ADD07802 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 196
ID ADC78077 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 197
ID ADD04617 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 198
ID ADC82693 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
FN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 199
 ID ADD06312 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003073816-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 200
 ID ADC80573 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003092103-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 201
 ID ADD11080 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 202
 ID ADD10353 standard; protein; 373 AA.
 DE Human secreted/transmembrane PRO polypeptide #32.
 PN US2003105011-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 203
 ID ADC47961 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 204
 ID ADD08873 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003073090-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 205
 ID ADC77831 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US200308066-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 206
 ID ADC80021 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003087358-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 207
 ID ADD07122 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2002193300-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 208

ID ADD11313 standard; protein; 373 AA.
 DE Human secreted/transmembrane PRO polypeptide #32.
 PN US2003105013-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 209
 ID ADD09490 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003194775-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 210
 ID ADC83369 standard; protein; 373 AA.
 DE Human PRO polypeptide #140.
 PN US2003059783-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 211
 ID ADD50794 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003105291-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 212
 ID ADD41203 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003203438-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 213
 ID ADD52342 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003194769-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 214
 ID ADD51040 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003105290-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 215
 ID ADD53082 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003194792-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 216
 ID ADD53634 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003203437-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 7; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 217
 ID ADD5476 standard; protein; 373 AA.
 DE Human PRO polypeptide #140.

PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 218
ID ADD37106 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 219
ID ADD56434 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 220
ID ADD51790 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 221
ID ADD02589 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 222
ID ADD05521 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 223
ID ADD02023 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 224
ID ADD54205 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 225
ID ADD54872 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 226
ID ADD50275 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 227
ID ADD51286 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 228
ID ADE49093 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 229
ID ADD92522 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 230
ID ADD91418 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 231
ID ADE04032 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 232
ID ADE31891 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 233
ID ADE27026 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 234
ID ADE32329 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 235
ID ADE22261 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 236
ID ADD50275 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

ID ADD79485 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 237
ID ADE35147 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 238
ID ADE16261 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 239
ID ADD72876 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 240
ID ADE42021 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 241
ID ADE17838 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 242
ID ADD91970 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 243
ID ADE33433 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 244
ID ADE33985 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 245
ID ADD80037 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 246
ID ADD93074 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 247
ID ADD72234 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 248
ID ADE19494 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 249
ID ADE18942 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 250
ID ADE43138 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 251
ID ADD95927 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 252
ID ADE22813 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 253
ID ADD78931 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 254
ID ADE26493 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.

PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 255
ID AD832881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 256
ID ADB42573 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 257
ID AD816885 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 258
ID ADD80589 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 259
ID ADD89617 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 260
ID ADE40901 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 261
ID ADE04700 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 262
ID ADE92829 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 263
ID ADP46899 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195333-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 264
ID ADF67430 standard; protein; 373 AA.
DE Human PRO363 amino acid sequence SEQ ID NO:503.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 265
ID ADG21538 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 266
ID ADG23179 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 267
ID ADF97514 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 268
ID ADG80578 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 269
ID ADG52656 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 270
ID ADG59976 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003208915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 271
ID ADG80026 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 272
ID ADH55318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Wed May 11 07:24:23 2005

Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 273
ID ADH5970 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 274
ID ADI3684 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 275
ID ADI60736 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 276
ID ADI64089 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 277
ID ADI65038 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 278
ID ADI63537 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 279
ID ADH81951 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 280
ID ADI00177 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 281
ID ADH81399 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 282
ID ADD76573 standard; protein; 373 AA.

ID ADM82568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 283
ID ADNI1967 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 284
ID ADNI6596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 285
ID ADNI5415 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 286
ID ADNI14863 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 287
ID ADC48833 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
RESULT 288
ID ADC81125 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
RESULT 289
ID ADE21004 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
RESULT 290
ID ADE05848 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
RESULT 291
ID ADD76573 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 292
ID ADD75077 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 293
ID ADD75823 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 294
ID ADD85055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 295
ID ADD86981 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 296
ID ADD20758 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 297
ID ADD39055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 298
ID ADD87937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 299
ID ADD86341 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 300
ID ADE505602 standard; protein; 373 AA.
DE Human PRO polypeptide #65.

PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 301
ID ADD73587 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 302
ID ADE75789 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 303
ID ADE48393 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 304
ID ADD78427 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 305
ID ADE41314 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 306
ID ADE23365 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 307
ID ADE21250 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 308
ID ADD77365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 309
ID ADE20512 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100733-A1.

PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 310
 ID ADD75577 standard; protein; 373 AA.
 DE Human PRO polypeptide #65.
 PN US2003100064-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 311
 ID ADD74093 standard; protein; 373 AA.
 DE Human PRO polypeptide #65.
 PN US2003100708-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 312
 ID ADD74339 standard; protein; 373 AA.
 DE Human PRO polypeptide #65.
 PN US2003100709-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 313
 ID ADD76069 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003100718-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 314
 ID ADD85561 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003100721-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 315
 ID ADE23917 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003092110-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 316
 ID ADE24560 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003092111-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 317
 ID ADD87385 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003203439-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 318
 ID ADE05110 standard; protein; 373 AA.
 DE Human PRO polypeptide #65.
 PN US2003100726-A1.
 PD 29-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 319
 ID ADD75323 standard; protein; 373 AA.
 DE Human PRO polypeptide #65.
 PN US2003100714-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 320
 ID ADD76867 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003100715-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 321
 ID ADD86635 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003100719-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 322
 ID ADE89251 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003199062-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 323
 ID ADD78103 standard; protein; 373 AA.
 DE Novel human secreted and transmembrane protein PRO363.
 PN US2003100731-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 324
 ID ADE18390 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003194794-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 325
 ID ADE88699 standard; protein; 373 AA.
 DE Human PRO polypeptide #194.
 PN US2003199054-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1908; DB 8; Length 373;
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;
 RESULT 326
 ID ADE89494 standard; protein; 373 AA.
 DE Human secreted/transmembrane protein, PRO363.
 PN US2003130181-A1.
 PD 10-JUL-2003.
 PA (ASHK/) ASHKENAZI A J.
 PA (BAKE/) BAKER K P.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.

PA (GERB//) GERBER H. 100.0%; Score 1908; DB 8; Length 373;
PA (GERR//) GERRITSEN M E. 100.0%; Pred. No. 3.7e-145;
PA (GOD//) GODDARD A. 100.0%;
PA (GODO//) GODOWSKI P J. 100.0%;
PA (GIRM//) GIRMALDI J C. 100.0%;
PA (GURN//) GURNEY A L. 100.0%;
PA (HILL//) HILLAN K J. 100.0%;
PA (KLJA//) KLJAVIN I J. 100.0%;
PA (KUOS//) KUO S S. 100.0%;
PA (NAPI//) NAPIER M A. 100.0%;
PA (PANJ//) PAN J. 100.0%;
PA (PAON//) PAONI N F. 100.0%;
PA (ROYM//) ROY M A. 100.0%;
PA (SHEL//) SHELTON D L. 100.0%;
PA (STEW//) STEWART T A. 100.0%;
PA (TUMA//) TUMAS D. 100.0%;
PA (WILL//) WILLIAMS P M. 100.0%;
PA (WOOD//) WOOD W I. 100.0%;
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 327
ID ADP77611 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 328
ID ADP77957 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 329
ID ADD85315 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 330
ID ADP73847 standard; protein; 373 AA.
DE Human PRO polypeptide #85.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 331
ID ADD74585 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 332
ID ADP77113 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 333
ID ADP77113 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH//) GENENTECH INC. 100.0%; Score 1908; DB 8; Length 373;
Query Match 100.0%; Pred. No. 3.7e-145;
Best Local Similarity 100.0%;
RESULT 334
ID ADD85807 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100720-A1.
PD 29-MAY-2003.

[illegible]

Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 343
ID ADE93381 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 344
ID ADF24018 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 345
ID ADF40450 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 346
ID ADF23394 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 347
ID ADF33377 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 348
ID ADF34962 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 349
ID ADF26844 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 350
ID ADF27480 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 351
ID ADE92277 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 352
ID ADE90578 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 353
ID ADF41074 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 354
ID ADF32753 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 355
ID ADF25119 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 356
ID ADF26220 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 357
ID ADF34009 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 358
ID ADF46246 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 359
ID ADE91725 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 360
ID ADG11879 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
FN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 361

ID ADG05643 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 362
ID ADG27197 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 363
ID ADG02304 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 364
ID ADG22090 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 365
ID ADG20160 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 366
ID ADF98066 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 367
ID ADG24283 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 368
ID ADF98637 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 369
ID ADG03468 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 370
ID ADF99189 standard; protein; 373 AA.

DE Human PRO polypeptide #194.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 371
ID ADG16774 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 372
ID ADG05233 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 373
ID ADG19500 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 374
ID ADG11260 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 375
ID ADG13337 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 376
ID ADG08394 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 377
ID ADG15564 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 378
ID ADG12039 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 379
ID ADF96962 standard; protein; 373 AA.
DE Human PRO polypeptide #194.


```
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 380
ID ADG06147 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 381
ID ADG23731 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 382
ID ADG04020 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 383
ID ADG24921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 384
ID ADF94596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 385
ID ADG07218 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 386
ID ADG07770 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 387
ID ADG06692 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 388
ID AGS5265 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194778-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 389
ID ADG60929 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 390
ID ADG62033 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 391
ID ADG82234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 392
ID ADG57473 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 393
ID ADG56921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 394
ID ADG55817 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 395
ID ADG58577 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 396
ID ADG70943 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1908; DB 8; Length 373;
  Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 397
ID ADH39036 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096965-A1.
PD 22-MAY-2003.
```


PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 398
ID ADG58025 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 399
ID ADG53609 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 400
ID ADG71495 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 401
ID ADG50232 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 402
ID ADG81682 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 403
ID ADH19749 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 404
ID ADH30644 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 405
ID ADH12011 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 406
ID ADG49608 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 407
ID ADG51480 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 408
ID ADG52433 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 409
ID ADG54161 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 410
ID ADG48984 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 411
ID ADG81130 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 412
ID ADG56369 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 413
ID ADH12635 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 414
ID ADG48360 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 415
ID ADH21242 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 416

DE ADG61481 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 417
ID ADH20282 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 418
ID ADH28568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 419
ID ADG54713 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 420
ID ADG59753 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 421
ID ADG50856 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 422
ID ADH43497 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 423
ID ADG58800 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 424
ID ADG34126 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 425
ID ADG62256 standard; protein; 373 AA.

DE Human secreted/transmembrane protein, PRO363.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 426
ID ADI81177 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 427
ID ADI33596 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 428
ID ADH69690 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 429
ID ADH25281 standard; protein; 373 AA.
DE Human neutrotrimin homologue related protein sequence SEQ ID NO:59.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 430
ID ADG09920 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 431
ID ADI15391 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 432
ID ADG09268 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 433
ID ADI14723 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Pred. No. 3.7e-145;
RESULT 434
ID ADI29851 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.

PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 435
ID AD118318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 436
ID ADM27248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 437
ID ADJ63599 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 438
ID ADJ77494 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 439
ID ADK82842 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
FN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 440
ID ADK66606 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
FN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 441
ID ADJ65616 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 442
ID ADM27752 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 443
ID ADM17058 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2004048332-A1.

PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 444
ID ADJ06892 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
FN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 445
ID ADM42476 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 446
ID ADN05373 standard; protein; 373 AA.
DE Antipsoriatic protein sequence #858.
FN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 447
ID ADM28338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 448
ID ADO36720 standard; protein; 373 AA.
DE Human UKW polypeptide, SEQ ID NO:2.
FN EP1416279-A1.
PD 06-MAY-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 449
ID ADI95820 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
FN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 450
ID ADI96372 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
FN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 451
ID AAB48146 standard; protein; 373 AA.
DE Human A236 variant 2 polypeptide.
FN WO2000069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 99.8%; Score 1905; DB 4; Length 373;
Best Local Similarity 99.7%; Pred. No. 6.5e-145;
RESULT 452
ID AAB48147 standard; protein; 373 AA.
DE Human A236 variant 3 polypeptide.
FN WO2000069885-A2.
PD 23-NOV-2000.

Wed May 11 07:24:23 2005

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.8%; Score 1905; DB 4; Length 373;
Best Local Similarity 99.7%; Pred. No. 6.5e-145;
RESULT 453
ID AAB48145 standard; protein; 373 AA.
DE Human A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.8%; Score 1905; DB 4; Length 373;
Best Local Similarity 99.7%; Pred. No. 6.5e-145;
RESULT 454
ID AAB48126 standard; protein; 373 AA.
DE Mouse A236 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 92.4%; Score 1763.5; DB 4; Length 373;
Best Local Similarity 92.7%; Pred. No. 1.7e-133;
RESULT 455
ID AAB26449 standard; protein; 373 AA.
DE Mouse A236 protein.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZWAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 92.4%; Score 1763.5; DB 5; Length 373;
Best Local Similarity 92.7%; Pred. No. 1.7e-133;
RESULT 456
ID AAB48149 standard; protein; 373 AA.
DE Mouse A236 variant 2 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 92.3%; Score 1760.5; DB 4; Length 373;
Best Local Similarity 92.5%; Pred. No. 2.9e-133;
RESULT 457
ID AAB48150 standard; protein; 373 AA.
DE Mouse A236 variant 3 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 92.3%; Score 1760.5; DB 4; Length 373;
Best Local Similarity 92.5%; Pred. No. 2.9e-133;
RESULT 458
ID AAB48148 standard; protein; 373 AA.
DE Mouse A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 92.3%; Score 1760.5; DB 4; Length 373;
Best Local Similarity 92.5%; Pred. No. 2.9e-133;
RESULT 459
ID AAB5862 standard; protein; 373 AA.
DE Murine adipocytes-derived protein.
PN WO200166720-A1.
PD 13-SEP-2001.
PA (KITA/) KITAMURA T.
PA (TSUR/) TSURUGA H.
Query Match 92.2%; Score 1759.5; DB 4; Length 373;
Best Local Similarity 92.5%; Pred. No. 3.5e-133;
RESULT 460
ID ABO00483 standard; protein; 141 AA.
DE Novel human polypeptide #70.
PN WO2003023013-A2.

PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 36.3%; Score 692; DB 6; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
RESULT 461
ID ABO0802 standard; protein; 139 AA.
DE Polypeptide encoded by novel human contig #53.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 35.1%; Score 670; DB 6; Length 139;
Best Local Similarity 99.3%; Pred. No. 6.3e-46;
RESULT 462
ID ABB83928 standard; protein; 365 AA.
DE PCAR SEQ ID NO 4.
PN US2002059654-A1.
PD 16-MAY-2002.
PA (BUHL/) BUHLER T.
PA (GADI/) GADIANT R A.
PA (KORN/) KORN R.
PA (MOVV/) MOVVA R.
Query Match 24.7%; Score 471; DB 5; Length 365;
Best Local Similarity 32.6%; Pred. No. 2.6e-29;
RESULT 463
ID AAW69697 standard; protein; 365 AA.
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYRY) UNIV NEW YORK STATE.
Query Match 24.4%; Score 465; DB 2; Length 365;
Best Local Similarity 31.6%; Pred. No. 8e-29;
RESULT 464
ID AAW57212 standard; protein; 365 AA.
DE Human coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 13-MAR-1998.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 24.4%; Score 465; DB 2; Length 365;
Best Local Similarity 31.6%; Pred. No. 8e-29;
RESULT 465
ID AAB47270 standard; protein; 365 AA.
DE Human CAR.
PN US6245966-B1.
PD 12-JUN-2001.
PA (UYTE-) UNIV TECHNOLOGY CORP.
Query Match 24.4%; Score 465; DB 4; Length 365;
Best Local Similarity 31.6%; Pred. No. 8e-29;
RESULT 466
ID ABB08040 standard; protein; 365 AA.
DE Human coxsackie-adenovirus receptor (CAR).
PN WO200229072-A2.
PD 11-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
Query Match 24.4%; Score 465; DB 5; Length 365;
Best Local Similarity 31.6%; Pred. No. 8e-29;
RESULT 467
ID ABJ37063 standard; protein; 365 AA.
DE Human breast cancer / ovarian cancer related protein #39.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 24.4%; Score 465; DB 6; Length 365;
Best Local Similarity 31.6%; Pred. No. 8e-29;
RESULT 468
ID ADB97544 standard; protein; 365 AA.
DE Human CAR wild-type protein.
PN WO2003070915-A2.
PD 28-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 24.4%; Score 465; DB 7; Length 365;
Best Local Similarity 31.6%; Pred. No. 8e-29;
RESULT 469

ID ADN95226 standard; protein; 365 AA.
 DE Human BEC/LEC-related protein sequence SeqID148.
 PN WO2003080640-A1.
 PD 02-OCT-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 24.4%; Score 465; DB 7; Length 365;
 Best Local Similarity 31.6%; Pred. No. 8e-29;
 RESULT 470
 ID ABUL2046 standard; protein; 505 AA.
 DE Human NOV4a CS59871-01 protein SEQ ID 12.
 PN WO200281625-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 24.4%; Score 465; DB 6; Length 505;
 Best Local Similarity 31.7%; Pred. No. 1.3e-28;
 RESULT 471
 ID ADR66297 standard; protein; 358 AA.
 DE Human prostatic carcinoma derived protein SEQ ID 151 #2.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 Query Match 24.1%; Score 459; DB 8; Length 358;
 Best Local Similarity 31.8%; Pred. No. 2.4e-28;
 RESULT 472
 ID ADR66858 standard; protein; 358 AA.
 DE Human prostatic carcinoma derived DNA SEQ ID 151 #4.
 PN WO2004076614-A2.
 PD 10-SEP-2004.
 PA (HINZ/) HINZMANN B.
 PA (DAHL/) DAHL E.
 PA (ROSE/) ROSENTHAL A.
 PA (HERM/) HERMANN K.
 PA (PILA/) PILARSKY C.
 Query Match 24.1%; Score 459; DB 8; Length 358;
 Best Local Similarity 31.8%; Pred. No. 2.4e-28;
 RESULT 473
 ID ABA48123 standard; peptide; 86 AA.
 DE Human A236 immunoglobulin domain.
 PN WO200069885-A2.
 PD 23-NOV-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 23.9%; Score 456; DB 4; Length 86;
 Best Local Similarity 100.0%; Pred. No. 5.8e-29;
 RESULT 474
 ID AAW57213 standard; protein; 376 AA.
 DE Mouse coxsackievirus and adenovirus receptor.
 PN WO9811221-A2.
 PD 19-MAR-1998.
 PA (DAND) DANA FARBER CANCER INST INC.
 Query Match 23.8%; Score 453.5; DB 2; Length 376;
 Best Local Similarity 32.0%; Pred. No. 7.1e-28;
 RESULT 475
 ID AAY72878 standard; protein; 352 AA.
 DE Human PRO5723 protein encoded by DNA82361 cDNA clone.
 PN WO200116319-A2.
 PD 08-MAR-2001.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 4; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 476
 ID AAB50930 standard; protein; 352 AA.
 DE Human PRO5723 protein.
 PN WO200073452-A2.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 4; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 477

ID AAB65294 standard; protein; 352 AA.
 DE Human PRO5723 protein sequence SEQ ID NO:505.
 PN WO200073454-A1.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 4; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 478
 ID ABB84956 standard; protein; 352 AA.
 DE Human PRO5723 protein sequence SEQ ID NO:280.
 PN WO200200690-A2.
 PD 03-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 5; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 479
 ID ABB95562 standard; protein; 352 AA.
 DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
 PN WO200208284-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 22.7%; Score 433; DB 5; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 480
 ID ABU58109 standard; protein; 352 AA.
 DE Human PRO polypeptide #141.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 481
 ID ABU59187 standard; protein; 352 AA.
 DE Novel human secreted or transmembrane protein PRO5723.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 482
 ID ABU82699 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein PRO5723.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 483
 ID ABU60618 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein, #177.
 PN US2002160384-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 484
 ID ABU80846 standard; protein; 352 AA.
 DE Human PRO polypeptide #108.
 PN US2003036635-A1.
 PD 20-FEB-2003.

Wed May 11 07:24:23 2005

PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 485
 ID ABO33812 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003045687-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 486
 ID ABU14000 standard; protein; 352 AA.
 DE Human PRO5723 polypeptide.
 PN US2002103125-A1.
 PD 01-AUG-2002.
 PA (GETH) GENENTECH LTD.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 487
 ID ABU72585 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003003531-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 488
 ID ABG74762 standard; protein; 352 AA.
 DE Human PRO5723 protein.
 PN US2002192752-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 489
 ID ABUS9334 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein, #177.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 490
 ID ABO26031 standard; protein; 352 AA.
 DE Human PRO5723 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 491
 ID ABUS9040 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003088063-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 492
 ID ABUS9040 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein, #177.
 PN US2002142961-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 493
 ID ABUS92418 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003022187-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 494
 ID ABUS9483 standard; protein; 352 AA.
 DE Novel human secreted or transmembrane protein PRO3301.
 PN US2003027985-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 495
 ID ABUS2249 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003017476-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 496
 ID ABUS10955 standard; protein; 352 AA.
 DE Human PRO polypeptide #141.
 PN US2002123463-A1.
 PD 05-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 497
 ID ABUS1707 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2002177164-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 498
 ID ABUS8646 standard; protein; 352 AA.
 DE Human secreted and transmembrane polypeptide PRO5723.
 PN US2002197615-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 499
 ID ABO34160 standard; protein; 352 AA.
 DE Human PRO5723 polypeptide.
 PN US2003017981-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 500
 ID ABUS72335 standard; protein; 352 AA.
 DE Human PRO5723 protein.
 PN US2003050448-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 501
 ID ADA38016 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein PRO5723.
 PN US2003008297-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 502
 ID ADA21702 standard; protein; 352 AA.
 DE Human secreted/transmembrane polypeptide PRO5723.
 PN US2003054404-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 6; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 503
 ID ADA10489 standard; protein; 352 AA.
 DE Human secreted/transmembrane protein, PRO5723.
 PN US2003059831-A1.
 PD 27-MAR-2003.

Query Match 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 504
ID ADA18033 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 505
ID ADA28141 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 506
ID ADA94721 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 507
ID ADA38946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 508
ID ABJ72463 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 509
ID ADA93067 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 510
ID AB034358 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO 5723.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 6; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 511
ID AB053246 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 512
ID ADA22628 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 513
ID AB022616 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;

Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 514
ID ADA06794 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #141.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 515
ID ABJ72165 standard; protein; 352 AA.
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 516
ID ADA39487 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 517
ID ADB83706 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 518
ID ADB80812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 519
ID ADB73353 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 520
ID ADB96513 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 521
ID ADB78435 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 522
ID ADB85083 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 523
ID ADB78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.

PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 524
ID ADB87255 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 525
ID ADB84837 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 526
ID ADB83952 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 527
ID ADB73107 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 528
ID ADC57985 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 529
ID ADC55349 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 530
ID ADC12216 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 531
ID ADC56638 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 532
ID ADC11683 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 533
ID ADC36945 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 534
ID ADC21935 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 535
ID ADC49666 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 536
ID ADC49165 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 537
ID ADC49682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 538
ID ADC47543 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 539
ID ADC14805 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 540
ID ADC47288 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 541
ID ADD08337 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 542
ID ADC82162 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003083461-A1.

PD 01-MAY-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 543
ID ADD07804 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 544
ID ADC78163 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 545
ID ADC82695 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 546
ID ADD06398 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 547
ID AD10569 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 548
ID ADD08875 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 549
ID ADC77917 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 550
ID ADD07124 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 551
ID AD11529 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;

RESULT 552
ID ADC83371 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 553
ID ADD50880 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 554
ID AD15380 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003059437-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 555
ID AD51126 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 556
ID ADD5478 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 557
ID ADD37322 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 558
ID ADD56436 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 559
ID ADD50607 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 560
ID ADD54874 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 561
ID ADD50361 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096970-A1.

Wed May 11 07:24:23 2005

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 562
ID ADD51372 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 563
ID ADE31893 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 564
ID ADE27028 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 565
ID ADE26495 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 566
ID ADF67432 standard; protein; 352 AA.
DE Human PRO5723 amino acid sequence SEQ ID NO:505.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 567
ID ADE94085 standard; protein; 352 AA.
DE Immune disease treatment/diagnosis related PRO5723.
PN US2003082199-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 568
ID ADI35686 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 569
ID ADI00179 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 7; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 570
ID ADC48919 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 571
ID ADE21090 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 572
ID ADE05934 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 573
ID ADD75163 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 574
ID ADD75909 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 575
ID ADD85141 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 576
ID ADD86967 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 577
ID ADE20844 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 578
ID ADE39141 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 579
ID ADE05688 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 580
ID ADD73673 standard; protein; 352 AA.
DE Human PRO polypeptide #108.

PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 581
ID AD85647 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 582
ID AD841530 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 583
ID AD821336 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 584
ID ADD77451 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 585
ID AD820598 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 586
ID ADD75663 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 587
ID ADD74179 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 588
ID ADD74425 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 589
ID ADD76155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100718-A1.

PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 590
ID AD85647 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 591
ID AD805196 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 592
ID ADD75409 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 593
ID ADD76953 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 594
ID ADD86721 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 595
ID ADD78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 596
ID ADD77697 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 597
ID ADD77943 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.7%; Score 433; DB 8; Length 352;
RESULT 598
ID ADD85401 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100725-A1.
PD 29-MAY-2003.


```
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 599
DE Human PRO polypeptide #108.
ID ADD73933 standard; protein; 352 AA.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 600
DE Human PRO polypeptide #108.
ID ADD74671 standard; protein; 352 AA.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 601
DE Novel human secreted and transmembrane protein PRO5723.
ID ADD77199 standard; protein; 352 AA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 602
DE Novel human secreted and transmembrane protein PRO5723.
ID ADD85893 standard; protein; 352 AA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 603
DE Human PRO polypeptide #108.
ID ADE05442 standard; protein; 352 AA.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 604
DE Human PRO polypeptide #108.
ID ADD74917 standard; protein; 352 AA.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 605
DE Human PRO5723 polypeptide.
ID ADF35631 standard; protein; 352 AA.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 606
ID ADG11881 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 607
ID AGD05729 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 608
ID ADG27283 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 609
ID ADG11346 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 610
ID ADG12125 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 611
ID ADF94682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 612
ID ADG06778 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 613
ID ADH39122 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 614
ID ADH19751 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 615
ID ADH21244 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 616
ID ADH20284 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 22.7%; Score 433; DB 8; Length 352;
Best Local Similarity 33.8%; Pred. No. 2.9e-26;
RESULT 617
```


ID ADH43713 standard; protein; 352 AA.
 DE Human PRO polypeptide #140.
 PN US2003224984-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 618
 ID ADG34212 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2004006206-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 619
 ID ADI33682 standard; protein; 352 AA.
 DE Human PRO polypeptide #108.
 PN US2003096960-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 620
 ID ADH69776 standard; protein; 352 AA.
 DE Human PRO polypeptide #108.
 PN US2004019183-A1.
 PD 29-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 621
 ID ADI29937 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2003096961-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 622
 ID ADM27334 standard; protein; 352 AA.
 DE Novel human secreted and transmembrane protein PRO5723.
 PN US2004044179-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 623
 ID ADK83058 standard; protein; 352 AA.
 DE Human PRO polypeptide #140.
 PN US2004043927-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 624
 ID ADK66692 standard; protein; 352 AA.
 DE Human PRO polypeptide #108.
 PN US2004044180-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 22.7%; Score 433; DB 8; Length 352;
 Best Local Similarity 33.8%; Pred. No. 2.9e-26;
 RESULT 625
 ID ABUI2047 standard; protein; 422 AA.
 DE Human NOV5a CG59883-01 protein SEQ ID 14.
 PN WO200281625-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 22.2%; Score 424.5; DB 6; Length 422;
 Best Local Similarity 29.9%; Pred. No. 1.8e-25;
 RESULT 626
 ID AAW69698 standard; protein; 352 AA.

DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.
 PN WO9833819-A1.
 PD 06-AUG-1998.
 PA (UUNY) UNIV NEW YORK STATE.
 Query Match 22.1%; Score 422.5; DB 2; Length 352;
 Best Local Similarity 29.7%; Pred. No. 2e-25;
 RESULT 627
 ID ABB83927 standard; protein; 261 AA.
 DE C-terminally truncated pCAR SEQ ID NO 2.
 PN US2002059654-A1.
 PD 16-MAY-2002.
 PA (BUHL/) BUHLER T.
 PA (GADI/) GADIENT R A.
 PA (KORN/) KORN R.
 PA (MOVV/) MOVVA R.
 Query Match 19.8%; Score 378.5; DB 5; Length 261;
 Best Local Similarity 34.6%; Pred. No. 4.8e-22;
 RESULT 628
 ID ADL67136 standard; protein; 430 AA.
 DE Human B7-H5 protein SEQ ID NO:6.
 PN WO2004022594-A2.
 PD 18-MAR-2004.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 Query Match 19.0%; Score 362.5; DB 8; Length 430;
 Best Local Similarity 29.5%; Pred. No. 1.8e-20;
 RESULT 629
 ID ABU08259 standard; protein; 431 AA.
 DE Human voltage-gated sodium channel beta subunit HIPHUM30.
 PN GB2376235-A.
 PD 11-DEC-2002.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 18.9%; Score 361; DB 6; Length 431;
 Best Local Similarity 30.2%; Pred. No. 2.4e-20;
 RESULT 630
 ID ABR82054 standard; protein; 431 AA.
 DE Human cell adhesion molecule BT-IgSF protein SEQ ID NO:2.
 PN EPI321475-A1.
 PD 25-JUN-2003.
 PA (MORG) MORINAGA MILK IND CO LTD.
 Query Match 18.9%; Score 361; DB 6; Length 431;
 Best Local Similarity 30.2%; Pred. No. 2.4e-20;
 RESULT 631
 ID ABB10359 standard; protein; 426 AA.
 DE Human CDNA SEQ ID NO: 667.
 PN WO200154474-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 18.9%; Score 360; DB 4; Length 426;
 Best Local Similarity 30.2%; Pred. No. 2.9e-20;
 RESULT 632
 ID ABP66946 standard; protein; 426 AA.
 DE Human polypeptide SEQ ID NO 667.
 PN US2002090672-A1.
 PD 11-JUL-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 18.9%; Score 360; DB 5; Length 426;
 Best Local Similarity 30.2%; Pred. No. 2.9e-20;
 RESULT 633
 ID ADC42862 standard; protein; 431 AA.
 DE RENAP protein #22.
 PN WO2003027228-A2.
 PD 03-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 18.9%; Score 360; DB 7; Length 431;
 Best Local Similarity 30.2%; Pred. No. 2.9e-20;
 RESULT 634
 ID ADI0601 standard; protein; 431 AA.
 DE Human coxsackie and adenovirus receptor like 1 (CXADR11) protein.
 PN WO2003104275-A2.
 PD 18-DEC-2003.
 PA (ONCO-) ONCOTHERAPY SCI INC.

PA (UYTY) UNIV TOKYO.
 Query Match 18.9%; Score 360; DB 8; Length 431;
 Best Local Similarity 30.2%; Pred. No. 2.9e-20;
 RESULT 635
 ID AAU83699 standard; protein; 290 AA.
 DE Human PRO protein, Seq ID NO 216.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PA (GETH) GENENTECH INC.
 Query Match 18.7%; Score 357; DB 5; Length 290;
 Best Local Similarity 31.5%; Pred. No. 3e-20;
 RESULT 636
 ID ADL67140 standard; protein; 428 AA.
 DE Mouse B7-H5 protein SEQ ID NO:10.
 PN WO2004022594-A2.
 PD 18-MAR-2004.
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 Query Match 18.5%; Score 352.5; DB 8; Length 428;
 Best Local Similarity 29.4%; Pred. No. 1.2e-19;
 RESULT 637
 ID ADP29332 standard; protein; 330 AA.
 DE Human secreted protein SEQ ID #99.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 18.4%; Score 350.5; DB 8; Length 330;
 Best Local Similarity 27.3%; Pred. No. 1.2e-19;
 RESULT 638
 ID AAW82731 standard; protein; 397 AA.
 DE Adenovirus PACSG2SCAR.sig chimeric protein.
 PN WO9854346-A1.
 PD 03-DEC-1998.
 PA (GENV-) GENVEC INC..
 Query Match 18.4%; Score 350.5; DB 2; Length 397;
 Best Local Similarity 28.2%; Pred. No. 1.5e-19;
 RESULT 639
 ID AAB48124 standard; peptide; 65 AA.
 DE Human A236 immunoglobulin domain.
 PN WO200069885-A2.
 PD 23-NOV-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 18.3%; Score 350; DB 4; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 RESULT 640
 ID AAW82729 standard; protein; 264 AA.
 DE Adenovirus pACTSG2-SCAR protein.
 PN WO9854346-A1.
 PD 03-DEC-1998.
 PA (GENV-) GENVEC INC.
 Query Match 18.0%; Score 342.5; DB 2; Length 264;
 Best Local Similarity 33.9%; Pred. No. 3.9e-19;
 RESULT 641
 ID AAW82730 standard; protein; 277 AA.
 DE Adenovirus SCAR.RGD protein.
 PN WO9854346-A1.
 PD 03-DEC-1998.
 PA (GENV-) GENVEC INC.
 Query Match 17.9%; Score 341; DB 2; Length 277;
 Best Local Similarity 34.6%; Pred. No. 5.5e-19;
 RESULT 642
 ID ADA50170 standard; protein; 412 AA.
 DE Human CAR/SCF fusion protein.
 PN US2003092068-A1.
 PD 15-MAY-2003.
 PA (ITOH/) ITOH A.
 PA (HANA/) HANAZONO Y.
 PA (OKAD/) OKADA T.
 PA (OZAW/) OZAWA K.
 Query Match 17.9%; Score 341; DB 6; Length 412;
 Best Local Similarity 34.6%; Pred. No. 9.4e-19;
 RESULT 643
 ID ADA50171 standard; protein; 412 AA.
 DE Human CAR/mouse SCF fusion protein.

PN US2003092068-A1.
 PD 15-MAY-2003.
 PA (ITOH/) ITOH A.
 PA (HANA/) HANAZONO Y.
 PA (OKAD/) OKADA T.
 PA (OZAW/) OZAWA K.
 Query Match 17.9%; Score 341; DB 6; Length 412;
 Best Local Similarity 34.6%; Pred. No. 9.4e-19;
 RESULT 644
 ID ADA50172 standard; protein; 493 AA.
 DE Human CAR/mouse anti-CD34 antibody fusion protein.
 PN US2003092068-A1.
 PD 15-MAY-2003.
 PA (ITOH/) ITOH A.
 PA (HANA/) HANAZONO Y.
 PA (OKAD/) OKADA T.
 PA (OZAW/) OZAWA K.
 Query Match 17.9%; Score 341; DB 6; Length 493;
 Best Local Similarity 34.6%; Pred. No. 1.2e-18;
 RESULT 645
 ID ABU62399 standard; protein; 466 AA.
 DE Chimeric CAR/Hg/Pro-A gene product.
 PN US6524572-B1.
 PD 25-FEB-2003.
 PA (RAIN-) RAINBOW THERAPEUTIC CO.
 Query Match 17.8%; Score 340.5; DB 6; Length 466;
 Best Local Similarity 27.0%; Pred. No. 1.2e-18;
 RESULT 646
 ID ADA50158 standard; protein; 393 AA.
 DE Human CAR/mouse SCF mature fusion protein.
 PN US2003092068-A1.
 PD 15-MAY-2003.
 PA (ITOH/) ITOH A.
 PA (HANA/) HANAZONO Y.
 PA (OKAD/) OKADA T.
 PA (OZAW/) OZAWA K.
 Query Match 17.6%; Score 335; DB 6; Length 393;
 Best Local Similarity 35.4%; Pred. No. 2.7e-18;
 RESULT 647
 ID ADA50157 standard; protein; 393 AA.
 DE Human CAR/SCF mature fusion protein.
 PN US2003092068-A1.
 PD 15-MAY-2003.
 PA (ITOH/) ITOH A.
 PA (HANA/) HANAZONO Y.
 PA (OKAD/) OKADA T.
 PA (OZAW/) OZAWA K.
 Query Match 17.6%; Score 335; DB 6; Length 393;
 Best Local Similarity 35.4%; Pred. No. 2.7e-18;
 RESULT 648
 ID ADA50159 standard; protein; 474 AA.
 DE Human CAR/mouse anti-CD34 antibody mature fusion protein.
 PN US2003092068-A1.
 PD 15-MAY-2003.
 PA (ITOH/) ITOH A.
 PA (HANA/) HANAZONO Y.
 PA (OKAD/) OKADA T.
 PA (OZAW/) OZAWA K.
 Query Match 17.6%; Score 335; DB 6; Length 474;
 Best Local Similarity 35.4%; Pred. No. 3.5e-18;
 RESULT 649
 ID AAB65841 standard; protein; 365 AA.
 DE Murine mature INTERCEPT 258 SEQ ID NO: 40.
 PN WO200078808-A1.
 PD 28-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 16.8%; Score 321; DB 4; Length 365;
 Best Local Similarity 28.4%; Pred. No. 3.3e-17;
 RESULT 650
 ID AAB65840 standard; protein; 394 AA.
 DE Murine INTERCEPT 258 SEQ ID NO: 39.
 PN WO200078808-A1.
 PD 28-DEC-2000.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 321; DB 4; Length 394;
Best Local Similarity 28.4%; Pred. No. 3.6e-17;
RESULT 651
ID AAB65908 standard; protein; 394 AA.
DE Murine secreted protein related protein SEQ ID NO: 142.
PN W0200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 320; DB 4; Length 394;
Best Local Similarity 28.4%; Pred. No. 4.4e-17;
RESULT 652
ID AAB65910 standard; protein; 394 AA.
DE Murine secreted protein related protein SEQ ID NO: 146.
PN W0200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 320; DB 4; Length 394;
Best Local Similarity 28.4%; Pred. No. 4.4e-17;
RESULT 653
ID AAB65911 standard; protein; 394 AA.
DE Murine secreted protein related protein SEQ ID NO: 148.
PN W0200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 320; DB 4; Length 394;
Best Local Similarity 28.4%; Pred. No. 4.4e-17;
RESULT 654
ID AAB65909 standard; protein; 394 AA.
DE Murine secreted protein related protein SEQ ID NO: 144.
PN W0200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.6%; Score 317; DB 4; Length 394;
Best Local Similarity 28.2%; Pred. No. 7.6e-17;
RESULT 655
ID ADF83097 standard; protein; 326 AA.
DE Human cortical thymocyte receptor CTXL, overexpressed in cancer.
PN W02003100000-A2.
PD 04-DEC-2003.
PA (TULA-) TULARIK INC.
Query Match 16.5%; Score 315.5; DB 8; Length 326;
Best Local Similarity 30.0%; Pred. No. 7.8e-17;
RESULT 656
ID AAB61480 standard; protein; 325 AA.
DE Human CTH protein.
PN W0200100672-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.5%; Score 314.5; DB 4; Length 325;
Best Local Similarity 29.4%; Pred. No. 9.3e-17;
RESULT 657
ID AAY87251 standard; protein; 327 AA.
DE Human signal peptide containing protein HSP-28 SEQ ID NO: 28.
PN W020000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 16.2%; Score 309.5; DB 3; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 658
ID AAY94857 standard; protein; 327 AA.
DE Human protein clone HP10568.
PN W0200005367-A2.
PD 03-FEB-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 16.2%; Score 309.5; DB 3; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 659
ID AAY97585 standard; protein; 327 AA.
DE Human secreted protein PRO7154.
PN W0200075317-A2.
PD 14-DEC-2000.

PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 4; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 660
ID ABB90354 standard; protein; 327 AA.
DE Human polypeptide SEQ ID NO 2730.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.2%; Score 309.5; DB 5; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 661
ID AAU83709 standard; protein; 327 AA.
DE Human PRO protein, Seq ID No 236.
PN W0200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 5; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 662
ID ABU80856 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 6; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 663
ID ABO33822 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 6; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 664
ID ABU82165 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 6; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 665
ID ABJ72345 standard; protein; 327 AA.
DE Human PRO7154 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 6; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 666
ID ABJ72473 standard; protein; 327 AA.
DE Human PRO7154 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 6; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 667
ID ABO34368 standard; protein; 327 AA.
DE Human secreted/transmembrane polypeptide PRO 7154.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 6; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 668
ID ABJ72175 standard; protein; 327 AA.
DE Human membrane bound receptor/protein PRO7154 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 669
ID ADB83726 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 670
ID ADB80832 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 671
ID ADB73373 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 672
ID ADB78455 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 673
ID ADB85103 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 674
ID ADB78209 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 675
ID ADB87275 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 676
ID ADB84857 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 677
ID ADB83972 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;

Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 678
ID ADB73127 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 679
ID ADC36965 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 680
ID ADC21955 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 681
ID ADC49986 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 682
ID ADC49185 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 683
ID ADC49702 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 684
ID ADC47563 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 685
ID ADC47308 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 686
ID ADC78183 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;
RESULT 687
ID ADB83972 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 7; Length 327;

RESULT 687
ID ADD06418 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 688
ID ADC77937 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US200308066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 689
ID ADD50900 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 690
ID ADD51146 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 691
ID ADD50627 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 692
ID ADD50381 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 693
ID ADD51392 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 7; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 694
ID ADC48939 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 695
ID ADE21110 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 696
ID ADE05954 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 697
ID ADD75183 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 698
ID ADD75929 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 699
ID ADD85161 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 700
ID ADD86987 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 701
ID ADE20864 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 702
ID ADE39161 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 703
ID ADE05708 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 704
ID ADD73693 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 705
ID ADD78533 standard; protein; 327 AA.

Wed May 11 07:24:23 2005

```
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100737-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 706
ID ADE21356 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100736-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 707
ID ADD77471 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100732-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 708
ID ADE20618 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100733-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 709
ID ADD75683 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100664-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 710
ID ADD74199 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100708-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 711
ID ADD74445 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100709-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 712
ID ADD76175 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100719-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 713
ID ADD85667 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100721-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 714
ID ADE05216 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100713-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 715
ID ADD75429 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100714-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 716
ID ADD76973 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100715-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 717
ID ADD86741 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100719-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 718
ID ADD78209 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100731-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 719
ID ADD77717 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100729-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 720
ID ADD77963 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100730-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 721
ID ADD85421 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
PD US2003100725-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 722
ID ADD73953 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100710-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 723
ID ADD74691 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
PD US2003100713-A1.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
```



```
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 724
ID AD077219 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 725
ID AD085913 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 726
ID AD085462 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 727
ID AD074937 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 728
ID AD050749 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 729
ID AD027303 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 730
ID AD011366 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 731
ID AD012145 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 732
ID AD094702 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 733
ID ADG06798 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 734
ID ADH39142 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 735
ID ADG34232 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 736
ID ADI33702 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 737
ID ADH69796 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 738
ID ADI29957 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 739
ID ADM27354 standard; protein; 327 AA.
DE Novel human secreted and transmembrane protein PRO7154.
FN US200404179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 740
ID ADK66712 standard; protein; 327 AA.
DE Human PRO polypeptide #118.
FN US200404180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 309.5; DB 8; Length 327;
Best Local Similarity 30.2%; Pred. No. 2.4e-16;
RESULT 741
ID AAB53307 standard; protein; 365 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:847.
FN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
```


Query Match
Best Local Similarity 16.2%; Score 309.5; DB 3; Length 365;
RESULT 742
ID AAG75613 standard; protein; 365 AA.
DE Human colon cancer antigen protein SEQ ID NO:6377.
FN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 16.2%; Score 309.5; DB 4; Length 365;
RESULT 743
ID AAW14146 standard; protein; 319 AA.
DE Human A33 antigen.
FN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 2; Length 319;
RESULT 744
ID AAY23323 standard; protein; 319 AA.
DE Amino acid sequence of the A33 antigen.
FN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 2; Length 319;
RESULT 745
ID AAB65863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
FN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 4; Length 319;
RESULT 746
ID ADA10947 standard; protein; 319 AA.
DE Human CDNA differentially expressed in colon cancer #43 product.
FN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE-) LASEK A W.
PA (JONE-) JONES D A.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 6; Length 319;
RESULT 747
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
FN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK-) ASHKENAZI A.
PA (FONG-) FONG S.
PA (GODD-) GODDARD A.
PA (GURN-) GURNEY A L.
PA (NAPI-) NAPIER M A.
PA (TUMA-) TUMAS D.
PA (WOOD-) WOOD W I.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 7; Length 319;
RESULT 748
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.
FN WO2003042861-A2.
PD 22-MAY-2003.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 7; Length 319;
RESULT 749
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
FN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 8; Length 319;
RESULT 750
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO:563.
FN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 8; Length 319;
RESULT 751
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
FN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 5; Length 336;
RESULT 752
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
FN US6699688-B1.
PD 02-MAR-2004.
PA (UINY-) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 16.1%; Score 308; DB 8; Length 316;
RESULT 753
ID AAY95024 standard; protein; 325 AA.
DE Human clone vc51_1 deletion variant ORF1, SEQ ID NO:124.
FN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 16.1%; Score 308; DB 3; Length 325;
RESULT 754
ID AAY76303 standard; protein; 389 AA.
DE Fragment of human secreted protein encoded by gene 29.
FN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 3; Length 389;
RESULT 755
ID ADE11956 standard; protein; 389 AA.
DE Human secreted polypeptide #210.
FN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE-) RUBEN S M.
PA (FLOF-) FLORENCE K A.
PA (NIJY-) NI J.
PA (ROSE-) ROSEN C A.
PA (CART-) CARTER K C.
PA (MOOR-) MOORE P A.
PA (OLSE-) OLSEN H S.
PA (SHIV-) SHI Y.
PA (YOUN-) YOUNG P E.
PA (WEIY-) WEI Y.
PA (BREW-) BREWER L A.
PA (SOPP-) SOPPET D R.
PA (LAPL-) LAPLEUR D W.
PA (ENDE-) ENDRESS G A.
PA (EBNE-) EBNER R.
PA (BIRS-) BIRSE C E.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 7; Length 389;
RESULT 756
ID AAY05286 standard; protein; 390 AA.
DE EGF-like homologue PRO246.
FN WO9914327-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 2; Length 390;
RESULT 757
ID AAY13351 standard; protein; 390 AA.

RESULT 750
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO:563.
FN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 8; Length 319;
RESULT 751
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
FN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 16.2%; Score 308.5; DB 5; Length 336;
RESULT 752
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
FN US6699688-B1.
PD 02-MAR-2004.
PA (UINY-) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 16.1%; Score 308; DB 8; Length 316;
RESULT 753
ID AAY95024 standard; protein; 325 AA.
DE Human clone vc51_1 deletion variant ORF1, SEQ ID NO:124.
FN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 16.1%; Score 308; DB 3; Length 325;
RESULT 754
ID AAY76303 standard; protein; 389 AA.
DE Fragment of human secreted protein encoded by gene 29.
FN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 3; Length 389;
RESULT 755
ID ADE11956 standard; protein; 389 AA.
DE Human secreted polypeptide #210.
FN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE-) RUBEN S M.
PA (FLOF-) FLORENCE K A.
PA (NIJY-) NI J.
PA (ROSE-) ROSEN C A.
PA (CART-) CARTER K C.
PA (MOOR-) MOORE P A.
PA (OLSE-) OLSEN H S.
PA (SHIV-) SHI Y.
PA (YOUN-) YOUNG P E.
PA (WEIY-) WEI Y.
PA (BREW-) BREWER L A.
PA (SOPP-) SOPPET D R.
PA (LAPL-) LAPLEUR D W.
PA (ENDE-) ENDRESS G A.
PA (EBNE-) EBNER R.
PA (BIRS-) BIRSE C E.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 7; Length 389;
RESULT 756
ID AAY05286 standard; protein; 390 AA.
DE EGF-like homologue PRO246.
FN WO9914327-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 2; Length 390;
RESULT 757
ID AAY13351 standard; protein; 390 AA.

DE Amino acid sequence of protein PRO246.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 2; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 758
ID AAY27096 standard; protein; 390 AA.
DE Human viral receptor protein (ACVRP).
PN US942606-A.
PD 24-AUG-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 2; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 759
ID AAY94999 standard; protein; 390 AA.
DE Human secreted protein vcs1_1, SEQ ID NO:38.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 3; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 760
ID AAY88574 standard; protein; 390 AA.
DE Human PRO246 amino acid sequence.
PN WO200015666-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 3; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 761
ID AAB80219 standard; protein; 390 AA.
DE Human PRO246 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 762
ID AAB31207 standard; protein; 390 AA.
DE Amino acid sequence of human polypeptide PRO246.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 763
ID AAB90818 standard; protein; 390 AA.
DE Human shear stress-response protein SEQ ID NO: 144.
PN WO200125427-A1.
PD 12-APR-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 764
ID AAU12340 standard; protein; 390 AA.
DE Human PRO246 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 765
ID AAB53082 standard; protein; 390 AA.
DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 766
ID AAB68599 standard; protein; 390 AA.

DE PRO246.
PN WO200105836-A1.
PD 25-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 767
ID AAB88358 standard; protein; 390 AA.
DE Human membrane or secretory protein clone PSEC0086.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 4; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 768
ID ABU71597 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 769
ID ABO17784 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 770
ID ABU71452 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 771
ID ADA56949 standard; protein; 390 AA.
DE Human secreted protein #232.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 772
ID ABO25178 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 773
ID ABU81038 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 774
ID ABU71898 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 775
ID ABO01781 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 776
ID ABU66738 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 777
ID ABUS4354 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 778
ID ADA40800 standard; protein; 390 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 779
ID ABU67296 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 780
ID ABO47369 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 781
ID ABR47754 standard; protein; 390 AA.
DE Human secreted protein, SEQ ID 645.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 782
ID ABUS9819 standard; protein; 390 AA.
DE Novel secreted and transmembrane protein PRO246.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 783
ID ABO25009 standard; protein; 390 AA.
DE Human secreted/transmembrane protein (PRO) #169.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 784
ID ABU64506 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002160374-A1.

PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 785
ID ABU72064 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 786
ID ABU67352 standard; protein; 390 AA.
DE Human secreted protein PRO246.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 787
ID ABU67165 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 788
ID ABO14872 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 789
ID ABU67014 standard; protein; 390 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 338.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 790
ID ABU69629 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 791
ID ABU79807 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 792
ID ABO14811 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 793
ID ADA45857 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003022328-A1.
PD 30-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 794
ID ADA76288 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 795
ID AD829244 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
FN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 796
ID ADA18938 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 797
ID ADA61561 standard; protein; 390 AA.
DE Homo sapiens.
FN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 798
ID AD819346 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
FN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 799
ID ADB27887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 800
ID ADA86366 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
FN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 801
ID ADB15930 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 802
ID ADA47716 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 803
ID ADA18100 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
FN US2003039571-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 804
ID ABO32763 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
FN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 805
ID ADA67511 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 806
ID ADB30518 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 807
ID ADA85814 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
FN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 808
ID ADA97026 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 809
ID ADA79330 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 810
ID ADA87469 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
FN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 811
ID ADB16671 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
FN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;

Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 812
ID ABO34823 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 813
ID ADA16075 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 814
ID ADA91763 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 815
ID ADB14826 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 816
ID ADA47282 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 817
ID ADB18787 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 818
ID ADA94002 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077732-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 819
ID ADB19898 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 820
ID ADB13210 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 821
ID ABO43317 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 822
ID ADA74464 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 823
ID ADA42220 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 824
ID ADB24697 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 825
ID ADA82221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 826
ID ADA75184 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 827
ID ADA85262 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 828
ID ADA84710 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 829
ID ABO17501 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 830
ID ABO17501 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;

ID ADB29966 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 831
ID ADA80494 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 832
ID ADA75736 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 833
ID ADA46961 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 834
ID ADB25257 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 835
ID ADA93433 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 836
ID ADB26783 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 837
ID ADB31070 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 838
ID ADA60998 standard; protein; 390 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 839
ID ADB24145 standard; protein; 390 AA.

DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 840
ID ADA96474 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 841
ID ADA81046 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 842
ID ADA95922 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 843
ID ADB26231 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 844
ID ADB21716 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 845
ID ADA77495 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 846
ID ADB18235 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 847
ID ADA86918 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 848
ID ADA16499 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.


```
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 849
ID ADA12928 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 850
ID ADA411796 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 851
ID ADA88021 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 852
ID ADA46409 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 853
ID ADA17143 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 854
ID ADA42646 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 855
ID ADB28439 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 856
ID ADB28991 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 857
ID ADA76943 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 858
ID ADA88573 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 859
ID ADA97578 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 860
ID ADB27335 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 861
ID ADB22268 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 862
ID ABO19865 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 863
ID ABO17562 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 864
ID ADA66959 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 865
ID ADB22820 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 866
ID ADB23593 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
```


Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 867
ID ADB92315 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 868
ID ADB15378 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 869
ID ADB38630 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 870
ID ADB38078 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 871
ID ADB66550 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 872
ID ADB89630 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 873
ID ADB90362 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 874
ID ADB77565 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 875
ID ADB39463 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;

RESULT 876
ID ADB74701 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 877
ID ADB47086 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 878
ID ADB86693 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 879
ID ADB77298 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 880
ID ADB34455 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 881
ID ADB35559 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 882
ID ADB33903 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 883
ID ADB35007 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 884
ID ADB36111 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 885
ID ADB39463 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;

ID ADB46506 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 886
ID ADC28347 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 887
ID ADC39547 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 888
ID ADC40061 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 889
ID ADC18989 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 890
ID ADC34185 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 891
ID ADC29240 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 892
ID ADC28771 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 893
ID ADC40656 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 894
ID ADC19313 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 895
ID ADC33761 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 896
ID ADC12831 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 897
ID ADC50379 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 898
ID ADC71926 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 899
ID ADC59905 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 900
ID ADC52912 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 901
ID ADC57266 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 902
ID ADC60457 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 903
ID ADC5932 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 904
ID ADC65459 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 905
ID ADC54557 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 906
ID ADC53518 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 907
ID ADC59041 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 908
ID ADC55919 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 909
ID ADC58489 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 910
ID ADC1283 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 911
ID ADD03163 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 912
ID ADC90155 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087348-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 913
ID ADC69574 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 914
ID ADC48463 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 915
ID ADD09992 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 916
ID ADD04567 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 917
ID ADC80523 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 918
ID ADD11030 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 919
ID ADC47911 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 920
ID ADD04838 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 921
ID ADC79971 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087358-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 922
ID ADD09440 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 923
ID ADD03844 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 924
ID ADD03420 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 925
ID ADD41153 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 926
ID ADD52292 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 927
ID ADD53032 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 928
ID ADD53584 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 929
ID ADD51740 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 930
ID ADD02539 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 931
ID ADD01973 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 932
ID ADD54155 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 933
ID ADD92472 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 934
ID ADD91368 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 935
ID ADE03982 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 936
ID ADE32279 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 937
ID ADE22211 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 938
ID ADD79435 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 939
ID ADE41971 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;

ID ADE04650 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US200319034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 959
ID ADE92779 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 960
ID ADG21488 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 961
ID ADG23129 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 962
ID ADF97464 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 963
ID ADG80528 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 964
ID ADG79976 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 965
ID ADG63791 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 966
ID ADH59155 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 967
ID ADH55268 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

DE Novel human secreted and transmembrane protein PRO246.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 968
ID ADH55820 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 969
ID ADI37934 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 970
ID ADI64039 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 971
ID ADI64988 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 972
ID ADI63487 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 973
ID ADH81901 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 974
ID ADH81349 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 975
ID ADJ26202 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 976
ID ADM82518 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.

PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 977
ID ADN15917 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 978
ID ADN16546 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 979
ID ADN15365 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 980
ID ADN14813 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 7; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 981
ID ADC81075 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 982
ID ADE79117 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 983
ID ADD76523 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 984
ID ADD87887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 985
ID ADD86291 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203440-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 986
ID ADE79541 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 987
ID ADE75739 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 988
ID ADE73217 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 989
ID ADE23315 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 990
ID ADE23867 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 991
ID ADE24510 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 992
ID ADB87335 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 993
ID ADE89201 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 994
ID ADE41205 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003104558-A1.
PD 05-JUN-2003.


```
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 995
ID ADE73752 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 996
ID ADE18340 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 997
ID ADE88649 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 998
ID ADE99306 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 999
ID ADE94669 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199037-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1000
ID ADE91080 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1001
ID ADE95221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1002
ID ADE93331 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1003
ID ADE34912 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1004
ID ADE98425 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1005
ID ADE92227 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1006
ID ADE90528 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1007
ID ADE91675 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1008
ID ADE98852 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1009
ID ADG40322 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS J P.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1010
ID ADF73716 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1011
ID ADG02254 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.1%; Score 307.5; DB 8; Length 390;
RESULT 1012
```


ID ADG22040 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1013
ID ADG20110 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1014
ID ADF98016 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1015
ID ADG24233 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1016
ID ADF98587 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1017
ID ADG03418 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1018
ID ADF99139 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1019
ID ADG16724 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1020
ID ADG05183 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1021
ID ADG19450 standard; protein; 390 AA.

DE Human PRO polypeptide #169.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1022
ID ADF73292 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1023
ID ADG13287 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1024
ID ADG08344 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1025
ID ADG15514 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1026
ID ADF96912 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1027
ID ADG06097 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1028
ID ADG23681 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1029
ID ADG03970 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1030
ID ADG24871 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.


```

PD US2003207427-A1.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1031
ID ADG07168 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1032
ID ADG07720 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1033
ID ADG55215 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1034
ID ADG60879 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1035
ID ADG61983 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1036
ID ADG92135 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1037
ID ADG82184 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1038
ID ADG57423 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1039
ID ADG56871 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1040
ID ADG55767 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1041
ID ADG58527 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1042
ID ADG70893 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1043
ID ADG92562 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1044
ID ADG57975 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1045
ID ADG53559 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1046
ID ADG71445 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1047
ID ADG81632 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1048
ID ADH30594 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 16.1%; Score 307.5; DB 8; Length 390;
  Best Local Similarity 29.2%; Pred. No. 4.4e-16;

```


Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1049
ID ADG63640 standard; protein; 390 AA.
DE Novel human secreted and transmembrane polypeptide PRO246.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1050
ID ADH11961 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1051
ID ADG52383 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1052
ID ADG54111 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1053
ID ADG81080 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1054
ID ADG56319 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1055
ID ADH12585 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1056
ID ADG61431 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1057
ID ADH28518 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1058
ID ADG54663 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1059
ID ADG59703 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1060
ID ADH20351 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1061
ID ADH07206 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1062
ID ADH59751 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1063
ID ADH06779 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1064
ID ADI81127 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1065
ID ADI18521 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003152999-A1.

	PA	(DESN/) DESNOYERS L.	
	PA	(GODD/) GODDARD A.	
	PA	(GODO/) GOWSKI P J.	
	PA	(GURN/) GURNEY A L.	
	PA	(MATH/) MATHER J P.	
	PA	(WILL/) WILLIAMS P M.	
	PA	(WOOD/) WOOD W I.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1075	
	ID	ADI18268 standard; protein; 390 AA.	
	DE	Novel human secreted and transmembrane protein PRO246.	
	PN	US2003207349-A1.	
	PD	06-NOV-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1076	
	ID	ADJ99468 standard; protein; 390 AA.	
	DE	Human secreted/transmembrane protein, #9.	
	PN	US2003187238-A1.	
	PD	02-OCT-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1077	
	ID	ADL08661 standard; protein; 390 AA.	
	DE	Human secreted/transmembrane protein, #9.	
	PN	US2003186358-A1.	
	PD	02-OCT-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1078	
	ID	ADM25006 standard; protein; 390 AA.	
	DE	Human secreted/transmembrane protein, #9.	
	PN	US2003096233-A1.	
	PD	22-MAY-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1079	
	ID	ADJ63549 standard; protein; 390 AA.	
	DE	Novel human secreted and transmembrane protein PRO246.	
	PN	US2004039164-A1.	
	PD	26-FEB-2004	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1080	
	ID	ADM29752 standard; protein; 390 AA.	
	DE	Human secreted/transmembrane protein, #9.	
	PN	US2003190611-A1.	
	PD	09-OCT-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1081	
	ID	ADJ77444 standard; protein; 390 AA.	
	DE	Human PRO polypeptide #169.	
	PN	US2004038336-A1.	
	PD	26-FEB-2004	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1082	
	ID	ADJ65566 standard; protein; 390 AA.	
	DE	Human PRO polypeptide #169.	
	PN	US2004038335-A1.	
	PD	26-FEB-2004	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1083	
	ID	ADI14673 standard; protein; 390 AA.	
	DE	Novel human secreted and transmembrane protein PRO246.	
	PN	US2003207393-A1.	
	PD	06-NOV-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1073	
	ID	ADI14673 standard; protein; 390 AA.	
	DE	Novel human secreted and transmembrane protein PRO246.	
	PN	US2003207393-A1.	
	PD	06-NOV-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1072	
	ID	ADI65668 standard; protein; 390 AA.	
	DE	Human secreted/transmembrane protein, #9.	
	PN	US2003148371-A1.	
	PD	07-AUG-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1071	
	ID	ADG09218 standard; protein; 390 AA.	
	DE	Novel human secreted and transmembrane protein PRO246.	
	PN	US2004009547-A1.	
	PD	15-JAN-2004	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390;
		Best Local Similarity	29.2%; Pred. No. 4.4e-16;
		RESULT 1070	
	ID	ADI15341 standard; protein; 390 AA.	
	DE	Novel human secreted and transmembrane protein PRO246.	
	PN	US2003207382-A1.	
	PD	06-NOV-2003	
	PA	(GETH) GENENTECH INC.	
		Query Match	16.1%; Score 307.5; DB 8; Length 390

RESULT 1083
ID ADM27702 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1084
ID ADM42426 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1085
ID ADO06074 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1086
ID ADM28288 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1087
ID ADR10926 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1088
ID ADR17835 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1089
ID ADI95770 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1090
ID ADI96322 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1091
ID ADT03511 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003159222-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1092
ID ADS74474 standard; protein; 390 AA.
DE Human secreted/transmembrane protein #9.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1093
ID ABO53064 standard; protein; 390 AA.
DE Human putative spliceosome associated protein (SAP) #41.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 16.0%; Score 305.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 6.4e-16;
RESULT 1094
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 304.5; DB 2; Length 268;
Best Local Similarity 31.9%; Pred. No. 4.6e-16;
RESULT 1095
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.


```

PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 16.0%; Score 304.5; DB 7; Length 268;
RESULT 1096
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.0%; Score 304.5; DB 2; Length 270;
RESULT 1097
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.0%; Score 304.5; DB 2; Length 273;
RESULT 1098
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 16.0%; Score 304.5; DB 2; Length 273;
RESULT 1099
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 16.0%; Score 304.5; DB 7; Length 273;
RESULT 1100
ID ABB11937 standard; peptide; 321 AA.
DE Human viral receptor protein homologue, SEQ ID NO:2307.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 15.9%; Score 303.5; DB 4; Length 321;
RESULT 1101
ID AAM40551 standard; protein; 321 AA.
DE Human polypeptide SEQ ID NO 5482.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 15.9%; Score 303.5; DB 4; Length 321;
RESULT 1102
ID ADS11818 standard; protein; 321 AA.
DE Human therapeutic contig protein - SEQ ID 2055.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 15.9%; Score 303.5; DB 8; Length 321;
RESULT 1103
ID AAB08903 standard; protein; 327 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:60.
PN WO20017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 15.9%; Score 303.5; DB 3; Length 327;
RESULT 1104
ID ADB64882 standard; protein; 317 AA.
DE Human protein encoded by clone PLACE60070500.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 15.9%; Score 303; DB 7; Length 317;
RESULT 1105
ID ADS08316 standard; protein; 538 AA.
DE Novel protein (useful for identifying genetic disorders) #471.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 15.8%; Score 302; DB 7; Length 538;
RESULT 1106
ID AAE06610 standard; protein; 390 AA.
DE Human protein having hydrophobic domain, HP10801.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA ) SAGAMI CHEM RES CENT.
Query Match
Best Local Similarity 15.7%; Score 299.5; DB 4; Length 390;
RESULT 1107
ID ADM05828 standard; protein; 406 AA.
DE Human protein of the invention SEQ ID NO:4513.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 15.5%; Score 296.5; DB 7; Length 406;
RESULT 1108
ID ADO43535 standard; protein; 348 AA.
DE Amino acid sequence of an additional human A34 clone.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 15.5%; Score 295; DB 8; Length 348;
RESULT 1109
ID ADP55948 standard; protein; 370 AA.
DE Human PRO protein sequence SEQ ID NO:1924.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 15.5%; Score 295; DB 8; Length 370;
RESULT 1110
ID AAY08621 standard; protein; 387 AA.
DE Human secreted protein AJ26_3.
PN WO9926972-A1.
PD 03-JUN-1999.
PA (GENY ) GENETICS INST INC.
Query Match
Best Local Similarity 15.5%; Score 295; DB 2; Length 387;
RESULT 1111
ID AAY67312 standard; protein; 387 AA.
DE Human secreted protein AJ26_3 amino acid sequence.
PN WO9960020-A1.
PD 25-NOV-1999.
PA (GENY ) GENETICS INST INC.
Query Match
Best Local Similarity 15.5%; Score 295; DB 3; Length 387;
```


Best Local Similarity 26.6%; Pred. No. 4.4e-15;
RESULT 1112
ID ADC38775 standard; protein; 387 AA.
DE Human secreted protein #62.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 15.5%; Score 295; DB 7; Length 387;
Best Local Similarity 26.6%; Pred. No. 4.4e-15;
RESULT 1113
ID AD043531 standard; protein; 387 AA.
DE Amino acid sequence of a full length human A34 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 15.5%; Score 295; DB 8; Length 387;
Best Local Similarity 26.6%; Pred. No. 4.4e-15;
RESULT 1114
ID AD043533 standard; protein; 402 AA.
DE Amino acid sequence of a human A34 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 15.5%; Score 295; DB 8; Length 402;
Best Local Similarity 26.6%; Pred. No. 4.7e-15;
RESULT 1115
ID AD065260 standard; protein; 407 AA.
DE Novel human protein sequence #233.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 15.5%; Score 295; DB 8; Length 407;
Best Local Similarity 27.5%; Pred. No. 4.7e-15;
RESULT 1116
ID ABM84859 standard; protein; 344 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5108.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.4%; Score 294; DB 8; Length 344;
Best Local Similarity 29.3%; Pred. No. 4.5e-15;
RESULT 1117
ID ADC42841 standard; protein; 423 AA.
DE RENAP protein #1.
PN WO2003027228-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.3%; Score 291; DB 7; Length 423;
Best Local Similarity 24.4%; Pred. No. 1e-14;
RESULT 1118
ID ADP29419 standard; protein; 244 AA.
DE Human secreted protein SEQ ID #186.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 15.1%; Score 288.5; DB 8; Length 244;
Best Local Similarity 28.3%; Pred. No. 7.8e-15;
RESULT 1119
ID AB885732 standard; protein; 192 AA.
DE Rat coxsackie-adenovirus receptor (CAR).
PN JP2001149095-A.
PD 05-JUN-2001.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (HIRO-) ZH HIROSHIMAKEN SANGYO GIJUTSU SHINKO KI.
Query Match 15.1%; Score 288; DB 4; Length 192;
Best Local Similarity 33.5%; Pred. No. 6.2e-15;
RESULT 1120
ID ADC78359 standard; protein; 389 AA.
DE Human PRO246 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 15.1%; Score 287.5; DB 3; Length 389;

Best Local Similarity 28.2%; Pred. No. 1.8e-14;
RESULT 1121
ID ADN39990 standard; protein; 413 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C360.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.9%; Score 285; DB 7; Length 413;
Best Local Similarity 25.7%; Pred. No. 3.1e-14;
RESULT 1122
ID ADR46674 standard; protein; 413 AA.
DE Cancer-associated protein, SEQ ID 87.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 14.9%; Score 285; DB 8; Length 413;
Best Local Similarity 25.7%; Pred. No. 3.1e-14;
RESULT 1123
ID ADN39989 standard; protein; 631 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C359.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 14.9%; Score 285; DB 7; Length 631;
Best Local Similarity 25.7%; Pred. No. 5.5e-14;
RESULT 1124
ID ADR46673 standard; protein; 631 AA.
DE Cancer-associated protein, SEQ ID 86.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 14.9%; Score 285; DB 8; Length 631;
Best Local Similarity 25.7%; Pred. No. 5.5e-14;
RESULT 1125
ID ADP30373 standard; protein; 377 AA.
DE Human secreted protein SEQ ID #1140.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 14.9%; Score 284.5; DB 8; Length 377;
Best Local Similarity 26.6%; Pred. No. 3e-14;
RESULT 1126
ID AAB65905 standard; protein; 370 AA.
DE Human secreted protein related protein SEQ ID NO: 136.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.4%; Score 275; DB 4; Length 370;
Best Local Similarity 29.6%; Pred. No. 1.7e-13;
RESULT 1127
ID ADO43537 standard; protein; 370 AA.
DE Amino acid sequence of a human A33-like 3 protein.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 14.4%; Score 274; DB 8; Length 370;
Best Local Similarity 29.6%; Pred. No. 2e-13;
RESULT 1128
ID AAW14158 standard; protein; 318 AA.
DE Mouse A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 14.3%; Score 272.5; DB 2; Length 318;
Best Local Similarity 28.8%; Pred. No. 2.2e-13;
RESULT 1129
ID AAB65833 standard; protein; 341 AA.
DE Murine mature INTERCEPT 258 SEQ ID NO: 29.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.2%; Score 271; DB 4; Length 341;
Best Local Similarity 29.3%; Pred. No. 3.2e-13;

RESULT 1130
ID AAB65832 standard; protein; 370 AA.
DE Human INTERCEPT 258 SEQ ID NO: 28.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 14.2%; Score 271; DB 4; Length 370;
Pred. No. 3.6e-13;
RESULT 1131
ID AAB65904 standard; protein; 370 AA.
DE Human secreted protein related protein SEQ ID NO: 134.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 14.2%; Score 271; DB 4; Length 370;
Pred. No. 3.6e-13;
RESULT 1132
ID AAB65907 standard; protein; 370 AA.
DE Human secreted protein related protein SEQ ID NO: 140.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 14.2%; Score 270; DB 4; Length 370;
Pred. No. 4.3e-13;
RESULT 1133
ID AAB65906 standard; protein; 370 AA.
DE Human secreted protein related protein SEQ ID NO: 138.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 14.1%; Score 269; DB 4; Length 370;
Pred. No. 5.2e-13;
RESULT 1134
ID AAU18038 standard; protein; 294 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 183.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 13.9%; Score 265; DB 4; Length 294;
Pred. No. 7.9e-13;
RESULT 1135
ID ADB31662 standard; protein; 294 AA.
DE Human novel protein SEQ ID NO 183.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 13.9%; Score 265; DB 7; Length 294;
Pred. No. 7.9e-13;
RESULT 1136
ID ADO43538 standard; protein; 228 AA.
DE Amino acid sequence of a human A33-like 3 protein fragment.
PN WO2004037999-A2.
PD 06-MAY-2004.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 13.0%; Score 247.5; DB 8; Length 228;
Pred. No. 1.4e-11;
RESULT 1137
ID ADM87310 standard; protein; 273 AA.
DE Human protein SEQ ID NO:403.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 12.7%; Score 242.5; DB 8; Length 273;
Pred. No. 4.7e-11;
RESULT 1138
ID ADN2700 standard; protein; 205 AA.
DE Human receptor and membrane-associated protein #3.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 12.3%; Score 235; DB 8; Length 205;
Pred. No. 1.3e-10;
RESULT 1139

ID AAB08940 standard; protein; 245 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:97.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.0%; Score 228.5; DB 3; Length 245;
Pred. No. 5.4e-10;
RESULT 1140
ID AAB08926 standard; protein; 246 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:83.
PN WO200017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 12.0%; Score 228.5; DB 3; Length 246;
Pred. No. 5.4e-10;
RESULT 1141
ID ADL67138 standard; protein; 242 AA.
DE Human B7-H5(ECD) protein SEQ ID NO:8.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match
Best Local Similarity 11.9%; Score 227; DB 8; Length 242;
Pred. No. 7e-10;
RESULT 1142
ID ADR20065 standard; protein; 346 AA.
DE Human immune response associated protein (IRAP), seq id 25.
PN WO2004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 11.9%; Score 226.5; DB 8; Length 346;
Pred. No. 1.3e-09;
RESULT 1143
ID ADL67142 standard; protein; 238 AA.
DE Mouse B7-H5(ECD) protein SEQ ID NO:12.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match
Best Local Similarity 11.8%; Score 225.5; DB 8; Length 238;
Pred. No. 9.1e-10;
RESULT 1144
ID ABP41477 standard; protein; 226 AA.
DE Human ovarian antigen HOFNF27, SEQ ID NO:2609.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 11.2%; Score 214; DB 5; Length 226;
Pred. No. 7.2e-09;
RESULT 1145
ID AAB61417 standard; protein; 162 AA.
DE Human TANGO 244 protein.
PN WO200100672-A1.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 10.9%; Score 207.5; DB 4; Length 162;
Pred. No. 1.5e-08;
RESULT 1146
ID AAB65843 standard; protein; 249 AA.
DE Murine INTERCEPT 258 extracellular domain SEQ ID NO: 42.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 10.8%; Score 202; DB 4; Length 249;
Pred. No. 7.6e-08;
RESULT 1147
ID AAO16453 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (huJAM3).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 10.4%; Score 198.5; DB 6; Length 310;
Pred. No. 2e-07;
RESULT 1148
ID AAI96294 standard; protein; 310 AA.

DE Human IGFAM-6 immunoglobulin.
PN WO200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.4%; Score 197.5; DB 3; Length 310;
Best Local Similarity 26.7%; Pred. No. 2.4e-07;
RESULT 1149
ID ADP56683 standard; protein; 299 AA.
DE Human junction adhesion molecule 3 (hJAM3) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 10.4%; Score 197.5; DB 8; Length 310;
Best Local Similarity 26.7%; Pred. No. 2.4e-07;
RESULT 1150
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 197; DB 2; Length 299;
Best Local Similarity 24.8%; Pred. No. 2.5e-07;
RESULT 1151
ID AAY23321 standard; protein; 299 AA.
DE Amino acid sequence of the PRO301 polypeptide.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 2; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1152
ID AAW74464 standard; protein; 299 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 10.3%; Score 196; DB 2; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1153
ID AAY13364 standard; protein; 299 AA.
DE Amino acid sequence of protein PRO301.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 2; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1154
ID AAY76011 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:189.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.3%; Score 196; DB 3; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1155
ID AAY76076 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:331.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1156
ID AAY70670 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 3; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1157
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200053753-A2.

PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 3; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1158
ID AAY5344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 3; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1159
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1160
ID AAM93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1161
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1162
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1163
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1164
ID AAU0823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1165
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 4; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1166
ID AAB53086 standard; protein; 299 AA.
DE Human angio genesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.

Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1183
ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1184
ID ABU81052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1185
ID ABU71911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1186
ID ABO01794 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1187
ID ABU66752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1188
ID ABU54367 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1189
ID ABU67291 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1190
ID ABO47382 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1191
ID ABU59833 standard; protein; 299 AA.
DE Novel secreted and transmembrane protein PRO301.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1192
ID ABO25023 standard; protein; 299 AA.
DE Human secreted/transmembrane protein (PRO) #183.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1193
ID ABU64519 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #23.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1194
ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1195
ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1196
ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1197
ID ABO14885 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1198
ID ABU07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1199
ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (hujAM1).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1200
ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1201

Wed May 11 07:24:23 2005

us-09-978-544a-59.rag.spdi

ID ABU69642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1202
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1203
ID AB014824 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1204
ID AD45885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1205
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1206
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1207
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1208
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1209
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1210
ID ADB27915 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1211
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1212
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1213
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1214
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1215
ID ABO32776 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1216
ID ADA67539 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1217
ID ADB30546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1218
ID ADA85842 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1219
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2003082705-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1220
 ID ADA79358 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003082763-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1221
 ID ADA87497 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003087345-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1222
 ID ADB16699 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003087349-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1223
 ID ABO34836 standard; protein; 299 AA.
 DE Human PRO polypeptide #21.
 PN US2003044793-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1224
 ID ADA16155 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003049621-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1225
 ID ADA91791 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003082694-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1226
 ID ADB14854 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003087351-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1227
 ID ADA47263 standard; protein; 299 AA.
 DE Human secreted/transmembrane polypeptide PRO301.
 PN US2003044844-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1228
 ID ADB18815 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003073211-A1.

PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1229
 ID ADA94030 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003077722-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1230
 ID ADB19926 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003082691-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1231
 ID ADB13238 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003082710-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1232
 ID ABO43331 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003044945-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1233
 ID ADA74492 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003068798-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1234
 ID ADA42300 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003054401-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1235
 ID ADB24725 standard; protein; 299 AA.
 DE Human PRO polypeptide SEQ ID NO 366.
 PN US2003077713-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1236
 ID ADA82249 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003082701-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.3%; Score 196; DB 6; Length 299;
 Best Local Similarity 24.8%; Pred. No. 3e-07;
 RESULT 1237
 ID ADA75212 standard; protein; 299 AA.
 DE Human PRO polypeptide #183.
 PN US2003073216-A1.
 PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1238
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1239
ID ADA84738 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1240
ID ABO17514 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
FN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1241
ID ADB29994 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1242
ID ADA80522 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1243
ID ADA75764 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1244
ID ADA46989 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1245
ID ADB25285 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1246
ID ADA93461 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1247
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1248
ID ADB31098 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1249
ID ADA61026 standard; protein; 299 AA.
DE Homo sapiens.
FN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1250
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1251
ID ADA96502 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1252
ID ADA81074 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1253
ID ADA95950 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1254
ID ADB26259 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1255
ID ADB21744 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 6; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1256
ID ADB21744 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1256
ID ADA7523 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1257
ID ADB18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1258
ID ADA86946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1259
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1260
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1261
ID ADA41876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1262
ID ADA88049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1263
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1264
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1265
ID ADA42726 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1266
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1267
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1268
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1269
ID ADA8601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1270
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1271
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1272
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1273
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1274
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.

Wed May 11 07:24:23 2005

```
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1275
  ID ADA66987 standard; protein; 299 AA.
  DE Human PRO polypeptide #183.
  PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1276
  ID ADB22848 standard; protein; 299 AA.
  DE Human PRO polypeptide #183.
  PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1277
  ID ADB23621 standard; protein; 299 AA.
  DE Human PRO polypeptide SEQ ID NO 366.
  PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1278
  ID ADA92343 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1279
  ID ADB15406 standard; protein; 299 AA.
  DE Human PRO polypeptide #183.
  PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1280
  ID ADB38658 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1281
  ID ADB38106 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1282
  ID ADB66578 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003082889-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1283
  ID ADB89658 standard; protein; 299 AA.
  DE Human PRO polypeptide #183.
  PN US2003082698-A1.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1284
  ID ADB90390 standard; protein; 299 AA.
  DE Human PRO polypeptide #183.
  PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1285
  ID ADB77645 standard; protein; 299 AA.
  DE Human secreted/transmembrane protein, #25.
  PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1286
  ID ADB39491 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1287
  ID ADB74781 standard; protein; 299 AA.
  DE Human secreted/transmembrane protein, #25.
  PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1288
  ID ADB47114 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1289
  ID ADB86721 standard; protein; 299 AA.
  DE Human PRO polypeptide #183.
  PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1290
  ID ADB77326 standard; protein; 299 AA.
  DE Novel human secreted and transmembrane protein PRO301.
  PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1291
  ID ADB34483 standard; protein; 299 AA.
  DE Human PRO polypeptide SEQ ID NO 366.
  PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
  RESULT 1292
  ID ADB35587 standard; protein; 299 AA.
  DE Human PRO polypeptide SEQ ID NO 366.
  PN US2003077719-A1.
PD 24-APR-2003.
```


PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1293
ID ADB31931 standard; protein; 299 AA.
DE Human PRO polypeptide SQ ID NO 366.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1294
ID ADB35035 standard; protein; 299 AA.
DE Human PRO polypeptide SQ ID NO 366.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1295
ID ADB36139 standard; protein; 299 AA.
DE Human PRO polypeptide SQ ID NO 366.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1296
ID ADB46534 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1297
ID ADC28427 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1298
ID ADC39627 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1299
ID ADC40141 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1300
ID ADC18969 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1301
ID ADC34265 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1302
ID ADC29320 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1303
ID ADC28851 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1304
ID ADC40736 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1305
ID ADC19393 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1306
ID ADC33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1307
ID ADC12911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1308
ID ADC50407 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1309
ID ADC71954 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1310
ID ADC59933 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1311
ID ADC34265 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 1320

ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
FN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1321

ID ADC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1322

ID ADD03191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1323

ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1324

ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1325

ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1326

ID ADD10020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1327

ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1328

ID ADC80551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1329

ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
FN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1330
ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1331
ID ADC47939 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1332
ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1333
ID ADC79999 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1334
ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1335
ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1336
ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1337
ID ADD03500 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1338
ID ADD41181 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1339
ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1340
ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1341
ID ADD53612 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1342
ID ADD37096 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1343
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1344
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1345
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1346
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1347
ID ADD92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.


```
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1348
ID ADD91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1349
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1350
ID ADE32307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1351
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1352
ID ADD79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1353
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1354
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1355
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1356
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.

PN 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1357
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1358
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1359
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1360
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1361
ID ADE34752 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1362
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1363
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1364
ID ADD95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1365
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
```


PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1366
ID AD78909 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1367
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1368
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1369
ID AD80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1370
ID AD89595 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1371
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1372
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1373
ID ADE92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1374
ID ADG21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1375
ID ADG23157 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1376
ID ADE97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1377
ID ADG80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1378
ID ADG80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1379
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1380
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1381
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1382
ID ADH5296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1383

ID ADH55848 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1384
ID ADI38014 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1385
ID ADI64067 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1386
ID ADI65016 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1387
ID ADI63515 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1388
ID ADH81929 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1389
ID ADH81377 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1390
ID ADJ26282 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1391
ID ADM82546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1392
ID ADN15945 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1393
ID ADN16574 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1394
ID ADN15393 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1395
ID ADN14841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1396
ID ADC81103 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1397
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1398
ID ADD76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1399
ID ADD87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1400
ID ADD86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1401
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.

PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1402
ID ADE75767 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1403
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1404
ID ADE41304 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1405
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1406
ID ADE23895 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1407
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1408
ID ADD87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1409
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1410
ID ADE41186 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003104558-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1411
ID ADE73832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1412
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1413
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1414
ID ADE99386 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1415
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1416
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1417
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1418
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1419
ID ADE34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.

RESULT 1428
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1429
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1430
ID ADF98044 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1431
ID ADG24261 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1432
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1433
ID ADG03446 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1434
ID ADF99167 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1435
ID ADG16752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1436
ID ADG05211 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1437
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

ID ADG19478 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1438
ID ADF73372 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1439
ID ADG13315 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1440
ID ADG08372 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1441
ID ADG15542 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1442
ID ADF96940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1443
ID ADG06125 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1444
ID ADG23709 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1445
ID ADG03998 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1446
ID ADG24899 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1447
ID ADG07196 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1448
ID ADG07748 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1449
ID ADG55243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1450
ID ADG60907 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1451
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1452
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003207145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1453
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1454
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1455
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

Wed May 11 07:24:23 2005

PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1456
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1457
ID ADG58555 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1458
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1459
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1460
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1461
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1462
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1463
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1464
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1465
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1466
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1467
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1468
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1469
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1470
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1471
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1472
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1473
ID ADH28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1474
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1475
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1476
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1477
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1478
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHUR J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1479
ID ADH59831 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1480
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHUR J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1481
ID ADH1155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1482
ID ADI18601 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1483
ID ADI65321 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1484
ID ADI37584 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1485
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1486
ID ADH97380 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1487
ID ADI15369 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1488
ID ADG09246 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1489
ID ADI65748 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.3%; Score 196; DB 8; Length 299;
RESULT 1490
ID ADI14701 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207383-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1491
ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1492
ID ADI18296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1493
ID ADJ99548 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1494
ID ADL08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1495
ID ADI47176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1496
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1497
ID ADK40844 standard; protein; 299 AA.
DE Human platelet F11 receptor #1.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UNNY) UNIV NEW YORK STATE RES FOUND.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1498
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20040319164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1500
ID ADL77818 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1499
ID ADM29832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 196; DB 8; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;

101	163.5	8.6	312	4	US-09-906-700-64	Sequence 64, Appl	174	141.5	7.4	316	4	US-09-910-174B-24	Sequence 24, Appl
102	163.5	8.6	312	4	US-09-903-603A-64	Sequence 64, Appl	175	141.5	7.4	316	4	US-09-620-461-24	Sequence 24, Appl
103	163.5	8.6	312	4	US-09-904-920A-64	Sequence 64, Appl	176	141.5	7.4	342	2	US-08-724-394A-6	Sequence 6, Appl
104	163.5	8.6	312	4	US-09-909-064-64	Sequence 64, Appl	177	141	7.4	527	4	US-09-910-174B-10	Sequence 10, Appl
105	163.5	8.6	312	4	US-09-905-381A-64	Sequence 64, Appl	178	141	7.4	527	4	US-09-620-461-10	Sequence 10, Appl
106	163.5	8.6	312	4	US-09-906-618-64	Sequence 64, Appl	179	137.5	7.2	540	2	US-08-724-394A-4	Sequence 4, Appl
107	163.5	8.6	312	4	US-09-953-499-9	Sequence 9, Appl	180	137	7.2	802	3	US-09-173-151A-33	Sequence 33, Appl
108	163.5	8.6	439	3	US-09-383-586-32	Sequence 32, Appl	181	136.5	7.2	350	4	US-09-651-200-25	Sequence 25, Appl
109	163.5	8.6	439	4	US-09-823-038A-32	Sequence 32, Appl	182	136.5	7.2	350	4	US-09-910-174B-17	Sequence 17, Appl
110	162	8.5	584	4	US-09-910-174B-16	Sequence 16, Appl	183	136.5	7.2	350	4	US-09-620-461-17	Sequence 17, Appl
111	158	8.3	394	4	US-09-855-323-17	Sequence 17, Appl	184	135.5	7.1	514	4	US-09-949-016-11380	Sequence 11380, A
112	158	8.2	394	4	US-09-855-323-17	Sequence 17, Appl	185	135.5	7.1	517	4	US-09-723-368-4	Sequence 4, Appl
113	156	8.2	394	4	US-09-656-952-20	Sequence 20, Appl	186	135.5	7.1	1070	4	US-09-961-403-3	Sequence 3, Appl
114	156	8.2	1059	4	US-09-907-794A-290	Sequence 290, Appl	187	135	7.1	290	4	US-09-910-174B-19	Sequence 19, Appl
115	156	8.2	1059	4	US-09-905-125A-290	Sequence 290, Appl	188	135	7.1	290	4	US-09-620-461-19	Sequence 19, Appl
116	156	8.2	1059	4	US-09-902-775A-290	Sequence 290, Appl	189	135	7.1	518	4	US-09-919-172-20	Sequence 20, Appl
117	156	8.2	1059	4	US-09-906-700-290	Sequence 290, Appl	190	135	7.1	581	2	US-08-724-394A-3	Sequence 3, Appl
118	156	8.2	1059	4	US-09-903-603A-290	Sequence 290, Appl	191	135	7.1	590	3	US-09-310-463-22	Sequence 22, Appl
119	156	8.2	1059	4	US-09-904-920A-290	Sequence 290, Appl	192	135	7.1	590	3	US-08-842-248A-22	Sequence 22, Appl
120	156	8.2	1059	4	US-09-909-064-290	Sequence 290, Appl	193	135	7.1	837	4	US-09-949-016-6515	Sequence 6515, Ap
121	156	8.2	1059	4	US-09-905-381A-290	Sequence 290, Appl	194	134.5	7.0	738	6	5264554-2	Patent No. 5264554
122	156	8.2	1059	4	US-09-906-618-290	Sequence 290, Appl	195	134.5	7.0	738	6	5264554-2	Patent No. 5264554
123	156	8.2	1119	4	US-09-907-794A-294	Sequence 294, Appl	196	134.5	7.0	1051	3	US-08-986-485-5	Sequence 5, Appl
124	156	8.2	1119	4	US-09-905-125A-294	Sequence 294, Appl	197	134	7.0	529	4	US-09-910-174B-13	Sequence 13, Appl
125	156	8.2	1119	4	US-09-902-775A-294	Sequence 294, Appl	198	134	7.0	529	4	US-09-620-461-13	Sequence 13, Appl
126	156	8.2	1119	4	US-09-906-700-294	Sequence 294, Appl	199	133.5	7.0	182	3	US-09-724-864-50	Sequence 50, Appl
127	156	8.2	1119	4	US-09-903-603A-294	Sequence 294, Appl	200	133	7.0	1248	4	US-09-949-016-10595	Sequence 10595, A
128	156	8.2	1119	4	US-09-904-920A-294	Sequence 294, Appl	201	133	7.0	1248	4	US-09-949-016-10596	Sequence 10596, A
129	156	8.2	1119	4	US-09-909-064-294	Sequence 294, Appl	202	133	7.0	1297	3	US-09-540-245A-17	Sequence 17, Appl
130	156	8.2	1119	4	US-09-905-381A-294	Sequence 294, Appl	203	133	7.0	1311	1	US-08-340-011-5	Sequence 5, Appl
131	156	8.2	1119	4	US-09-906-618-294	Sequence 294, Appl	204	133	7.0	1311	3	US-08-901-710-5	Sequence 5, Appl
132	155	8.1	313	4	US-09-700-397-4	Sequence 4, Appl	205	133	7.0	1311	3	US-09-169-079-5	Sequence 5, Appl
133	155	8.1	344	4	US-09-700-397-4	Sequence 4, Appl	206	132	6.9	296	4	US-09-667-135-36	Sequence 36, Appl
134	153.5	8.0	321	4	US-09-754-465A-2	Sequence 2, Appl	207	131.5	6.9	581	2	US-08-724-394A-2	Sequence 2, Appl
135	153.5	8.0	321	4	US-09-953-499-2	Sequence 2, Appl	208	131	6.9	288	4	US-09-651-200-14	Sequence 14, Appl
136	152.5	8.0	526	4	US-09-910-174B-9	Sequence 9, Appl	209	131	6.9	450	4	US-09-907-794A-320	Sequence 320, App
137	152.5	8.0	526	4	US-09-620-461-9	Sequence 9, Appl	210	131	6.9	450	4	US-09-908-125A-320	Sequence 320, App
138	152.5	8.0	526	4	US-09-949-016-6122	Sequence 9, Appl	211	131	6.9	450	4	US-09-902-775A-320	Sequence 320, App
139	152.5	8.0	540	4	US-09-949-016-6122	Sequence 9, Appl	212	131	6.9	450	4	US-09-906-700-320	Sequence 320, App
140	151.5	7.9	95	3	US-09-949-016-11644	Sequence 11644, A	213	131	6.9	450	4	US-09-903-603A-320	Sequence 320, App
141	151.5	7.9	1101	3	US-08-986-485-17	Sequence 17, Appl	214	131	6.9	450	4	US-09-904-920A-320	Sequence 320, App
142	151	7.9	1101	3	US-08-986-485-17	Sequence 17, Appl	215	131	6.9	450	4	US-09-909-064-320	Sequence 320, App
143	150	7.9	501	2	US-08-408-095-31	Sequence 31, Appl	216	131	6.9	450	4	US-09-905-381A-320	Sequence 320, App
144	150	7.9	205	3	US-09-462-270-4	Sequence 4, Appl	217	131	6.9	450	4	US-09-906-618-320	Sequence 320, App
145	150	7.9	319	4	US-09-910-174B-12	Sequence 12, Appl	218	131	6.9	4391	4	US-10-006-011A-2	Sequence 1, Appl
146	150	7.9	319	4	US-09-620-461-12	Sequence 12, Appl	219	130.5	6.8	458	4	US-09-435-956A-1	Sequence 10547, A
147	150	7.9	357	4	US-09-910-174B-14	Sequence 14, Appl	220	130	6.8	588	4	US-09-949-016-10547	Sequence 6, Appl
148	150	7.9	513	4	US-09-620-461-14	Sequence 14, Appl	221	129	6.8	1338	3	US-08-750-141A-3	Sequence 7344, Ap
149	150	7.9	513	4	US-09-910-174B-18	Sequence 18, Appl	222	129	6.8	1338	3	US-09-119-014D-6	Sequence 9, Appl
150	149	7.9	513	4	US-09-620-461-18	Sequence 18, Appl	223	128.5	6.7	646	4	US-09-949-016-7344	Sequence 11044, A
151	148.5	7.8	610	2	US-09-656-952-2	Sequence 2, Appl	224	128	6.7	615	2	US-08-752-307B-9	Sequence 3, Appl
152	148.5	7.8	738	3	US-08-724-394A-5	Sequence 5, Appl	225	128	6.7	615	3	US-09-991-326-9	Sequence 2, Appl
153	148.5	7.8	738	4	US-09-336-536-73	Sequence 32, Appl	226	128	6.7	819	4	US-09-949-016-11044	Sequence 6, Appl
154	147.5	7.7	315	4	US-09-910-174B-28	Sequence 28, Appl	227	128	6.7	819	4	US-09-949-016-11044	Sequence 9, Appl
155	147.5	7.7	315	4	US-09-910-174B-28	Sequence 28, Appl	228	128	6.7	819	4	US-09-949-016-11044	Sequence 9, Appl
156	147	7.7	344	4	US-09-620-461-28	Sequence 19, Appl	229	128	6.7	1501	2	US-08-447-464-3	Sequence 11044, A
157	146.5	7.7	404	4	US-09-656-952-19	Sequence 3, Appl	230	127.5	6.7	288	2	US-08-147-772-2	Sequence 3, Appl
158	146.5	7.7	404	4	US-09-638-649-3	Sequence 3, Appl	231	127.5	6.7	288	2	US-08-716-679-3	Sequence 3, Appl
159	146.5	7.7	404	4	US-09-949-016-11025	Sequence 11025, A	232	127.5	6.7	288	2	US-08-456-104-6	Sequence 2, Appl
160	145	7.6	193	4	US-09-638-648-3	Sequence 4, Appl	233	127.5	6.7	288	2	US-08-101-524-23	Sequence 23, Appl
161	143.5	7.5	731	4	US-09-243D-4	Sequence 15, Appl	234	127.5	6.7	288	2	US-08-153-262-2	Sequence 6, Appl
162	143.5	7.5	731	4	US-09-910-174B-15	Sequence 15, Appl	235	127.5	6.7	288	3	US-08-751-767A-6	Sequence 2, Appl
163	143	7.5	405	4	US-09-620-461-15	Sequence 4, Appl	236	127.5	6.7	288	3	US-08-479-744A-29	Sequence 29, Appl
164	143	7.5	405	4	US-09-620-461-15	Sequence 4, Appl	237	127.5	6.7	288	3	US-08-280-757B-29	Sequence 29, Appl
165	143	7.5	523	4	US-09-910-174B-11	Sequence 11, Appl	238	127.5	6.7	288	3	US-09-159-135-2	Sequence 2, Appl
166	143	7.5	523	4	US-09-910-174B-11	Sequence 11, Appl	239	127.5	6.7	288	3	US-08-205-697A-19	Sequence 19, Appl
167	142.5	7.5	816	4	US-09-949-016-110904	Sequence 2, Appl	240	127.5	6.7	288	3	US-08-702-525-19	Sequence 19, Appl
168	142.5	7.5	340	4	US-09-651-200-2	Sequence 2, Appl	241	127.5	6.7	288	3	US-08-450-798-2	Sequence 2, Appl
169	142.5	7.5	441	4	US-09-651-200-4	Sequence 4, Appl	242	127.5	6.7	288	3	US-08-403-253A-2	Sequence 2, Appl
170	142.5	7.5	534	4	US-09-651-200-6	Sequence 6, Appl	243	127.5	6.7	288	4	US-09-651-200-13	Sequence 13, Appl
171	142	7.4	329	4	US-09-651-200-24	Sequence 24, Appl	244	127.5	6.7	288	4	US-09-667-135-34	Sequence 34, Appl
172	142	7.4	304	4	US-09-651-200-19	Sequence 19, Appl	245	127.5	6.7	288	4	US-08-435-816A-2	Sequence 2, Appl
173	142	7.4	511	4	US-09-949-016-7020	Sequence 7020, Ap	246	127.5	6.7	288	4	US-09-425-762-29	Sequence 29, Appl
					Sequence 10054, A							US-09-837-867A-19	Sequence 19, Appl

247	127.5	6.7	288	4	US-09-910-174B-5	Sequence 5, Appli	320	120	6.3	698	2	US-08-602-725-36	Sequence 36, Appli
248	127.5	6.7	288	4	US-09-620-461-5	Sequence 5, Appli	321	120	6.3	702	4	US-09-949-016-6484	Sequence 6484, Ap
249	127.5	6.7	288	4	US-08-453-386A-2	Sequence 2, Appli	322	120	6.3	734	2	US-08-389-459A-17	Sequence 17, Appli
250	127.5	6.7	288	4	US-09-206-132-6	Sequence 6, Appli	323	120	6.3	734	3	US-08-987-867A-17	Sequence 17, Appli
251	127.5	6.7	288	4	US-09-425-516-29	Sequence 29, Appli	324	120	6.3	740	4	US-09-949-016-8168	Sequence 8168, Ap
252	127.5	6.7	288	5	PCT-US95-02576-19	Sequence 19, Appli	325	120	6.3	795	4	US-09-949-016-7119	Sequence 7119, Ap
253	127.5	6.7	288	4	US-09-778-510-6	Sequence 6, Appli	326	120	6.3	806	3	US-09-383-630-3	Sequence 3, Appli
254	127.5	6.7	398	4	US-09-907-794A-84	Sequence 84, Appli	327	120	6.3	1953	4	US-09-917-254-92	Sequence 92, Appli
255	127.5	6.7	398	4	US-09-905-125A-84	Sequence 84, Appli	328	119.5	6.3	631	3	US-09-345-468-12	Sequence 12, Appli
256	127.5	6.7	398	4	US-09-902-775A-84	Sequence 84, Appli	329	119.5	6.3	631	3	US-09-414-453A-12	Sequence 12, Appli
257	127.5	6.7	398	4	US-09-906-700-84	Sequence 84, Appli	330	119.5	6.3	631	3	US-09-310-463-20	Sequence 20, Appli
258	127.5	6.7	398	4	US-09-903-603A-84	Sequence 84, Appli	331	119.5	6.3	631	3	US-08-842-248A-20	Sequence 20, Appli
259	127.5	6.7	398	4	US-09-904-920A-84	Sequence 84, Appli	332	119	6.2	328	4	US-09-949-016-6428	Sequence 6428, Ap
260	127.5	6.7	398	4	US-09-909-064-84	Sequence 84, Appli	333	119	6.2	329	4	US-09-149-476-483	Sequence 483, App
261	127.5	6.7	398	4	US-09-905-381A-84	Sequence 84, Appli	334	119	6.2	332	4	US-09-949-016-7327	Sequence 7327, Ap
262	127.5	6.7	398	4	US-09-906-618-84	Sequence 84, Appli	335	119	6.2	780	1	US-08-232-538-14	Sequence 14, Appli
263	127.5	6.7	416	4	US-09-638-649-1	Sequence 1, Appli	336	119	6.2	780	2	US-08-786-164-14	Sequence 14, Appli
264	127.5	6.7	416	4	US-08-755-235-2	Sequence 2, Appli	337	118.5	6.2	365	4	US-09-949-016-7591	Sequence 7591, Ap
265	127.5	6.7	416	4	US-09-638-648-1	Sequence 1, Appli	338	118.5	6.2	373	4	US-09-823-038A-60	Sequence 60, Appli
266	127.5	6.7	432	4	US-09-778-510-2	Sequence 2, Appli	339	118.5	6.2	729	1	US-07-640-029-3	Sequence 3, Appli
267	127.5	6.7	455	4	US-09-949-016-6949	Sequence 6949, Ap	340	118.5	6.2	731	1	US-07-921-807B-5	Sequence 5, Appli
268	127.5	6.7	455	4	US-09-949-016-11026	Sequence 11026, A	341	118.5	6.2	731	1	US-08-441-944A-5	Sequence 5, Appli
269	127	6.7	184	3	US-08-630-172-2	Sequence 2, Appli	342	118.5	6.2	731	3	US-08-439-992A-3	Sequence 3, Appli
270	127	6.7	184	3	US-09-375-419-2	Sequence 2, Appli	343	118.5	6.2	733	1	US-07-640-029-4	Sequence 4, Appli
271	127	6.7	252	4	US-09-270-767-44627	Sequence 44627, A	344	118.5	6.2	733	1	US-07-921-807B-6	Sequence 6, Appli
272	127	6.7	418	3	US-08-630-172-18	Sequence 18, Appli	345	118.5	6.2	733	3	US-08-441-944A-6	Sequence 6, Appli
273	127	6.7	418	3	US-09-375-419-18	Sequence 18, Appli	346	118.5	6.2	733	3	US-08-439-992A-4	Sequence 4, Appli
274	127	6.7	1461	3	US-09-976-594-531	Sequence 531, App	347	118.5	6.2	817	1	US-07-640-029-2	Sequence 2, Appli
275	127	6.7	1651	3	US-09-540-245A-18	Sequence 18, Appli	348	118.5	6.2	820	1	US-07-921-807B-3	Sequence 3, Appli
276	126	6.6	498	4	US-09-354-151-2	Sequence 2, Appli	349	118.5	6.2	820	1	US-08-441-944A-3	Sequence 3, Appli
277	125	6.6	801	3	US-09-383-630-6	Sequence 6, Appli	350	118.5	6.2	820	3	US-08-439-992A-1	Sequence 1, Appli
278	125	6.6	1018	1	US-08-408-093-6	Sequence 6, Appli	351	118.5	6.2	822	1	US-07-997-133-1	Sequence 1, Appli
279	125	6.6	1018	1	US-08-408-420A-6	Sequence 6, Appli	352	118.5	6.2	822	1	US-07-921-807B-4	Sequence 4, Appli
280	125	6.6	1018	1	US-08-714-901-6	Sequence 6, Appli	353	118.5	6.2	822	1	US-08-459-296-2	Sequence 2, Appli
281	125	6.6	1018	3	US-08-040-741-6	Sequence 6, Appli	354	118.5	6.2	822	1	US-08-441-944A-4	Sequence 4, Appli
282	125	6.6	1044	4	US-09-949-016-10321	Sequence 10321, A	355	118.5	6.2	822	2	US-08-451-822A-12	Sequence 12, Appli
283	124.5	6.5	365	4	US-09-949-016-6907	Sequence 6907, Ap	356	118.5	6.2	822	3	US-08-439-992A-2	Sequence 2, Appli
284	124.5	6.5	391	4	US-09-949-016-7325	Sequence 7325, Ap	357	118.5	6.2	822	3	US-08-323-430-12	Sequence 12, Appli
285	124.5	6.5	972	3	US-08-750-141A-2	Sequence 2, Appli	358	118	6.2	191	4	US-09-270-767-33678	Sequence 33678, A
286	124.5	6.5	972	4	US-09-944-807-10	Sequence 10, Appli	359	118	6.2	191	4	US-09-270-767-48895	Sequence 48895, A
287	124	6.5	473	3	US-09-171-945-131	Sequence 131, Appli	360	118	6.2	364	4	US-08-896-537A-3	Sequence 3, Appli
288	124	6.5	519	3	US-08-996-338-21	Sequence 21, Appli	361	118	6.2	1911	1	US-08-348-006B-5	Sequence 5, Appli
289	124	6.5	519	4	US-09-556-972-21	Sequence 21, Appli	362	118	6.2	1911	2	US-08-800-825A-5	Sequence 5, Appli
290	124	6.5	537	1	US-08-604-333-4	Sequence 4, Appli	363	118	6.2	1911	3	US-09-158-657-5	Sequence 5, Appli
291	124	6.5	537	3	US-09-110-618-4	Sequence 4, Appli	364	118	6.2	1911	5	PCT-US94-10166-5	Sequence 5, Appli
292	124	6.5	537	3	US-09-173-151A-29	Sequence 29, Appli	365	117.5	6.2	269	4	US-09-949-016-6121	Sequence 6121, Ap
293	124	6.5	537	4	US-09-578-178-4	Sequence 4, Appli	366	117.5	6.2	276	4	US-09-949-016-7261	Sequence 7261, Ap
294	124	6.5	537	4	US-09-577-806-4	Sequence 8, Appli	367	117.5	6.2	336	4	US-09-949-016-7715	Sequence 7715, Ap
295	124	6.5	537	4	US-09-621-502-8	Sequence 8, Appli	368	117.5	6.2	526	1	US-08-471-570-4	Sequence 4, Appli
296	124	6.5	596	2	US-08-752-307B-13	Sequence 13, Appli	369	117.5	6.2	526	1	US-08-471-570-10	Sequence 10, Appli
297	124	6.5	596	3	US-09-707-802-13	Sequence 13, Appli	370	117.5	6.2	652	1	US-09-540-245A-16	Sequence 16, Appli
298	124	6.5	596	3	US-09-991-326-13	Sequence 13, Appli	371	117.5	6.2	1381	3	US-09-270-767-42034	Sequence 42034, A
299	124	6.5	731	1	US-08-070-165F-10	Sequence 10, Appli	372	117	6.1	278	4	US-09-383-632-2	Sequence 2, Appli
300	124	6.5	731	2	US-08-885-418-10	Sequence 10, Appli	373	117	6.1	431	3	US-09-038-832-4	Sequence 4, Appli
301	123.5	6.5	398	4	US-09-778-510-4	Sequence 4, Appli	374	117	6.1	447	4	US-09-949-016-8211	Sequence 8211, Ap
302	123.5	6.5	589	2	US-08-724-394A-1	Sequence 1, Appli	375	117	6.1	638	3	US-08-470-335-240	Sequence 240, App
303	123	6.4	729	1	US-08-070-165F-6	Sequence 6, Appli	376	116.5	6.1	638	4	US-08-467-602-297	Sequence 297, App
304	123	6.4	729	2	US-08-885-418-6	Sequence 6, Appli	377	116.5	6.1	638	4	US-08-411-295F-223	Sequence 223, App
305	123	6.4	1395	3	US-09-540-245A-15	Sequence 15, Appli	378	116.5	6.1	672	4	US-08-467-602-339	Sequence 339, App
306	122.5	6.4	935	3	US-08-928-383B-18	Sequence 18, Appli	379	116.5	6.1	672	4	US-08-411-295F-265	Sequence 265, App
307	122.5	6.4	816	1	US-07-640-029-1	Sequence 1, Appli	380	116.5	6.1	820	1	US-08-166-717D-6	Sequence 6, Appli
308	122.5	6.4	1209	4	US-08-130-158A-2	Sequence 2, Appli	381	116.5	6.1	855	3	US-08-470-335-241	Sequence 241, App
309	122	6.4	821	2	US-08-451-822A-13	Sequence 13, Appli	382	116.5	6.1	855	4	US-08-467-602-298	Sequence 298, App
310	122	6.4	821	3	US-08-323-430-13	Sequence 13, Appli	383	116.5	6.1	855	4	US-08-411-295F-224	Sequence 224, App
311	121.5	6.4	605	2	US-08-752-307B-8	Sequence 8, Appli	384	116.5	6.1	855	4	US-08-467-602-340	Sequence 340, App
312	121.5	6.4	605	3	US-09-707-802-8	Sequence 8, Appli	385	116.5	6.1	889	4	US-08-470-335-242	Sequence 242, App
313	121.5	6.4	605	3	US-09-991-326-8	Sequence 8, Appli	386	116.5	6.1	889	4	US-08-411-295F-266	Sequence 266, App
314	121.5	6.4	643	1	US-08-471-570-6	Sequence 6, Appli	387	116.5	6.1	902	3	US-08-470-335-242	Sequence 242, App
315	121.5	6.4	769	3	US-08-471-570-8	Sequence 8, Appli	388	116.5	6.1	902	4	US-08-467-602-296	Sequence 296, App
316	121	6.3	374	3	US-09-046-736-4	Sequence 4, Appli	389	116.5	6.1	902	4	US-08-411-295F-222	Sequence 222, App
317	120	6.3	607	2	US-08-752-307B-12	Sequence 12, Appli	390	116.5	6.1	936	4	US-08-467-602-338	Sequence 338, App
318	120	6.3	607	3	US-09-707-802-12	Sequence 12, Appli	391	116.5	6.1	936	4	US-08-411-295F-264	Sequence 264, App
319	120	6.3	607	3	US-09-991-326-12	Sequence 12, Appli	392	116	6.1	216	4	US-09-666-267B-8	Sequence 8, Appli

393	116	6.1	292	4	US-09-800-729-175	Sequence 175, App	466	112.5	5.9	965	4	US-08-467-602-358	Sequence 358, App
394	116	6.1	1018	1	US-08-452-052-2	Sequence 2, Appli	467	112.5	5.9	965	4	US-08-411-295F-284	Sequence 284, App
395	116	6.1	1745	4	US-09-800-729-89	Sequence 89, Appl	468	112.5	5.9	423	4	US-09-778-510-22	Sequence 22, Appl
396	115.5	6.1	315	4	US-09-949-016-11121	Sequence 11121, A	469	112	5.9	642	1	US-08-217-295-1	Sequence 1, Appli
397	115.5	6.1	315	4	US-09-949-016-11122	Sequence 11122, A	470	112	5.9	647	3	US-08-470-335-243	Sequence 243, App
398	115	6.0	143	4	US-09-949-016-9006	Sequence 9006, Ap	471	112	5.9	647	3	US-08-467-602-308	Sequence 308, App
399	115	6.0	313	4	US-09-756-983-15	Sequence 15, Appl	472	112	5.9	647	4	US-08-411-295F-234	Sequence 234, App
400	115	6.0	459	3	US-08-470-335-239	Sequence 239, App	473	112	5.9	681	4	US-08-467-602-350	Sequence 350, App
401	115	6.0	459	4	US-08-467-602-239	Sequence 239, App	474	112	5.9	864	3	US-08-411-295F-276	Sequence 276, App
402	115	6.0	459	4	US-08-411-295F-225	Sequence 225, App	475	112	5.9	864	3	US-08-470-335-244	Sequence 244, App
403	115	6.0	493	4	US-08-467-602-341	Sequence 341, App	476	112	5.9	864	4	US-08-467-602-309	Sequence 309, App
404	115	6.0	493	4	US-08-411-295F-267	Sequence 267, App	477	112	5.9	864	4	US-08-411-295F-235	Sequence 235, App
405	114.5	6.0	269	4	US-10-000-489-78	Sequence 78, Appl	478	112	5.9	898	4	US-08-467-602-351	Sequence 351, App
406	114.5	6.0	449	3	US-09-310-463-38	Sequence 38, Appl	479	112	5.9	898	4	US-08-411-295F-277	Sequence 277, App
407	114.5	6.0	626	4	US-09-949-016-6213	Sequence 6213, Ap	480	112	5.9	911	3	US-08-470-335-245	Sequence 245, App
408	114.5	6.0	664	4	US-09-949-016-7850	Sequence 7850, Ap	481	112	5.9	911	4	US-08-467-602-310	Sequence 310, App
409	114	6.0	468	3	US-09-292-097-2	Sequence 2, Appli	482	112	5.9	911	4	US-08-470-335-250	Sequence 250, App
410	114	6.0	468	4	US-09-933-561-2	Sequence 13, Appl	483	112	5.9	945	4	US-08-467-602-352	Sequence 352, App
411	114	6.0	945	5	PCT-US95-08493-13	Sequence 43068, A	484	112	5.9	945	4	US-08-467-602-352	Sequence 278, App
412	113.5	5.9	280	4	US-09-270-767-43068	Sequence 3, Appli	485	111.5	5.8	306	3	US-08-205-697A-17	Sequence 17, Appl
413	113.5	5.9	307	4	US-09-137-970B-3	Sequence 6729, Ap	486	111.5	5.8	306	4	US-08-702-525-17	Sequence 17, Appl
414	113.5	5.9	417	4	US-09-949-016-6729	Sequence 8, Appli	487	111.5	5.8	306	4	US-09-651-200-17	Sequence 17, Appl
415	113.5	5.9	669	1	US-07-847-743B-8	Sequence 8, Appli	488	111.5	5.8	306	4	US-09-667-135-35	Sequence 35, Appl
416	113.5	5.9	669	1	US-08-456-201-8	Sequence 13, Appl	489	111.5	5.8	306	5	PCT-US95-02576-17	Sequence 17, Appl
417	113.5	5.9	669	1	US-08-456-201-8	Sequence 8, Appli	490	111.5	5.8	307	3	US-08-996-338-25	Sequence 25, Appl
418	113.5	5.9	669	2	US-08-310-161-11	Sequence 11, Appl	491	111.5	5.8	307	4	US-09-556-972-25	Sequence 23, Appl
419	113.5	5.9	669	2	US-08-456-241-8	Sequence 8, Appli	492	111.5	5.8	312	4	US-09-684-708A-23	Sequence 27, Appl
420	113.5	5.9	669	2	US-08-456-241-13	Sequence 11, Appl	493	111.5	5.8	312	4	US-09-684-708A-23	Sequence 18832, A
421	113.5	5.9	669	2	US-08-440-401-11	Sequence 11, Appl	494	111.5	5.8	342	4	US-09-248-796A-18832	Sequence 5, Appli
422	113.5	5.9	669	2	US-08-419-878B-11	Sequence 11, Appl	495	111.5	5.8	345	4	US-09-638-649-5	Sequence 246, App
423	113.5	5.9	669	3	US-09-173-480B-11	Sequence 11, Appl	496	111.5	5.8	456	3	US-08-470-335-246	Sequence 303, App
424	113.5	5.9	669	3	PCT-US92-04295A-8	Sequence 8, Appli	497	111.5	5.8	456	4	US-08-467-602-303	Sequence 229, App
425	113.5	5.9	669	5	PCT-US92-04295A-13	Sequence 13, Appl	498	111.5	5.8	456	4	US-08-411-295F-229	Sequence 7564, Ap
426	113.5	5.9	205	4	US-09-451-291-11	Sequence 11, Appl	499	111.5	5.8	456	4	US-09-949-016-7564	Sequence 345, App
427	113	5.9	205	4	US-08-630-172-15	Sequence 15, Appl	500	111.5	5.8	456	4	US-08-467-602-345	Sequence 271, App
428	113	5.9	208	3	US-09-375-419-15	Sequence 15, Appl	501	111.5	5.8	490	4	US-08-411-295F-271	Sequence 2, Appli
429	113	5.9	208	3	US-09-460-384-36	Sequence 36, Appl	502	111.5	5.8	490	4	US-08-896-537A-2	Sequence 247, App
430	113	5.9	478	5	PCT-US95-08493-15	Sequence 15, Appl	503	111.5	5.8	551	4	US-08-470-335-247	Sequence 302, App
431	113	5.9	860	5	PCT-US95-08493-19	Sequence 19, Appl	504	111.5	5.8	635	3	US-08-467-602-302	Sequence 228, App
432	113	5.9	868	5	PCT-US95-08493-21	Sequence 21, Appl	505	111.5	5.8	635	4	US-08-411-295F-228	Sequence 250, App
433	113	5.9	1363	4	US-09-375-248-19	Sequence 19, Appl	506	111.5	5.8	635	4	US-08-470-335-250	Sequence 311, App
434	113	5.9	479	4	US-08-467-602-307	Sequence 307, App	507	111.5	5.8	644	4	US-08-467-602-311	Sequence 237, App
435	112.5	5.9	479	4	US-08-411-295F-233	Sequence 233, App	508	111.5	5.8	644	4	US-08-411-295F-237	Sequence 44877, A
436	112.5	5.9	490	4	US-09-667-135-28	Sequence 28, Appl	509	111.5	5.8	644	4	US-09-270-767-44877	Sequence 344, App
437	112.5	5.9	513	4	US-08-467-602-349	Sequence 349, App	510	111.5	5.8	669	4	US-08-467-602-344	Sequence 279, App
438	112.5	5.9	513	4	US-08-467-602-349	Sequence 275, App	511	111.5	5.8	669	4	US-08-467-602-353	Sequence 251, App
439	112.5	5.9	650	3	US-09-310-463-2	Sequence 2, Appli	512	111.5	5.8	678	4	US-08-411-295F-279	Sequence 21, Appl
440	112.5	5.9	650	4	US-08-842-248A-2	Sequence 22, Appl	513	111.5	5.8	678	4	US-08-467-602-342	Sequence 248, App
441	112.5	5.9	651	3	US-09-985-950-22	Sequence 22, Appl	514	111.5	5.8	782	4	US-09-684-708A-21	Sequence 300, App
442	112.5	5.9	651	4	US-09-546-049-22	Sequence 22, Appl	515	111.5	5.8	852	3	US-08-470-335-248	Sequence 300, App
443	112.5	5.9	658	4	US-08-467-602-305	Sequence 305, App	516	111.5	5.8	852	4	US-08-467-602-300	Sequence 226, App
444	112.5	5.9	667	4	US-08-411-295F-231	Sequence 231, App	517	111.5	5.8	852	4	US-08-411-295F-226	Sequence 251, App
445	112.5	5.9	667	4	US-08-467-602-314	Sequence 314, App	518	111.5	5.8	861	4	US-08-470-335-251	Sequence 312, App
446	112.5	5.9	667	4	US-08-411-295F-240	Sequence 240, App	519	111.5	5.8	861	4	US-08-467-602-312	Sequence 238, App
447	112.5	5.9	692	4	US-08-467-602-347	Sequence 347, App	520	111.5	5.8	861	4	US-08-411-295F-238	Sequence 342, App
448	112.5	5.9	692	4	US-08-411-295F-273	Sequence 273, App	521	111.5	5.8	866	4	US-08-467-602-342	Sequence 242, App
449	112.5	5.9	701	4	US-08-467-602-356	Sequence 356, App	522	111.5	5.8	886	4	US-08-411-295F-268	Sequence 284, App
450	112.5	5.9	701	4	US-08-411-295F-282	Sequence 305, App	523	111.5	5.8	886	4	US-08-467-602-354	Sequence 354, App
451	112.5	5.9	875	4	US-08-467-602-306	Sequence 306, App	524	111.5	5.8	895	4	US-08-411-295F-280	Sequence 280, App
452	112.5	5.9	875	4	US-08-411-295F-232	Sequence 232, App	525	111.5	5.8	895	4	US-08-470-335-249	Sequence 249, App
453	112.5	5.9	884	4	US-08-467-602-315	Sequence 315, App	526	111.5	5.8	895	4	US-08-467-602-301	Sequence 301, App
454	112.5	5.9	884	4	US-08-411-295F-241	Sequence 241, App	527	111.5	5.8	899	3	US-08-467-602-301	Sequence 227
455	112.5	5.9	909	4	US-08-467-602-348	Sequence 348, App	528	111.5	5.8	899	4	US-08-411-295F-227	Sequence 252, App
456	112.5	5.9	909	4	US-08-411-295F-274	Sequence 357, App	529	111.5	5.8	908	3	US-08-470-335-252	Sequence 313, App
457	112.5	5.9	918	4	US-08-467-602-357	Sequence 357, App	530	111.5	5.8	908	4	US-08-411-295F-239	Sequence 239, App
458	112.5	5.9	918	4	US-08-411-295F-283	Sequence 283, App	531	111.5	5.8	908	4	US-08-467-602-313	Sequence 343, App
459	112.5	5.9	922	4	US-08-467-602-304	Sequence 304, App	532	111.5	5.8	933	4	US-08-411-295F-239	Sequence 269, App
460	112.5	5.9	922	4	US-08-411-295F-230	Sequence 230, App	533	111.5	5.8	933	4	US-08-411-295F-269	Sequence 355, App
461	112.5	5.9	931	4	US-08-467-602-316	Sequence 316, App	534	111.5	5.8	942	4	US-08-467-602-355	Sequence 281, App
462	112.5	5.9	931	4	US-08-411-295F-242	Sequence 242, App	535	111.5	5.8	1241	3	US-08-411-295F-281	Sequence 2, Appli
463	112.5	5.9	956	4	US-08-467-602-346	Sequence 346, App	536	111.5	5.8	306	2	US-09-040-774-2	Sequence 4, Appli
464	112.5	5.9	956	4	US-08-467-602-346	Sequence 272, App	537	111.5	5.8				
465	112.5	5.9	956	4	US-08-411-295F-272	Sequence 272, App	538	110.5	5.8				

539	110.5	5.8	306	2	US-08-456-104-8	Sequence 8, Appli	612	108.5	5.7	625	2	US-08-456-241-26	Sequence 26, Appli
540	110.5	5.8	306	2	US-08-101-624-25	Sequence 25, Appli	613	108.5	5.7	625	5	PCT-US92-04295A-26	Sequence 26, Appli
541	110.5	5.8	306	3	US-08-153-262-4	Sequence 4, Appli	614	108.5	5.7	640	4	US-08-467-602-256	Sequence 256, App
542	110.5	5.8	306	3	US-08-479-744A-31	Sequence 31, Appli	615	108.5	5.7	640	4	US-08-411-295F-182	Sequence 182, App
543	110.5	5.8	306	3	US-08-280-757B-31	Sequence 31, Appli	616	108.5	5.7	645	4	US-09-949-016-6728	Sequence 6728, Ap
544	110.5	5.8	306	3	US-09-159-135-4	Sequence 4, Appli	617	108.5	5.7	645	4	US-08-653-961-4	Sequence 4, Appli
545	110.5	5.8	306	3	US-09-450-798-4	Sequence 4, Appli	618	108.5	5.7	687	4	US-08-467-602-254	Sequence 254, App
546	110.5	5.8	306	3	US-09-425-762-31	Sequence 31, Appli	619	108.5	5.7	687	4	US-08-411-295F-180	Sequence 180, App
547	110.5	5.8	306	4	US-08-453-386A-4	Sequence 4, Appli	620	108.5	5.7	746	3	US-08-434-000A-4	Sequence 4, Appli
548	110.5	5.8	306	4	US-09-206-132-8	Sequence 8, Appli	621	108.5	5.7	746	3	US-09-312-157-4	Sequence 4, Appli
549	110.5	5.8	306	4	US-09-425-516-31	Sequence 31, Appli	622	108.5	5.7	746	4	US-09-717-888-4	Sequence 4, Appli
550	110.5	5.8	758	2	US-08-874-678-1	Sequence 1, Appli	623	108.5	5.7	764	4	US-09-949-016-6254	Sequence 6254, Ap
551	110.5	5.8	758	3	US-08-643-839-1	Sequence 1, Appli	624	108	5.7	330	2	US-08-332-562A-81	Sequence 81, Appli
552	110.5	5.8	758	3	US-09-051-363-24	Sequence 24, Appli	625	108	5.7	330	2	US-08-332-562A-134	Sequence 134, App
553	110.5	5.8	758	3	US-09-348-886-1	Sequence 1, Appli	626	108	5.7	483	3	US-09-310-463-16	Sequence 16, Appli
554	110.5	5.8	868	1	US-08-374-834-1	Sequence 1, Appli	627	108	5.7	483	4	US-08-842-248A-16	Sequence 16, Appli
555	110.5	5.8	868	2	US-08-644-271-1	Sequence 1, Appli	628	108	5.7	623	4	US-09-949-016-11206	Sequence 11206, A
556	110.5	5.8	868	4	US-09-077-955-1	Sequence 1, Appli	629	108	5.7	645	4	US-08-653-961-2	Sequence 2, Appli
557	110.5	5.8	869	4	US-09-715-249-8	Sequence 8, Appli	630	107.5	5.6	231	1	US-08-188-091A-4	Sequence 4, Appli
558	110.5	5.8	1617	4	US-09-784-358-16	Sequence 16, Appli	631	107.5	5.6	303	4	US-09-651-200-23	Sequence 23, Appli
559	110.5	5.8	1691	4	US-09-784-358-2	Sequence 2, Appli	632	107.5	5.6	303	4	US-09-441-411-15	Sequence 15, Appli
560	110.5	5.8	1212	4	US-09-949-016-10458	Sequence 10458, A	633	107.5	5.6	303	4	US-09-441-411-20	Sequence 20, Appli
561	110	5.8	301	3	US-08-829-525-24	Sequence 24, Appli	634	107.5	5.6	309	2	US-08-456-104-4	Sequence 4, Appli
562	110	5.8	301	3	US-08-609-583A-24	Sequence 24, Appli	635	107.5	5.6	309	3	US-08-479-744A-23	Sequence 23, Appli
563	110	5.8	301	3	US-08-937-399-24	Sequence 24, Appli	636	107.5	5.6	309	3	US-08-280-757B-23	Sequence 23, Appli
564	110	5.8	301	4	US-09-310-367-24	Sequence 24, Appli	637	107.5	5.6	309	3	US-08-205-697A-21	Sequence 21, Appli
565	110	5.8	301	4	US-09-032-337-24	Sequence 24, Appli	638	107.5	5.6	309	3	US-08-702-525-21	Sequence 21, Appli
566	110	5.8	301	4	US-09-464-231-24	Sequence 24, Appli	639	107.5	5.6	309	4	US-09-651-200-22	Sequence 22, Appli
567	110	5.8	597	4	US-09-746-311B-381	Sequence 381, App	640	107.5	5.6	309	4	US-09-667-135-33	Sequence 33, Appli
568	110	5.8	924	1	US-08-481-130-28	Sequence 28, Appli	641	107.5	5.6	309	4	US-09-425-762-23	Sequence 23, Appli
569	110	5.8	924	1	US-08-656-984A-28	Sequence 28, Appli	642	107.5	5.6	309	4	US-08-837-867A-21	Sequence 21, Appli
570	110	5.8	924	1	US-08-485-604-28	Sequence 28, Appli	643	107.5	5.6	309	4	US-09-206-132-4	Sequence 4, Appli
571	110	5.8	924	2	US-08-487-595-28	Sequence 28, Appli	644	107.5	5.6	309	4	US-09-441-411-13	Sequence 13, Appli
572	109.5	5.7	320	3	US-08-205-697A-2	Sequence 2, Appli	645	107.5	5.6	309	4	US-09-441-411-18	Sequence 18, Appli
573	109.5	5.7	320	3	US-08-702-525-2	Sequence 2, Appli	646	107.5	5.6	309	4	US-09-441-411-24	Sequence 24, Appli
574	109.5	5.7	320	4	PCT-US95-02576-2	Sequence 2, Appli	647	107.5	5.6	309	4	US-09-425-516-23	Sequence 23, Appli
575	109.5	5.7	332	4	US-09-062-365-1	Sequence 1, Appli	648	107.5	5.6	309	5	PCT-US95-02576-21	Sequence 21, Appli
576	109	5.7	440	4	US-09-866-028-61	Sequence 61, Appli	649	107.5	5.6	314	3	US-08-702-525-13	Sequence 13, Appli
577	109	5.7	440	4	US-09-944-457-61	Sequence 61, Appli	650	107.5	5.6	314	3	US-08-702-525-13	Sequence 13, Appli
578	109	5.7	442	4	US-09-778-510-20	Sequence 20, Appli	651	107.5	5.6	314	4	US-09-837-867A-13	Sequence 13, Appli
579	109	5.7	442	4	US-09-930-803-1	Sequence 1, Appli	652	107.5	5.6	314	4	US-09-441-411-14	Sequence 14, Appli
580	109	5.7	652	3	US-09-310-463-4	Sequence 4, Appli	653	107.5	5.6	314	4	US-09-441-411-19	Sequence 19, Appli
581	109	5.7	652	3	US-08-842-248A-4	Sequence 4, Appli	654	107.5	5.6	323	4	PCT-US95-02576-13	Sequence 13, Appli
582	109	5.7	869	1	US-08-374-834-16	Sequence 16, Appli	655	107.5	5.6	323	4	US-09-684-708A-25	Sequence 25, Appli
583	109	5.7	869	2	US-08-644-271-29	Sequence 29, Appli	656	107.5	5.6	356	4	US-09-441-411-11	Sequence 11, Appli
584	109	5.7	869	2	US-09-077-955-33	Sequence 33, Appli	657	107.5	5.6	356	4	US-09-441-411-12	Sequence 12, Appli
585	109	5.7	869	4	US-08-222-616-33	Sequence 33, Appli	658	107.5	5.6	356	4	US-09-441-411-16	Sequence 16, Appli
586	109	5.7	1298	1	US-08-340-011-2	Sequence 32, Appli	659	107.5	5.6	356	4	US-09-441-411-17	Sequence 17, Appli
587	109	5.7	1298	1	US-08-901-710-2	Sequence 2, Appli	660	107.5	5.6	489	3	US-09-310-463-14	Sequence 14, Appli
588	109	5.7	1298	3	US-08-446-648-33	Sequence 33, Appli	661	107.5	5.6	489	4	US-08-842-248A-14	Sequence 14, Appli
589	109	5.7	1298	3	US-09-983-610-33	Sequence 33, Appli	662	107.5	5.6	489	4	US-09-949-016-6765	Sequence 6765, Ap
590	109	5.7	1298	4	US-09-169-079-2	Sequence 2, Appli	663	107.5	5.6	630	2	US-08-752-307B-14	Sequence 14, Appli
591	109	5.7	1298	4	PCT-US95-04228-33	Sequence 33, Appli	664	107.5	5.6	630	3	US-09-707-802-14	Sequence 14, Appli
592	109	5.7	1362	2	US-08-874-678-33	Sequence 33, Appli	665	107.5	5.6	630	3	US-09-931-326-14	Sequence 14, Appli
593	109	5.7	1362	2	US-08-643-839-33	Sequence 33, Appli	666	107.5	5.6	645	4	US-09-345-473B-15	Sequence 15, Appli
594	109	5.7	1362	3	US-08-643-839-33	Sequence 33, Appli	667	107.5	5.6	645	4	US-09-345-473B-16	Sequence 16, Appli
595	109	5.7	1362	3	US-08-348-886-33	Sequence 33, Appli	668	107.5	5.6	732	1	US-07-847-743B-9	Sequence 9, Appli
596	109	5.7	1363	1	US-08-340-011-4	Sequence 4, Appli	669	107.5	5.6	732	1	US-08-456-201-9	Sequence 9, Appli
597	109	5.7	1363	2	US-08-874-678-32	Sequence 32, Appli	670	107.5	5.6	732	2	US-08-456-241-9	Sequence 9, Appli
598	109	5.7	1363	3	US-08-643-839-32	Sequence 32, Appli	671	107.5	5.6	732	5	PCT-US92-04295A-9	Sequence 9, Appli
599	109	5.7	1363	3	US-08-901-710-4	Sequence 4, Appli	672	107.5	5.6	833	4	US-09-949-016-11496	Sequence 11496, A
600	109	5.7	1363	3	US-09-375-248-2	Sequence 32, Appli	673	107.5	5.6	1180	4	US-08-467-602-257	Sequence 257, App
601	109	5.7	1363	4	US-09-169-079-4	Sequence 4, Appli	674	107	5.6	244	4	US-08-411-295F-183	Sequence 183, App
602	109	5.7	1368	2	US-08-874-678-34	Sequence 34, Appli	675	107	5.6	244	4	US-09-949-016-9042	Sequence 9042, Ap
603	109	5.7	1368	3	US-08-643-839-34	Sequence 34, Appli	676	107	5.6	471	4	US-09-949-016-9043	Sequence 9043, Ap
604	109	5.7	1368	3	US-09-348-886-34	Sequence 34, Appli	677	107	5.6	471	4	US-09-949-016-9044	Sequence 9044, Ap
605	109	5.7	1368	3	US-08-602-725-34	Sequence 34, Appli	678	107	5.6	471	4	US-09-949-016-9045	Sequence 9045, Ap
606	108.5	5.7	344	2	US-08-467-602-255	Sequence 255, App	679	107	5.6	471	4	US-09-949-016-9046	Sequence 9046, Ap
607	108.5	5.7	423	4	US-08-411-295F-181	Sequence 181, App	680	107	5.6	471	4	US-09-949-016-9047	Sequence 9047, Ap
608	108.5	5.7	423	4	US-09-046-736-2	Sequence 2, Appli	681	107	5.6	471	4	US-09-949-016-9048	Sequence 9048, Ap
609	108.5	5.7	467	3	US-07-847-743B-26	Sequence 26, Appli	682	107	5.6	471	4	US-09-949-016-9049	Sequence 9049, Ap
610	108.5	5.7	625	1	US-08-456-201-26	Sequence 26, Appli	683	107	5.6	471	4	US-09-949-016-9050	Sequence 9050, Ap
611	108.5	5.7	625	1			684	107	5.6	471	4		

685	107	5.6	471	4	US-09-949-016-9051	Sequence 9051, Ap	758	104.5	5.5	241	4	US-08-411-295F-94	Sequence 94, Appl
686	107	5.6	479	4	US-09-723-368-2	Sequence 2, Appli	759	104.5	5.5	249	3	US-09-345-468-9	Sequence 9, Appli
687	107	5.6	479	4	US-09-949-016-6278	Sequence 6278, Ap	760	104.5	5.5	249	3	US-09-414-453A-9	Sequence 9, Appli
688	107	5.6	486	2	US-08-432-016-6	Sequence 6, Appli	761	104.5	5.5	264	4	US-08-467-602-265	Sequence 265, App
689	107	5.6	486	2	US-08-684-594-6	Sequence 6, Appli	762	104.5	5.5	264	4	US-08-411-295F-191	Sequence 191, App
690	107	5.6	522	4	US-09-949-016-7563	Sequence 7563, Ap	763	104.5	5.5	319	3	US-09-345-468-5	Sequence 5, Appli
691	106.5	5.6	349	4	US-09-924-103-4	Sequence 4, Appli	764	104.5	5.5	319	3	US-09-414-453A-5	Sequence 5, Appli
692	106.5	5.6	354	6	5169835-4	Patent No. 5169835	765	104.5	5.5	339	3	US-09-345-468-3	Sequence 3, Appli
693	106.5	5.6	354	6	5169835-4	Patent No. 5169835	766	104.5	5.5	339	3	US-09-414-453A-3	Sequence 3, Appli
694	106.5	5.6	389	4	US-08-467-602-213	Sequence 213, App	767	104.5	5.5	443	4	US-08-467-602-263	Sequence 263, App
695	106.5	5.6	389	4	US-08-411-295F-139	Sequence 139, App	768	104.5	5.5	443	4	US-08-411-295F-189	Sequence 189, App
696	106.5	5.6	606	4	US-08-467-602-214	Sequence 214, App	769	104.5	5.5	452	4	US-08-467-602-272	Sequence 272, App
697	106.5	5.6	606	4	US-08-411-295F-140	Sequence 140, App	770	104.5	5.5	452	4	US-08-411-295F-198	Sequence 198, App
698	106.5	5.6	653	4	US-08-467-602-212	Sequence 212, App	771	104.5	5.5	466	4	US-09-944-807-12	Sequence 12, Appl
699	106.5	5.6	653	4	US-08-411-295F-138	Sequence 138, App	772	104.5	5.5	466	4	US-09-949-016-6766	Sequence 6766, Ap
700	106.5	5.6	816	4	US-09-949-016-8119	Sequence 819, Ap	773	104.5	5.5	480	4	US-09-949-016-7272	Sequence 7272, Ap
701	106	5.6	283	4	US-09-904-615-106	Sequence 106, App	774	104.5	5.5	579	3	US-09-173-151A-2	Sequence 2, Appli
702	106	5.6	292	4	US-09-651-200-16	Sequence 16, Appl	775	104.5	5.5	609	4	US-09-949-016-7747	Sequence 7747, Ap
703	106	5.6	292	4	US-09-303-040-2	Sequence 2, Appli	776	104.5	5.5	609	4	US-09-949-016-7748	Sequence 7748, Ap
704	106	5.6	292	4	US-08-303-040-4	Sequence 4, Appli	777	104.5	5.5	609	4	US-09-949-016-7749	Sequence 7749, Ap
705	106	5.6	434	3	US-08-540-245A-19	Sequence 19, Appl	778	104.5	5.5	609	4	US-09-949-016-7750	Sequence 7750, Ap
706	105.5	5.5	457	1	US-08-416-478A-8	Sequence 8, Appli	779	104.5	5.5	609	4	US-09-949-016-7751	Sequence 7751, Ap
707	105.5	5.5	457	2	US-08-474-988B-8	Sequence 8, Appli	780	104.5	5.5	609	4	US-09-949-016-7752	Sequence 7752, Ap
708	105.5	5.5	457	2	US-08-394-442B-8	Sequence 8, Appli	781	104.5	5.5	609	4	US-09-949-016-7753	Sequence 7753, Ap
709	105.5	5.5	806	2	US-08-443-861-5	Sequence 5, Appli	782	104.5	5.5	609	4	US-09-949-016-7754	Sequence 7754, Ap
710	105.5	5.5	806	3	US-08-193-829B-5	Sequence 5, Appli	783	104.5	5.5	612	2	US-08-752-307B-11	Sequence 11, Appl
711	105.5	5.5	917	1	US-08-245-295-2	Sequence 2, Appli	784	104.5	5.5	612	2	US-09-707-802-11	Sequence 11, Appl
712	105.5	5.5	917	1	US-08-481-130-2	Sequence 2, Appli	785	104.5	5.5	612	3	US-09-991-326-11	Sequence 11, Appl
713	105.5	5.5	917	1	US-08-656-984A-2	Sequence 2, Appli	786	104.5	5.5	660	4	US-08-467-602-264	Sequence 264, App
714	105.5	5.5	917	1	US-08-485-604-2	Sequence 2, Appli	787	104.5	5.5	660	4	US-08-411-295F-190	Sequence 190, App
715	105.5	5.5	917	2	US-08-487-595-2	Sequence 2, Appli	788	104.5	5.5	669	4	US-08-467-602-273	Sequence 273, App
716	105.5	5.5	999	1	US-08-252-626A-2	Sequence 2, Appli	789	104.5	5.5	669	4	US-08-411-295F-199	Sequence 199, App
717	105.5	5.5	999	4	US-09-949-016-6718	Sequence 6718, Ap	790	104.5	5.5	686	3	US-09-173-151A-4	Sequence 4, Appli
718	105.5	5.5	1367	1	US-07-813-593-4	Sequence 4, Appli	791	104.5	5.5	707	4	US-08-467-602-262	Sequence 262, App
719	105.5	5.5	1367	1	US-07-977-451-6	Sequence 6, Appli	792	104.5	5.5	707	4	US-08-411-295F-188	Sequence 188, App
720	105.5	5.5	1367	1	US-07-946-507-4	Sequence 4, Appli	793	104.5	5.5	716	4	US-08-467-602-274	Sequence 274, App
721	105.5	5.5	1367	1	US-08-252-517-6	Sequence 6, Appli	794	104.5	5.5	716	4	US-08-411-295F-200	Sequence 200, App
722	105.5	5.5	1367	1	US-07-906-397A-6	Sequence 6, Appli	795	104.5	5.5	1268	3	US-08-506-296B-28	Sequence 28, Appl
723	105.5	5.5	1367	1	US-08-601-891-5	Sequence 6, Appli	796	104	5.5	212	3	US-08-702-525-63	Sequence 63, Appl
724	105.5	5.5	1367	2	US-08-443-861-2	Sequence 2, Appli	797	104	5.5	212	5	PCT-US95-02576-63	Sequence 63, Appl
725	105.5	5.5	1367	2	US-09-021-324-6	Sequence 2, Appli	798	104	5.5	226	5	US-08-702-525-65	Sequence 65, Appl
726	105.5	5.5	1367	3	US-08-193-829B-2	Sequence 2, Appli	799	104	5.5	226	5	PCT-US95-02576-65	Sequence 65, Appl
727	105.5	5.5	1367	4	US-08-872-136B-6	Sequence 6, Appli	800	104	5.5	227	4	US-09-305-258-947	Sequence 947, Appl
728	105.5	5.5	1367	5	PCT-US92-02750-8	Sequence 8, Appli	801	104	5.5	240	1	US-08-471-570-12	Sequence 12, Appl
729	105.5	5.5	1367	5	PCT-US92-05401-6	Sequence 6, Appli	802	104	5.5	270	3	US-09-430-503-26	Sequence 26, Appl
730	105.5	5.5	1367	5	PCT-US92-09893-6	Sequence 6, Appli	803	104	5.5	270	3	US-09-430-503-30	Sequence 30, Appl
731	105	5.5	210	4	US-08-467-602-215	Sequence 215, App	804	104	5.5	283	1	US-08-332-562A-136	Sequence 136, Appl
732	105	5.5	210	4	US-08-411-295F-141	Sequence 141, App	805	104	5.5	355	4	US-08-471-570-14	Sequence 14, Appl
733	105	5.5	277	4	US-09-354-151-3	Sequence 3, Appli	806	104	5.5	432	4	US-08-467-602-266	Sequence 266, App
734	105	5.5	323	4	US-09-651-200-21	Sequence 21, Appl	807	104	5.5	432	4	US-09-667-135-30	Sequence 30, Appl
735	105	5.5	323	4	US-09-441-411-22	Sequence 22, Appl	808	104	5.5	489	4	US-08-891-845-10	Sequence 10, Appl
736	105	5.5	323	5	PCT-US94-09642-2	Sequence 2, Appli	809	104	5.5	501	3	US-09-514-573-10	Sequence 10, Appl
737	105	5.5	329	2	US-08-456-104-2	Sequence 2, Appli	810	104	5.5	501	4	US-08-467-602-267	Sequence 267, App
738	105	5.5	329	2	US-08-101-624-2	Sequence 2, Appli	811	104	5.5	649	6	US-08-411-295F-193	Sequence 193, App
739	105	5.5	329	3	US-08-479-744A-2	Sequence 2, Appli	812	104	5.5	649	4	US-08-467-602-268	Sequence 268, App
740	105	5.5	329	3	US-08-280-757B-2	Sequence 2, Appli	813	104	5.5	696	4	US-08-467-602-268	Sequence 268, App
741	105	5.5	329	3	US-08-205-697A-23	Sequence 23, Appl	814	104	5.5	696	4	US-08-411-295F-194	Sequence 194, App
742	105	5.5	329	3	US-08-703-525-23	Sequence 23, Appl	815	104	5.5	768	4	US-08-891-845-2	Sequence 2, Appli
743	105	5.5	329	3	US-08-403-253A-4	Sequence 4, Appli	816	104	5.5	768	4	US-09-514-573-2	Sequence 2, Appli
744	105	5.5	329	4	US-08-435-816A-4	Sequence 4, Appli	817	103.5	5.4	192	2	US-08-867-680-2	Sequence 261, App
745	105	5.5	329	4	US-09-425-762-2	Sequence 2, Appli	818	103.5	5.4	241	4	US-08-467-602-261	Sequence 187, App
746	105	5.5	329	4	US-09-837-867A-23	Sequence 23, Appl	819	103.5	5.4	420	4	US-08-411-295F-187	Sequence 280, App
747	105	5.5	329	4	US-09-206-132-2	Sequence 2, Appli	820	103.5	5.4	420	4	US-08-411-295F-186	Sequence 186, App
748	105	5.5	329	4	US-09-441-411-26	Sequence 26, Appl	821	103.5	5.4	420	3	US-08-753-007A-9	Sequence 9, Appli
749	105	5.5	329	4	US-09-425-516-2	Sequence 2, Appli	822	103.5	5.4	422	4	US-09-398-496-9	Sequence 269, App
750	105	5.5	329	5	PCT-US95-02576-23	Sequence 23, Appl	823	103.5	5.4	429	4	US-08-467-602-269	Sequence 195, App
751	105	5.5	372	4	US-09-949-016-11132	Sequence 11132, A	824	103.5	5.4	429	4	US-08-411-295F-195	Sequence 258, App
752	105	5.5	1709	4	US-09-949-016-10503	Sequence 10503, A	825	103.5	5.4	637	4	US-08-467-602-258	Sequence 184, App
753	104.5	5.5	241	3	US-08-341-018-54	Sequence 54, Appl	826	103.5	5.4	637	4	US-08-411-295F-184	Sequence 10, Appl
754	104.5	5.5	241	3	US-08-470-335-195	Sequence 195, App	827	103.5	5.4	645	3	US-08-753-007A-10	Sequence 10, Appl
755	104.5	5.5	241	3	US-08-470-339-195	Sequence 195, App	828	103.5	5.4	645	3	US-09-398-496-10	Sequence 270, App
756	104.5	5.5	241	4	US-08-467-602-389	Sequence 389, App	829	103.5	5.4	646	4	US-08-467-602-270	
757	104.5	5.5	241	4	US-08-411-295F-47	Sequence 47, Appl	830	103.5	5.4				

831	103.5	5.4	646	4	US-08-411-295F-196	Sequence 196, App	904	102	5.3	281	4	US-09-310-367-10	Sequence 10, Appl
832	103.5	5.4	661	2	US-08-795-868-14	Sequence 14, Appl	905	102	5.3	281	4	US-09-032-337-10	Sequence 10, Appl
833	103.5	5.4	661	3	US-09-303-069-14	Sequence 14, Appl	906	102	5.3	281	4	US-09-464-231-10	Sequence 10, Appl
834	103.5	5.4	661	3	US-09-134-250-14	Sequence 14, Appl	907	102	5.3	286	4	US-09-270-767-44618	Sequence 44618, A
835	103.5	5.4	684	4	US-08-467-602-259	Sequence 259, App	908	102	5.3	321	3	US-09-361-434-17	Sequence 17, Appl
836	103.5	5.4	684	4	US-08-411-295F-185	Sequence 185, App	909	102	5.3	321	3	US-09-361-434-22	Sequence 22, Appl
837	103.5	5.4	693	4	US-08-467-602-271	Sequence 271, App	910	102	5.3	321	3	US-09-635-025-12	Sequence 22, Appl
838	103.5	5.4	693	4	US-08-411-295F-197	Sequence 197, App	911	102	5.3	321	3	US-09-635-025-12	Sequence 22, Appl
839	103.5	5.4	805	3	US-08-985-526-34	Sequence 34, Appl	912	102	5.3	329	4	US-09-667-135-32	Sequence 32, Appl
840	103.5	5.4	1447	3	US-09-041-886-25	Sequence 25, Appl	913	102	5.3	332	4	US-09-870-521-3	Sequence 3, Appl
841	103.5	5.4	1447	5	PCT-US94-05277-2	Sequence 2, Appl	914	102	5.3	388	3	US-09-188-930-275	Sequence 275, App
842	103	5.4	524	4	US-09-270-767-44009	Sequence 44009, A	915	102	5.3	388	4	US-09-312-283C-275	Sequence 275, App
843	103	5.4	558	4	US-09-667-135-31	Sequence 31, Appl	916	102	5.3	398	4	US-08-467-602-224	Sequence 224, App
844	103	5.4	645	1	US-07-847-743B-27	Sequence 27, Appl	917	102	5.3	398	4	US-08-411-295F-150	Sequence 150, App
845	103	5.4	645	1	US-08-456-201-27	Sequence 27, Appl	918	102	5.3	615	4	US-08-467-602-225	Sequence 225, App
846	103	5.4	645	1	US-08-428-926-4	Sequence 4, Appl	919	102	5.3	615	4	US-08-411-295F-151	Sequence 151, App
847	103	5.4	645	1	US-08-428-926-4	Sequence 4, Appl	920	102	5.3	662	4	US-08-467-602-226	Sequence 226, App
848	103	5.4	645	1	US-08-428-298-4	Sequence 4, Appl	921	102	5.3	662	4	US-08-411-295F-152	Sequence 152, App
849	103	5.4	645	1	US-08-339-517-4	Sequence 4, Appl	922	101.5	5.3	207	4	US-08-467-602-219	Sequence 219, App
850	103	5.4	645	2	US-08-456-241-27	Sequence 27, Appl	923	101.5	5.3	207	4	US-08-411-295F-145	Sequence 145, App
851	103	5.4	645	3	US-09-020-880-93	Sequence 93, Appl	924	101.5	5.3	226	4	US-09-311-784A-32	Sequence 32, Appl
852	103	5.4	645	3	US-09-101-544-93	Sequence 93, Appl	925	101.5	5.3	232	4	US-09-949-016-7589	Sequence 7589, Ap
853	103	5.4	645	4	US-09-097-681-3	Sequence 3, Appl	926	101.5	5.3	232	4	US-09-949-016-7590	Sequence 7590, Ap
854	103	5.4	645	5	PCT-US92-04295A-27	Sequence 27, Appl	927	101.5	5.3	386	4	US-08-467-602-218	Sequence 218, App
855	102.5	5.4	230	4	US-08-467-602-223	Sequence 223, App	928	101.5	5.3	386	4	US-08-411-295F-144	Sequence 144, App
856	102.5	5.4	230	4	US-08-411-295F-149	Sequence 149, App	929	101.5	5.3	603	4	US-08-467-602-216	Sequence 216, App
857	102.5	5.4	241	1	US-07-847-743B-30	Sequence 30, Appl	930	101.5	5.3	603	4	US-08-411-295F-142	Sequence 142, App
858	102.5	5.4	241	1	US-08-456-201-30	Sequence 30, Appl	931	101.5	5.3	650	4	US-08-467-602-217	Sequence 217, App
859	102.5	5.4	241	2	US-08-456-241-30	Sequence 30, Appl	932	101.5	5.3	650	4	US-08-411-295F-143	Sequence 143, App
860	102.5	5.4	241	5	PCT-US92-04295A-30	Sequence 30, Appl	933	101	5.3	1187	1	US-08-320-559-28	Sequence 28, Appl
861	102.5	5.4	309	4	US-09-667-135-6	Sequence 6, Appl	934	101	5.3	1187	5	US-08-545-860D-28	Sequence 28, Appl
862	102.5	5.4	309	4	US-09-910-174B-7	Sequence 7, Appl	935	101	5.3	1187	5	PCT-US94-04496-28	Sequence 28, Appl
863	102.5	5.4	309	4	US-09-620-461-7	Sequence 7, Appl	936	101	5.3	1210	3	US-08-320-559-26	Sequence 26, Appl
864	102.5	5.4	318	2	US-08-633-148-4	Sequence 4, Appl	937	101	5.3	1210	3	US-08-545-860D-26	Sequence 26, Appl
865	102.5	5.4	324	4	US-09-910-174B-6	Sequence 6, Appl	938	101	5.3	1210	5	US-09-538-092-1179	Sequence 1179, Ap
866	102.5	5.4	324	4	US-09-620-461-6	Sequence 6, Appl	939	101	5.3	1210	5	PCT-US94-04496-26	Sequence 26, Appl
867	102.5	5.4	325	4	US-09-651-200-20	Sequence 20, Appl	940	101	5.3	1212	1	US-08-072-574-10	Sequence 10, Appl
868	102.5	5.4	340	2	US-08-633-148-2	Sequence 2, Appl	941	101	5.3	1253	3	US-08-506-296B-14	Sequence 14, Appl
869	102.5	5.4	395	4	US-08-467-602-227	Sequence 227, App	942	100.5	5.3	313	4	US-09-701-623C-3	Sequence 3, Appl
870	102.5	5.4	395	4	US-08-411-295F-153	Sequence 153, App	943	100.5	5.3	351	1	US-09-756-983-18	Sequence 18, Appl
871	102.5	5.4	409	4	US-08-467-602-221	Sequence 221, App	944	100.5	5.3	718	3	US-08-190-802A-44	Sequence 44, Appl
872	102.5	5.4	409	4	US-08-411-295F-147	Sequence 147, App	945	100.5	5.3	718	3	US-08-477-346-44	Sequence 44, Appl
873	102.5	5.4	418	4	US-08-467-602-230	Sequence 230, App	946	100.5	5.3	718	3	US-08-473-089-44	Sequence 44, Appl
874	102.5	5.4	418	4	US-08-411-295F-156	Sequence 156, App	947	100.5	5.3	718	3	US-08-487-072A-44	Sequence 44, Appl
875	102.5	5.4	420	1	US-07-847-743B-29	Sequence 29, Appl	948	100.5	5.3	1391	4	US-10-080-505-11	Sequence 11, Appl
876	102.5	5.4	420	1	US-08-456-201-29	Sequence 29, Appl	949	100.5	5.3	1391	4	US-10-080-505-15	Sequence 15, Appl
877	102.5	5.4	420	2	US-08-456-241-29	Sequence 28, Appl	950	100.5	5.3	1474	4	US-09-677-046A-4	Sequence 4, Appl
878	102.5	5.4	420	5	PCT-US92-04295A-29	Sequence 29, Appl	951	100.5	5.3	1503	4	US-09-677-046A-6	Sequence 6, Appl
879	102.5	5.4	612	4	US-08-467-602-228	Sequence 228, App	952	100.5	5.3	1509	4	US-09-677-046A-2	Sequence 2, Appl
880	102.5	5.4	612	4	US-08-411-295F-154	Sequence 154, App	953	100	5.2	337	4	US-09-248-796A-15931	Sequence 15931, A
881	102.5	5.4	626	4	US-08-467-602-222	Sequence 222, App	954	100	5.2	424	6	5169835-6	Patent No. 5169835
882	102.5	5.4	626	4	US-08-411-295F-148	Sequence 148, App	955	100	5.2	424	6	5169835-6	Patent No. 5169835
883	102.5	5.4	635	4	US-08-467-602-231	Sequence 231, App	956	100	5.2	547	1	US-08-314-615-1	Sequence 1, Appl
884	102.5	5.4	635	4	US-08-411-295F-157	Sequence 157, App	957	100	5.2	547	1	US-08-314-362-1	Sequence 1, Appl
885	102.5	5.4	637	1	US-07-847-743B-28	Sequence 28, Appl	958	100	5.2	547	1	US-08-433-010-1	Sequence 1, Appl
886	102.5	5.4	637	1	US-08-456-201-28	Sequence 28, Appl	959	100	5.2	547	2	US-08-482-882-1	Sequence 1, Appl
887	102.5	5.4	637	2	US-08-456-241-28	Sequence 28, Appl	960	100	5.2	547	2	US-08-483-389-1	Sequence 1, Appl
888	102.5	5.4	637	5	PCT-US92-04295A-28	Sequence 28, Appl	961	100	5.2	547	2	US-08-487-113D-1	Sequence 1, Appl
889	102.5	5.4	659	4	US-08-467-602-229	Sequence 229, App	962	100	5.2	547	2	US-08-473-503-1	Sequence 1, Appl
890	102.5	5.4	659	4	US-08-411-295F-155	Sequence 155, App	963	100	5.2	547	2	US-08-483-932-1	Sequence 1, Appl
891	102.5	5.4	673	4	US-08-467-602-220	Sequence 220, App	964	100	5.2	547	2	US-08-720-420A-1	Sequence 1, Appl
892	102.5	5.4	673	4	US-08-411-295F-146	Sequence 146, App	965	100	5.2	547	3	US-08-714-017-1	Sequence 1, Appl
893	102.5	5.4	682	4	US-08-467-602-232	Sequence 232, App	966	100	5.2	547	3	US-08-863-790-1	Sequence 1, Appl
894	102.5	5.4	682	4	US-08-411-295F-158	Sequence 158, App	967	100	5.2	547	3	US-08-475-680-1	Sequence 1, Appl
895	102	5.3	176	4	US-09-270-767-59418	Sequence 59418, A	968	100	5.2	547	3	US-08-296-749-1	Sequence 1, Appl
896	102	5.3	270	3	US-08-430-503-28	Sequence 28, Appl	969	100	5.2	547	4	US-08-314-369-1	Sequence 1, Appl
897	102	5.3	270	3	US-09-430-503-32	Sequence 32, Appl	970	100	5.2	598	3	US-09-310-463-10	Sequence 10, Appl
898	102	5.3	281	1	US-08-487-748A-9	Sequence 9, Appl	971	100	5.2	598	4	US-08-842-248A-10	Sequence 10, Appl
899	102	5.3	281	1	US-08-487-748A-10	Sequence 10, Appl	972	100	5.2	615	3	US-08-985-950-16	Sequence 16, Appl
900	102	5.3	281	3	US-08-487-748A-10	Sequence 10, Appl	973	100	5.2	615	3	US-08-985-950-18	Sequence 18, Appl
901	102	5.3	281	3	US-08-480-070C-10	Sequence 10, Appl	974	100	5.2	615	4	US-09-546-049-16	Sequence 16, Appl
902	102	5.3	281	3	US-08-829-525-10	Sequence 10, Appl	975	100	5.2	615	4	US-09-546-049-16	Sequence 16, Appl
903	102	5.3	281	3	US-08-609-583A-10	Sequence 10, Appl	976	100	5.2	622	4	US-09-499-846-2	Sequence 2, Appl

977	100	5.2	643	5	PCT-US93-00031-19	Sequence 19, Appl	1050	96	5.0	769	3	US-09-312-157-10	Sequence 10, Appl
978	100	5.2	644	5	PCT-US93-00031-21	Sequence 21, Appl	1051	96	5.0	769	4	US-09-717-888-10	Sequence 10, Appl
979	100	5.2	647	3	US-09-009-490A-91	Sequence 91, Appl	1052	96	5.0	1180	1	US-08-486-270-8	Sequence 8, Appl
980	100	5.2	647	3	US-08-482-073-5	Sequence 5, Appl	1053	96	5.0	1180	3	US-08-367-264-8	Sequence 8, Appl
981	100	5.2	647	5	PCT-US93-00031-11	Sequence 11, Appl	1054	96	5.0	1180	3	US-08-660-148-2	Sequence 2, Appl
982	100	5.2	647	5	PCT-US93-00031-23	Sequence 23, Appl	1055	96	5.0	1180	4	US-09-153-757-8	Sequence 8, Appl
983	99.5	5.2	256	4	US-09-248-796A-14185	Sequence 14185, A	1056	96	5.0	1180	4	US-09-459-715-8	Sequence 8, Appl
984	99.5	5.2	322	4	US-09-667-135-2	Sequence 2, Appl	1057	95.5	5.0	94	3	US-08-928-383B-21	Sequence 21, Appl
985	99.5	5.2	322	4	US-09-910-174B-29	Sequence 29, Appl	1058	95.5	5.0	108	4	US-09-663-600A-191	Sequence 191, Appl
986	99.5	5.2	322	4	US-09-620-461-29	Sequence 29, Appl	1059	95.5	5.0	269	3	US-09-430-503-2	Sequence 2, Appl
987	99.5	5.2	347	4	US-09-667-135-4	Sequence 4, Appl	1060	95.5	5.0	269	3	US-09-430-503-4	Sequence 4, Appl
988	99.5	5.2	421	2	US-08-659-984A-1	Sequence 1, Appl	1061	95.5	5.0	269	3	US-09-430-503-6	Sequence 6, Appl
989	99.5	5.2	421	3	US-08-660-531-1	Sequence 1, Appl	1062	95.5	5.0	269	3	US-09-430-503-8	Sequence 8, Appl
990	99.5	5.2	444	2	US-08-659-984A-5	Sequence 5, Appl	1063	95.5	5.0	431	3	US-08-985-950-14	Sequence 14, Appl
991	99.5	5.2	444	3	US-08-660-531-5	Sequence 5, Appl	1064	95.5	5.0	431	3	US-08-985-950-20	Sequence 20, Appl
992	99.5	5.2	891	4	US-09-345-473B-25	Sequence 25, Appl	1065	95.5	5.0	431	4	US-09-546-049-14	Sequence 14, Appl
993	99	5.2	408	3	US-09-724-864-62	Sequence 62, Appl	1066	95.5	5.0	431	4	US-09-546-049-20	Sequence 20, Appl
994	99	5.2	419	6	5169835-2	Patent No. 5169835	1067	95.5	5.0	451	1	US-08-287-001A-2	Sequence 2, Appl
995	99	5.2	419	6	5169835-2	Patent No. 5169835	1068	95.5	5.0	451	5	PCT-US95-09941-2	Sequence 2, Appl
996	99	5.2	771	3	US-08-434-000A-8	Sequence 8, Appl	1069	95.5	5.0	583	2	US-08-432-016-2	Sequence 2, Appl
997	99	5.2	771	3	US-09-312-157-8	Sequence 8, Appl	1070	95.5	5.0	583	2	US-08-684-594-2	Sequence 2, Appl
998	99	5.2	771	3	US-09-717-888-8	Sequence 8, Appl	1071	95.5	5.0	640	4	US-09-949-016-7565	Sequence 9, Appl
999	99	5.2	1180	1	US-08-072-574-8	Sequence 8, Appl	1072	95	5.0	101	3	US-08-928-383B-9	Sequence 9, Appl
1000	98.5	5.2	290	4	US-09-910-174B-32	Sequence 32, Appl	1073	95	5.0	247	5	US-09-949-016-6225	Sequence 5, Appl
1001	98.5	5.2	290	4	US-09-451-291-3	Sequence 3, Appl	1074	95	5.0	247	5	PCT-US94-10257A-2	Sequence 2, Appl
1002	98.5	5.2	290	4	US-09-645-069-23	Sequence 23, Appl	1075	95	5.0	260	4	US-09-349-016-8243	Sequence 4, Appl
1003	98.5	5.2	290	4	US-08-752-307B-10	Sequence 10, Appl	1076	95	5.0	318	6	5223394-11	Sequence 11, Appl
1004	98.5	5.2	611	2	US-09-707-802-10	Sequence 10, Appl	1077	95	5.0	318	6	5223394-11	Sequence 11, Appl
1005	98.5	5.2	611	3	US-09-991-326-10	Sequence 10, Appl	1078	95	5.0	471	4	US-09-270-767-43916	Sequence 43916, A
1006	98	5.1	329	4	US-09-651-200-18	Sequence 18, Appl	1079	95	5.0	668	3	US-09-173-151A-35	Sequence 35, Appl
1007	98	5.1	329	4	US-09-303-040-6	Sequence 6, Appl	1080	95	5.0	828	1	US-08-261-304-2	Sequence 2, Appl
1008	98	5.1	351	5	PCT-US93-05703-2	Sequence 2, Appl	1081	95	5.0	906	4	US-09-417-039-11	Sequence 11, Appl
1009	98	5.1	488	4	US-09-499-846-12	Sequence 12, Appl	1082	95	5.0	1090	4	US-09-866-510-14	Sequence 14, Appl
1010	98	5.1	497	4	US-09-499-846-6	Sequence 6, Appl	1083	95	5.0	1106	1	US-08-180-195-2	Sequence 2, Appl
1011	98	5.1	497	4	US-09-499-846-10	Sequence 10, Appl	1084	95	5.0	1106	1	US-08-168-917-2	Sequence 2, Appl
1012	98	5.1	518	3	US-09-240-915-8	Sequence 8, Appl	1085	95	5.0	1106	1	US-08-477-329-2	Sequence 2, Appl
1013	98	5.1	518	3	US-09-591-435-8	Sequence 8, Appl	1086	95	5.0	1106	2	US-08-475-458-2	Sequence 2, Appl
1014	98	5.1	525	4	US-09-493-846-4	Sequence 4, Appl	1087	95	5.0	1106	2	US-08-460-510-2	Sequence 2, Appl
1015	98	5.1	525	4	US-09-493-846-8	Sequence 8, Appl	1088	95	5.0	1106	2	US-08-460-490-2	Sequence 2, Appl
1016	98	5.1	547	1	US-08-473-981A-6	Sequence 6, Appl	1089	95	5.0	1106	3	US-08-980-400-2	Sequence 2, Appl
1017	98	5.1	547	2	US-08-473-981A-6	Sequence 6, Appl	1090	95	5.0	1106	3	US-08-462-728-4	Sequence 2, Appl
1018	98	5.1	1212	1	US-08-486-270-10	Sequence 10, Appl	1091	95	5.0	1106	3	US-09-583-459A-2	Sequence 2, Appl
1019	98	5.1	1212	3	US-08-367-264-10	Sequence 10, Appl	1092	95	5.0	1106	3	US-09-583-210-2	Sequence 2, Appl
1020	98	5.1	1212	3	US-08-660-148-5	Sequence 5, Appl	1093	95	5.0	1106	3	US-09-583-449A-2	Sequence 2, Appl
1021	98	5.1	1212	4	US-09-153-757-10	Sequence 10, Appl	1094	95	5.0	1106	3	US-09-435-059-2	Sequence 2, Appl
1022	98	5.1	1212	4	US-09-459-715-10	Sequence 10, Appl	1095	95	5.0	1106	3	US-08-461-917-4	Sequence 4, Appl
1023	98	5.1	1212	4	US-09-695-481-7	Sequence 7, Appl	1096	95	5.0	1106	4	US-08-464-436-4	Sequence 4, Appl
1024	97.5	5.1	281	4	US-09-949-016-8447	Sequence 83, Appl	1097	95	5.0	1106	4	US-08-464-436-4	Sequence 4, Appl
1025	97.5	5.1	306	4	US-09-369-247-63	Sequence 83, Appl	1098	95	5.0	1106	4	US-09-866-510-18	Sequence 18, Appl
1026	97.5	5.1	307	2	US-08-332-562A-83	Sequence 83, Appl	1099	95	5.0	1106	4	US-09-866-510-20	Sequence 20, Appl
1027	97.5	5.1	313	4	US-09-949-016-10974	Sequence 7014, A	1100	95	5.0	1106	4	US-09-866-510-22	Sequence 22, Appl
1028	97.5	5.1	313	4	US-09-949-016-10974	Sequence 7014, A	1101	95	5.0	1106	5	PCT-US92-00730-2	Sequence 2, Appl
1029	97.5	5.1	315	4	US-09-949-016-10974	Sequence 7014, A	1102	95	5.0	1106	5	PCT-US92-00862-2	Sequence 2, Appl
1030	97.5	5.1	369	4	US-09-906-779-5	Sequence 5, Appl	1103	94.5	5.0	215	4	US-09-949-016-6658	Sequence 6658, A
1031	97.5	5.1	466	2	US-08-432-016-4	Sequence 5, Appl	1104	94.5	5.0	263	4	US-09-949-016-10819	Sequence 10819, A
1032	97.5	5.1	466	2	US-08-684-594-4	Sequence 4, Appl	1105	94.5	5.0	267	3	US-09-345-468-19	Sequence 19, Appl
1033	97.5	5.1	793	1	US-08-188-328-54	Sequence 4, Appl	1106	94.5	5.0	267	3	US-09-414-453A-19	Sequence 19, Appl
1034	97.5	5.1	793	1	US-08-332-643-48	Sequence 54, Appl	1107	94.5	5.0	282	4	US-09-404-879A-393	Sequence 393, Appl
1035	97.5	5.1	793	1	US-08-332-638-54	Sequence 48, Appl	1108	94.5	5.0	282	4	US-09-667-857-393	Sequence 393, Appl
1036	97	5.1	976	3	US-08-750-141A-1	Sequence 1, Appl	1109	94.5	5.0	292	3	US-09-345-468-18	Sequence 18, Appl
1037	97	5.1	232	3	US-09-361-434-7	Sequence 7, Appl	1110	94.5	5.0	292	3	US-09-414-453A-18	Sequence 18, Appl
1038	97	5.1	288	1	US-09-635-025-7	Sequence 1, Appl	1111	94.5	5.0	299	4	US-09-651-200-15	Sequence 15, Appl
1039	97	5.1	288	1	US-08-768-626-1	Sequence 1, Appl	1112	94.5	5.0	309	4	US-09-667-857-392	Sequence 392, Appl
1040	97	5.1	288	4	US-09-645-069-12	Sequence 12, Appl	1113	94.5	5.0	309	4	US-09-667-857-392	Sequence 392, Appl
1041	97	5.1	492	3	US-08-462-794-11	Sequence 11, Appl	1114	94.5	5.0	313	3	US-09-345-468-16	Sequence 16, Appl
1042	97	5.1	715	4	US-09-949-016-7423	Sequence 7423, A	1115	94.5	5.0	313	3	US-09-414-453A-16	Sequence 16, Appl
1043	96.5	5.1	261	4	US-09-270-767-32898	Sequence 32898, A	1116	94.5	5.0	329	5	PCT-US95-04353-3	Sequence 3, Appl
1044	96.5	5.1	261	4	US-09-270-767-32898	Sequence 32898, A	1117	94.5	5.0	582	4	US-09-702-705-334	Sequence 334, Appl
1045	96.5	5.1	340	3	US-09-188-930-184	Sequence 184, Appl	1118	94.5	5.0	582	4	US-09-736-457-334	Sequence 334, Appl
1046	96.5	5.1	340	3	US-09-312-283C-184	Sequence 184, Appl	1119	94.5	5.0	582	4	US-09-614-124B-334	Sequence 334, Appl
1047	96.5	5.1	613	4	US-09-949-016-7353	Sequence 7353, A	1120	94.5	5.0	582	4	US-09-671-325-334	Sequence 334, Appl
1048	96.5	5.1	613	4	US-09-949-016-7353	Sequence 7353, A	1121	94.5	5.0	582	4	US-09-671-325-334	Sequence 334, Appl
1049	96	5.0	769	3	US-08-434-000A-10	Sequence 10, Appl	1122	94.5	5.0	582	4	US-09-589-184-334	Sequence 334, Appl

1123	94.5	5.0	582	4	US-09-658-824-334	Sequence 334, App	1196	92	4.8	310	4	US-09-949-016-8501	Sequence 8501, Ap
1124	94.5	5.0	604	4	US-09-949-016-9548	Sequence 9548, Ap	1197	92	4.8	310	4	US-09-949-016-8896	Sequence 8896, Ap
1125	94.5	5.0	954	4	US-09-949-016-6147	Sequence 6147, Ap	1198	92	4.8	322	3	US-09-383-586-33	Sequence 33, Appl
1126	94.5	5.0	961	4	US-09-949-016-7230	Sequence 7230, Ap	1199	92	4.8	322	4	US-09-823-038A-33	Sequence 33, Appl
1127	94.5	5.0	1260	3	US-08-506-296B-21	Sequence 21, Appl	1200	92	4.8	328	1	US-08-225-477B-5	Sequence 5, Appl
1128	94	4.9	272	4	US-09-270-767-36013	Sequence 36013, A	1201	92	4.8	328	5	PCT-US95-04353-5	Sequence 5, Appl
1129	94	4.9	272	4	US-09-270-767-36013	Sequence 36013, A	1202	92	4.8	328	5	PCT-US95-04353-5	Sequence 5, Appl
1130	94	4.9	529	4	US-09-949-016-6204	Sequence 6204, A	1203	92	4.8	366	4	US-09-311-021-84	Sequence 84, Appl
1131	94	4.9	898	2	US-08-808-982-5	Sequence 5, Appl	1204	92	4.8	366	4	US-09-010-147B-20	Sequence 20, Appl
1132	94	4.9	898	2	US-08-808-982-5	Sequence 5, Appl	1205	92	4.8	703	4	US-10-116-326-6	Sequence 6, Appl
1133	93.5	4.9	96	3	US-08-478-208-4	Sequence 4, Appl	1206	92	4.8	762	4	US-10-116-326-6	Sequence 2, Appl
1134	93.5	4.9	96	3	US-08-478-208-4	Sequence 4, Appl	1207	92	4.8	778	4	US-10-116-326-2	Sequence 2, Appl
1135	93.5	4.9	256	4	US-09-949-016-7326	Sequence 7326, Ap	1208	92	4.8	778	4	US-10-003-690-2	Sequence 2, Appl
1136	93.5	4.9	355	2	US-08-450-555-2	Sequence 2, Appl	1209	92	4.8	904	4	US-09-976-594-615	Sequence 615, App
1137	93.5	4.9	2842	1	US-07-741-940-7	Sequence 7, Appl	1210	92	4.8	2409	6	5180808-2	Patent No. 5180808
1138	93.5	4.9	2842	1	US-08-289-548A-7	Sequence 7, Appl	1211	91.5	4.8	59	2	US-08-414-657D-52	Sequence 52, Appl
1139	93.5	4.9	2842	1	US-08-452-654-7	Sequence 7, Appl	1212	91.5	4.8	59	2	US-08-414-657D-53	Sequence 53, Appl
1140	93.5	4.9	2842	4	US-08-449-711-7	Sequence 7, Appl	1213	91.5	4.8	157	1	US-08-494-577-4	Sequence 4, Appl
1141	93.5	4.9	2843	1	US-07-741-940-2	Sequence 2, Appl	1214	91.5	4.8	157	1	US-08-494-577-5	Sequence 5, Appl
1142	93.5	4.9	2843	1	US-08-289-548A-2	Sequence 2, Appl	1215	91.5	4.8	157	2	US-08-795-868-4	Sequence 4, Appl
1143	93.5	4.9	2843	1	US-08-452-654-2	Sequence 2, Appl	1216	91.5	4.8	157	2	US-08-795-868-5	Sequence 5, Appl
1144	93.5	4.9	2843	1	US-08-452-655B-2	Sequence 2, Appl	1217	91.5	4.8	157	3	US-09-303-069-5	Sequence 5, Appl
1145	93.5	4.9	2843	1	US-08-452-655B-7	Sequence 7, Appl	1218	91.5	4.8	157	3	US-09-134-250-5	Sequence 5, Appl
1146	93.5	4.9	2843	2	US-08-370-235A-2	Sequence 2, Appl	1219	91.5	4.8	380	4	US-09-877-730-4	Sequence 4, Appl
1147	93.5	4.9	2843	3	US-08-450-582-2	Sequence 2, Appl	1220	91.5	4.8	439	3	US-08-985-950-12	Sequence 12, Appl
1148	93.5	4.9	2843	3	US-08-450-582-7	Sequence 7, Appl	1221	91.5	4.8	439	3	US-09-310-463-8	Sequence 8, Appl
1149	93.5	4.9	2843	4	US-08-449-731-2	Sequence 2, Appl	1222	91.5	4.8	439	4	US-08-842-248A-8	Sequence 8, Appl
1150	93.5	4.9	2843	4	US-10-092-138A-30	Sequence 30, Appl	1223	91.5	4.8	439	4	US-09-546-049-12	Sequence 12, Appl
1151	93.5	4.9	2843	4	US-09-538-092-1007	Sequence 1007, Ap	1224	91.5	4.8	777	2	US-08-874-678-3	Sequence 3, Appl
1152	93.5	4.9	2973	2	US-08-821-355A-7	Sequence 7, Appl	1225	91.5	4.8	777	3	US-08-643-839-3	Sequence 3, Appl
1153	93.5	4.9	2973	3	US-09-003-687A-7	Sequence 7, Appl	1226	91.5	4.8	777	3	US-09-348-886-3	Sequence 3, Appl
1154	93.5	4.9	2973	3	US-09-136-605-7	Sequence 7, Appl	1227	91.5	4.8	830	4	US-09-562-737-35	Sequence 35, Appl
1155	93	4.9	329	1	US-08-348-792-12	Sequence 12, Appl	1228	91.5	4.8	904	4	US-09-877-730-6	Sequence 6, Appl
1156	93	4.9	329	2	US-08-462-738-12	Sequence 12, Appl	1229	91.5	4.8	985	4	US-09-877-730-10	Sequence 10, Appl
1157	93	4.9	329	3	US-09-199-955-12	Sequence 12, Appl	1230	91.5	4.8	1069	4	US-09-877-730-2	Sequence 2, Appl
1158	93	4.9	329	3	US-08-880-875-12	Sequence 12, Appl	1231	91.5	4.8	1150	4	US-09-877-730-8	Sequence 8, Appl
1159	93	4.9	343	1	US-08-348-792-10	Sequence 10, Appl	1232	91	4.8	361	4	US-09-270-767-45128	Sequence 45128, A
1160	93	4.9	343	2	US-08-462-738-10	Sequence 10, Appl	1233	91	4.8	371	4	US-08-411-295F-308	Sequence 308, App
1161	93	4.9	343	3	US-09-199-955-10	Sequence 10, Appl	1234	91	4.8	405	4	US-08-467-602-384	Sequence 384, App
1162	93	4.9	343	3	US-08-880-875-10	Sequence 10, Appl	1235	91	4.8	405	4	US-08-411-295F-307	Sequence 307, App
1163	93	4.9	462	2	US-08-752-307B-7	Sequence 7, Appl	1236	91	4.8	624	2	US-08-642-406A-22	Sequence 22, Appl
1164	93	4.9	462	3	US-09-707-802-7	Sequence 7, Appl	1237	91	4.8	624	3	US-09-199-534-22	Sequence 22, Appl
1165	93	4.9	462	3	US-09-991-326-7	Sequence 7, Appl	1238	91	4.8	624	3	US-09-199-534-22	Sequence 22, Appl
1166	93	4.9	465	2	US-08-752-307B-5	Sequence 5, Appl	1239	91	4.8	709	4	US-09-541-094-14	Sequence 14, Appl
1167	93	4.9	465	3	US-09-707-802-5	Sequence 5, Appl	1240	91	4.8	1106	4	US-09-866-510-16	Sequence 16, Appl
1168	93	4.9	465	3	US-09-991-326-5	Sequence 5, Appl	1241	90.5	4.7	218	4	US-09-451-291-12	Sequence 12, Appl
1169	93	4.9	477	2	US-08-432-016-3	Sequence 3, Appl	1242	90.5	4.7	262	1	US-08-403-379A-1	Sequence 1, Appl
1170	93	4.9	477	2	US-08-684-594-3	Sequence 3, Appl	1243	90.5	4.7	262	2	US-08-929-414-1	Sequence 1, Appl
1171	93	4.9	624	4	US-09-270-767-42659	Sequence 42659, A	1244	90.5	4.7	262	2	US-08-557-309B-51	Sequence 51, Appl
1172	93	4.9	773	3	US-08-434-000A-2	Sequence 2, Appl	1245	90.5	4.7	263	3	US-08-834-306-51	Sequence 51, Appl
1173	93	4.9	773	3	US-09-312-157-2	Sequence 2, Appl	1246	90.5	4.7	263	3	US-08-993-674A-51	Sequence 51, Appl
1174	93	4.9	773	4	US-09-717-888-2	Sequence 2, Appl	1247	90.5	4.7	263	4	US-09-256-976-51	Sequence 51, Appl
1175	93	4.9	799	1	US-08-198-228-42	Sequence 42, Appl	1248	90.5	4.7	334	4	US-09-197-970B-7	Sequence 7, Appl
1176	93	4.9	799	1	US-08-332-638-42	Sequence 42, Appl	1249	90.5	4.7	335	1	US-08-348-792-2	Sequence 2, Appl
1177	93	4.9	915	4	US-09-538-092-63	Sequence 63, Appl	1250	90.5	4.7	335	2	US-08-462-738-2	Sequence 2, Appl
1178	92.5	4.8	192	4	US-09-545-216A-5	Sequence 5, Appl	1251	90.5	4.7	335	3	US-09-199-955-2	Sequence 2, Appl
1179	92.5	4.8	222	4	US-09-545-216A-6	Sequence 6, Appl	1252	90.5	4.7	335	3	US-08-880-875-2	Sequence 2, Appl
1180	92.5	4.8	326	4	US-09-545-216A-6	Sequence 6, Appl	1253	90.5	4.7	335	3	US-09-369-248A-3	Sequence 3, Appl
1181	92.5	4.8	828	4	US-10-092-138A-26	Sequence 26, Appl	1254	90.5	4.7	1565	6	5352450-2	Patent No. 5352450
1182	92.5	4.8	829	1	US-07-670-611-2	Sequence 2, Appl	1255	90.5	4.7	1565	6	5352450-2	Patent No. 5352450
1183	92.5	4.8	829	1	US-08-220-674-2	Sequence 2, Appl	1256	90	4.7	358	4	5223418-2	Patent No. 5223418
1184	92.5	4.8	829	1	US-08-445-186-2	Sequence 2, Appl	1257	90	4.7	394	6	5223418-2	Patent No. 5223418
1185	92.5	4.8	829	1	US-08-445-186-2	Sequence 2, Appl	1258	90	4.7	394	6	5223418-2	Patent No. 5223418
1186	92.5	4.8	829	2	US-08-446-550-2	Sequence 2, Appl	1259	90	4.7	402	3	US-09-292-097-16	Sequence 16, Appl
1187	92	4.8	175	4	US-08-763-902B-6	Sequence 6, Appl	1260	90	4.7	402	4	US-09-933-561-16	Sequence 16, Appl
1188	92	4.8	199	2	US-08-768-964-12	Sequence 12, Appl	1261	90	4.7	464	2	US-09-949-016-6747	Sequence 6747, Ap
1189	92	4.8	199	3	US-09-005-299-12	Sequence 12, Appl	1262	90	4.7	464	2	US-08-602-725-32	Sequence 32, Appl
1190	92	4.8	199	3	US-09-515-431-12	Sequence 12, Appl	1263	90	4.7	464	4	US-09-949-016-6116	Sequence 6116, Ap
1191	92	4.8	218	3	US-09-068-655-7	Sequence 7, Appl	1264	90	4.7	464	4	US-09-949-016-7525	Sequence 7525, Ap
1192	92	4.8	263	2	US-08-768-964-2	Sequence 2, Appl	1265	90	4.7	556	4	US-09-538-092-712	Sequence 712, App
1193	92	4.8	263	3	US-09-005-299-2	Sequence 2, Appl	1266	90	4.7	890	1	US-08-445-640-2	Sequence 2, Appl
1194	92	4.8	263	3	US-09-515-431-2	Sequence 2, Appl	1267	90	4.7	890	3	US-08-170-558-2	Sequence 2, Appl
1195	92	4.8	288	4	US-09-949-016-6579	Sequence 6579, Ap	1268	90	4.7	890	3	US-08-447-314-2	Sequence 2, Appl

1269	90	4.7	890	3	US-08-445-461-2	Sequence 2, Appli	1342	88	4.6	425	3	US-08-470-335-226	Sequence 226, App
1270	90	4.7	890	4	US-09-223-490-2	Sequence 2, Appli	1343	88	4.6	425	4	US-08-467-602-320	Sequence 320, App
1271	90	4.7	911	1	US-08-286-305A-1	Sequence 1, Appli	1344	88	4.6	425	4	US-08-411-295F-246	Sequence 246, App
1272	90	4.7	911	2	US-08-441-104A-1	Sequence 1, Appli	1345	88	4.6	445	4	US-08-467-602-328	Sequence 328, App
1273	90	4.7	911	3	US-08-440-816A-1	Sequence 1, Appli	1346	88	4.6	445	4	US-08-411-295F-254	Sequence 254, App
1274	90	4.7	911	4	US-09-417-381A-1	Sequence 1, Appli	1347	88	4.6	456	4	US-08-467-602-366	Sequence 366, App
1275	90	4.7	1356	1	US-08-810-116-8	Sequence 8, Appli	1348	88	4.6	456	4	US-08-411-295F-292	Sequence 292, App
1276	90	4.7	1356	2	US-07-930-548A-8	Sequence 8, Appli	1349	88	4.6	459	4	US-08-467-602-362	Sequence 362, App
1277	90	4.7	1356	3	US-09-098-707A-2	Sequence 2, Appli	1350	88	4.6	459	4	US-08-411-295F-288	Sequence 288, App
1278	90	4.7	1356	4	US-09-483-533-2	Sequence 2, Appli	1351	88	4.6	479	4	US-08-467-602-370	Sequence 370, App
1279	90	4.7	1356	5	US-09-949-016-6198	Sequence 6198, Ap	1352	88	4.6	479	4	US-08-411-295F-296	Sequence 296, App
1280	90	4.7	1456	4	US-09-949-016-9853	Sequence 9853, Ap	1353	88	4.6	601	3	US-08-470-335-233	Sequence 233, App
1281	90	4.7	2090	4	US-09-538-092-1081	Sequence 1081, Ap	1354	88	4.6	601	4	US-08-411-295F-249	Sequence 249, App
1282	90	4.7	2120	4	US-09-949-016-9768	Sequence 9768, Ap	1355	88	4.6	601	4	US-08-467-602-323	Sequence 323, App
1283	89.5	4.7	199	3	US-09-430-503-48	Sequence 48, Appli	1356	88	4.6	604	3	US-08-411-295F-255	Sequence 255, App
1284	89.5	4.7	662	1	US-08-261-304-7	Sequence 7, Appli	1357	88	4.6	604	4	US-08-470-335-227	Sequence 227, App
1285	89.5	4.7	735	5	PCR-US93-00031-13	Sequence 13, Appl	1358	88	4.6	604	4	US-08-467-602-318	Sequence 318, App
1286	89.5	4.7	736	5	PCR-US93-00031-15	Sequence 15, Appl	1359	88	4.6	604	4	US-09-345-473B-17	Sequence 17, Appl
1287	89.5	4.7	739	3	US-08-482-073-6	Sequence 6, Appli	1360	88	4.6	604	4	US-08-411-295F-244	Sequence 244, App
1288	89.5	4.7	739	5	PCR-US93-00031-9	Sequence 9, Appli	1361	88	4.6	610	3	US-08-470-335-236	Sequence 236, App
1289	89.5	4.7	740	5	PCR-US93-00031-17	Sequence 17, Appl	1362	88	4.6	610	4	US-08-467-602-332	Sequence 332, App
1290	89.5	4.7	757	3	US-08-434-000A-6	Sequence 6, Appli	1363	88	4.6	613	3	US-08-411-295F-258	Sequence 258, App
1291	89.5	4.7	757	3	US-09-312-157-6	Sequence 6, Appli	1364	88	4.6	613	4	US-08-467-602-329	Sequence 329, App
1292	89.5	4.7	757	4	US-09-717-888-6	Sequence 6, Appli	1365	88	4.6	613	4	US-08-411-295F-255	Sequence 255, App
1293	89.5	4.7	2753	4	US-09-949-016-7659	Sequence 7659, Ap	1366	88	4.6	622	2	US-08-356-786-16	Sequence 16, Appl
1294	89.5	4.7	2753	4	US-09-949-016-7660	Sequence 7660, Ap	1367	88	4.6	624	4	US-08-467-602-326	Sequence 326, App
1295	89.5	4.7	3730	4	US-09-949-016-9908	Sequence 9908, Ap	1368	88	4.6	624	4	US-08-411-295F-232	Sequence 232, App
1296	89.5	4.7	3924	4	US-09-538-092-1246	Sequence 1246, Ap	1369	88	4.6	633	4	US-08-467-602-335	Sequence 335, App
1297	89	4.7	174	2	US-08-768-964-13	Sequence 13, Appl	1370	88	4.6	633	4	US-08-411-295F-261	Sequence 261, App
1298	89	4.7	174	3	US-09-005-299-13	Sequence 13, Appl	1371	88	4.6	635	4	US-08-467-602-365	Sequence 365, App
1299	89	4.7	174	3	US-09-515-431-13	Sequence 13, Appl	1372	88	4.6	635	4	US-08-411-295F-291	Sequence 291, App
1300	89	4.7	238	2	US-08-768-964-7	Sequence 7, Appli	1373	88	4.6	638	4	US-08-467-602-360	Sequence 360, App
1301	89	4.7	238	3	US-09-005-299-7	Sequence 7, Appli	1374	88	4.6	638	4	US-08-411-295F-286	Sequence 286, App
1302	89	4.7	238	3	US-09-515-431-7	Sequence 7, Appli	1375	88	4.6	644	4	US-08-467-602-374	Sequence 374, App
1303	89	4.7	525	4	US-09-107-532A-5095	Sequence 5095, Ap	1376	88	4.6	644	4	US-08-411-295F-300	Sequence 300, App
1304	89	4.7	626	4	US-09-248-796A-27023	Sequence 27023, A	1377	88	4.6	647	4	US-08-467-602-371	Sequence 371, App
1305	89	4.7	671	4	US-09-266-225D-16	Sequence 16, Appl	1378	88	4.6	647	4	US-08-411-295F-297	Sequence 297, App
1306	89	4.7	907	4	US-09-949-016-9750	Sequence 9750, Ap	1379	88	4.6	658	4	US-08-467-602-368	Sequence 368, App
1307	89	4.7	907	4	US-09-949-016-9751	Sequence 9751, Ap	1380	88	4.6	658	4	US-08-411-295F-294	Sequence 294, App
1308	89	4.7	1457	4	US-09-436-874-2	Sequence 2, Appli	1381	88	4.6	667	4	US-08-467-602-377	Sequence 377, App
1309	89	4.7	1457	4	US-09-713-273A-18	Sequence 18, Appl	1382	88	4.6	667	4	US-08-411-295F-303	Sequence 303, App
1310	88.5	4.6	199	3	US-08-430-503-44	Sequence 44, Appl	1383	88	4.6	667	4	US-08-470-335-234	Sequence 234, App
1311	88.5	4.6	298	1	US-08-348-792-4	Sequence 4, Appli	1384	88	4.6	818	3	US-08-411-295F-259	Sequence 259, App
1312	88.5	4.6	298	2	US-08-462-738-4	Sequence 4, Appli	1385	88	4.6	818	4	US-08-470-335-231	Sequence 231, App
1313	88.5	4.6	298	3	US-09-199-955-4	Sequence 4, Appli	1386	88	4.6	818	4	US-08-411-295F-247	Sequence 247, App
1314	88.5	4.6	298	3	US-08-880-875-4	Sequence 4, Appli	1387	88	4.6	821	3	US-08-470-335-228	Sequence 228, App
1315	88.5	4.6	329	4	US-09-917-265A-59	Sequence 59, Appl	1388	88	4.6	821	4	US-08-467-602-319	Sequence 319, App
1316	88.5	4.6	329	4	US-09-917-265A-108	Sequence 108, App	1389	88	4.6	821	4	US-08-411-295F-245	Sequence 245, App
1317	88.5	4.6	491	4	US-09-107-532A-6115	Sequence 6115, Ap	1390	88	4.6	827	3	US-08-470-335-237	Sequence 237, App
1318	88.5	4.6	520	4	US-09-949-016-9918	Sequence 9918, Ap	1391	88	4.6	827	4	US-08-467-602-333	Sequence 333, App
1319	88.5	4.6	533	4	US-09-917-265A-62	Sequence 62, Appl	1392	88	4.6	827	4	US-08-411-295F-259	Sequence 259, App
1320	88.5	4.6	722	3	US-08-961-083-84	Sequence 84, Appl	1393	88	4.6	830	3	US-08-470-335-231	Sequence 231, App
1321	88.5	4.6	722	4	US-09-536-784-84	Sequence 84, Appl	1394	88	4.6	830	4	US-08-467-602-330	Sequence 330, App
1322	88.5	4.6	826	4	US-09-877-730-16	Sequence 16, Appl	1395	88	4.6	841	4	US-08-411-295F-256	Sequence 256, App
1323	88.5	4.6	907	4	US-09-877-730-20	Sequence 20, Appl	1396	88	4.6	841	4	US-08-467-602-327	Sequence 327, App
1324	88	4.6	197	2	US-08-756-387B-11	Sequence 11, Appl	1397	88	4.6	850	4	US-08-411-295F-253	Sequence 253, App
1325	88	4.6	197	3	US-08-285-873-11	Sequence 11, Appl	1398	88	4.6	850	4	US-08-467-602-336	Sequence 336, App
1326	88	4.6	197	3	US-09-944-277A-11	Sequence 11, Appl	1399	88	4.6	852	4	US-08-411-295F-262	Sequence 262, App
1327	88	4.6	257	1	US-07-869-933-11	Sequence 11, Appl	1400	88	4.6	852	4	US-08-467-602-363	Sequence 363, App
1328	88	4.6	257	2	US-08-756-387B-2	Sequence 2, Appli	1401	88	4.6	855	4	US-08-411-295F-289	Sequence 289, App
1329	88	4.6	257	3	US-09-103-663-11	Sequence 11, Appl	1402	88	4.6	855	4	US-08-467-602-361	Sequence 361, App
1330	88	4.6	257	3	US-09-285-873-2	Sequence 2, Appli	1403	88	4.6	855	4	US-08-411-295F-287	Sequence 287, App
1331	88	4.6	257	4	US-08-897-956A-1	Sequence 1, Appli	1404	88	4.6	861	4	US-08-467-602-375	Sequence 375, App
1332	88	4.6	257	4	US-09-944-277A-2	Sequence 2, Appli	1405	88	4.6	861	4	US-08-411-295F-301	Sequence 301, App
1333	88	4.6	288	4	US-09-248-796A-15438	Sequence 2, Appli	1406	88	4.6	864	4	US-08-467-602-372	Sequence 372, App
1334	88	4.6	339	3	US-09-719-243-2	Sequence 2, Appli	1407	88	4.6	864	4	US-08-411-295F-298	Sequence 298, App
1335	88	4.6	349	3	US-08-470-335-188	Sequence 188, App	1408	88	4.6	865	3	US-08-470-335-235	Sequence 235, App
1336	88	4.6	382	4	US-08-467-602-382	Sequence 382, App	1409	88	4.6	865	3	US-08-467-602-322	Sequence 322, App
1337	88	4.6	391	5	PCR-US95-15696-2	Sequence 2, Appli	1410	88	4.6	865	4	US-08-411-295F-248	Sequence 248, App
1338	88	4.6	411	3	US-08-470-339-189	Sequence 189, App	1411	88	4.6	868	3	US-08-470-335-229	Sequence 229, App
1339	88	4.6	414	3	US-08-470-339-188	Sequence 188, App	1412	88	4.6	868	4	US-08-467-602-317	Sequence 317, App
1340	88	4.6	422	4	US-08-467-602-324	Sequence 324, App	1413	88	4.6	868	4	US-08-411-295F-243	Sequence 243, App
1341	88	4.6	422	4	US-08-411-295F-250	Sequence 250, App	1414	88	4.6	874	3	US-08-470-335-238	Sequence 238, App


```

RESULT 3
US-08-928-383B-2
; Sequence 2, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996

```


PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0405 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1946351
 US-08-979-424-3

Query Match	24.4%	Score 465;	DB 2;	Length 365;
Best Local Similarity	31.6%;	Pred. No. 2.9e-36;		
Matches 122;	Conservative 69;	Mismatches 151;	Indels 44;	Gaps 9
Qy	1	MSILLLLLLSVYVG-----TLGHTIE-IKRVAEKVTLPCHHQHQLGPEKOTLDIEWLLT	54	
Db	1	MALLLCFVLLCGVDFARSLITPEEMIERAKGETAYLPCKFTLSPEDQGLDIEWLIS	60	
Qy	55	--DNEGQKVITYSSRHVYNNLTTEEQKGRVAPASNFL-AGDASLQIBLPKPSDBGRYTC	111	
Db	61	PADNQKVDQVILYSGDKIYDYDYPDLKGRVHFTSNDLKSGDASINVTNLQLSDTGYTC	120	
Qy	112	KVKNSGRVYWSHVILKVLVRPSKPCLEGELTEGSDLTLTQCESSGTEPIVYVQRIRE	171	
Db	121	KVKKAPGVANKIHLVLVRPSGARCYVDGSEETGSDFKIKCEPKGSLPQYEQKUI--	178	
Qy	172	KEGEDERLPKPSRIDYNHGPRVLLQNLTMYSGLYQCTAGNEAGKESCVRV-TVQYVQS	230	
Db	179	--SDSQMPTSLAEMTSSVISVNASSEYSGTYSCTVRNRVSGDQCLLRNVVPPSNK	235	
Qy	231	IGWVAGAVTGIVAGALLIFLVLVLLIRKDKERYEEEEERPNREIDAEAPKARL-----	284	
Db	236	AGLIAGAIIGTLLALALIGLIIFCCRKREBEKEVH-HDIREDPVPPKSRTSTARS	294	
Qy	285	--VKPSSSSSGSRSSRSSTSTRANSASRQTLSTDAAPQGLAQYSLVAGPEVRG	342	
Db	295	IGSNHSLGWSPSNMEGYSKTQYNQVPSDFERTPQSPITLP-----	336	
Qy	343	SEPKVHHANLTKAETTPSMIPSQSR	368	
Db	337	--PAKVAAPNLNRMGAIPVMTPAQSK	360	

```

RESULT 5
US-09-272-496-2
; Sequence 2, Application US/09272496
; Patent NO. 6245966
; GENERAL INFORMATION:
; APPLICANT: DeGregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272,496
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```

US-09-272-496-2

Query Match          24.4%; Score 465; DB 3; Length 365;
Best Local Similarity 31.6%; Pred. No. 2.9e-36;
Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;

Qy      1  MSLLLLLLSVYVG- ---TLGHTHTE- IKRVAEKEVTLPCHHQLGLPEKOTLDIEWLLT 54
Db      1  MALLLCFVLLCGVDFPARSISITPPEEMIEKAKETAYLPCKFTLSPEDQGLDIENLIS 60

Qy      55  --DNEGQKVITYTSSRHVYNNLTTEEQKGRVAFASNFL-AGDASLIQIBLPKPSDGRVTC 111
Db      61  PADNQKVDQVILLYSGDKIVDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120

Qy      112  KVXNSGRYVWSHVILKVLVRPSKPCLEGBLTGSDLTLOCSSSGTEPIVYVQRIRE 171
Db      121  KVKKAPGVANKKIHLVVLVPSGARCXYDGSSEITGSDPKICEPEKSLPQYEWQKL- - 178

Qy      172  KEGEDERLPPKSRIDYNHQRVLLQNLTMYSYGLYQCTAGNEAGKESCVCVRV-TVQYVQS 230
Db      179  --SDSQKPTSLAETSSTSVISVKNASSEYSGTYSTVNRVNSDQCLLRNVVPPSNK 235

Qy      231  IGWVAGAVTGIVAGALLIFLLVLLIIRKDXERYEEERPNEIREDAAAPKARL----- 284
Db      236  AGLTAGAIIIGTLALALIGIIFCCRKKRREEKEVEVH-HDIREDVPPPKSRSTARSX 294

Qy      285  --VKPSSSSGSRSSRSGSSSTRSTANSASRSQTLSTDAAPQPLCATQAYSLVGPVVRG 342
Db      295  IGSNHSSLLGSNSPSNMEGYSKTYQNVQPSDFEITPQSPTLP----- 336

Qy      343  SEPKKVHHANLTAKBTTPSMIPSOQR 368
Db      337  --PAKVAAPNLSSRMGAIPVMIPAQSK 360

```

```

RESULT 6
US-09-949-016-6064
; Sequence 6064, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6064
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6064

```

Query Match	24.4%;	Score 465;	DB 4;	Length 365;
Best Local Similarity	31.6%;	Pred. No. 2.9e-36;		
Matches 122;	Conservative 69;	Mismatches 151;	Indels 44;	Gaps 9;
Qy	1	MSLLLLLLLLSYVVG----	TLGHTHTE- IKRVAEKEVTLPC	HOLGLPEKDTLDIEWLLLT 54
Db	1	MAALLLCFVLLCGVVD	FARSLITPEEMI EKAKETAYLPCKFTLS	PDQSGPLDIEWLIS 60
Qy	55	--DNEGQNKVVITYSSRRVNNLT	TEEQGRVAFASNFL-AGDASIQIBELPKSP	DSRGTYTC 111
Db	61	PADNQKVDQVILLYSGDKIYDDY	YPDLKGRVHFTSNDLKS	GDASINVTNLQLSDIGTYQC 120
Qy	112	KVRNSGRYVWSHVILKVLVR	SPKPCBELEGELTSGSDLT	LQCESSSGTHPIVYVQWRIRE 171

Db 121 KVKAPGVANKKIHLVWLVKPSGARYVDGSEIGSDFKIKCEPKESLPLQYEWKLT-- 178
QY 172 KEGEDERLPPKSRIDYHNHPGRVILLONLTMSYSGLYOCTAGNEAKGSCVVRV-TVQYVQS 230
Db 179 ---SDSKMPTSLWAEMTSSVISKNASSEYSGTCTVRNRVGSQCLLRNVPPSNK 235
QY 231 IGMVAGVTGIVAGALLIFLLVWLLIRKDKERYEEERPNREDAEAPKARL----- 284
Db 236 AGLIAGAIIGTLLALALIGLIIFCCRKRREKYEKEVH-HDIREDPVPPKSTARSY 294
QY 285 --VKPSSSSGSRSSRSTRANSASRSQRTLTDAAPQGLATQAYSIVLGPEVRG 342
Db 295 IGSNHSLSGMSPSNMEGYSKTQNVPSDFERTPQSTLP----- 336
QY 343 SEPKKVHANLTKAETTPSMIPQSQR 368
Db 337 --PAKVAAPNLSRGAIPVMPAQSK 360

RESULT 7

US-09-949-016-11050
; Sequence 11050, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11050
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11050

Query Match 24.4%; Score 465; DB 4; Length 383;
Best Local Similarity 31.6%; Pred. No. 3.1e-36;
Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;

QY 1 MSLLLLLLLVSYVG-----TLGTHTE-IKRVAEKVTLPCHQHLGLPEKDTLDIEWLLT 54
Db 19 MALLLCFVLLCGVDFARSLSTITPEEMIEKAGETAYLPCKFTLSPEDQGLDIEWLLS 78
QY 55 --DNEGQKVITYSSRHVNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
Db 79 PADNQKVDQVILVSGDKIDYYPDLKGRVHFTSNDLKGSDASINVTNLQSLDICTYQC 138
QY 112 KVKNSGRYVSHVLKVLVPSKPKCELEGELTEGSDLTLCQESSSGTEPIVYVQRIRE 171
Db 139 KVKKAPGVANKKIHLVWLVKPSGARYVDGSEIGSDFKIKCEPKESLPLQYEWKLT-- 196
QY 172 KEGEDERLPPKSRIDYHNHPGRVILLONLTMSYSGLYOCTAGNEAKGSCVVRV-TVQYVQS 230
Db 197 ---SDSKMPTSLWAEMTSSVISKNASSEYSGTCTVRNRVGSQCLLRNVPPSNK 253
QY 231 IGMVAGVTGIVAGALLIFLLVWLLIRKDKERYEEERPNREDAEAPKARL----- 284
Db 254 AGLIAGAIIGTLLALALIGLIIFCCRKRREKYEKEVH-HDIREDPVPPKSTARSY 312
QY 285 --VKPSSSSGSRSSRSTRANSASRSQRTLTDAAPQGLATQAYSIVLGPEVRG 342
Db 313 IGSNHSLSGMSPSNMEGYSKTQNVPSDFERTPQSTLP----- 354

QY 343 SEPKKVHANLTKAETTPSMIPQSQR 368
Db 355 --PAKVAAPNLSRGAIPVMPAQSK 378

RESULT 8

US-08-928-383B-23
; Sequence 23, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cocksackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-928-383B-23

Query Match 24.0%; Score 458.5; DB 3; Length 365;
Best Local Similarity 32.3%; Pred. No. 1.2e-35;
Matches 122; Conservative 68; Mismatches 155; Indels 33; Gaps 10;

QY 3 LLLLLLLL--VSYVYGTGTHTEIKRVAE---EKVTLPCHHQLGLPEKDTLDIEWLL--TD 55
Db 4 LLCFVLLCGIADFTSGLSITTEQRIEKAGETAYLPCKFTLSPEDQGLDIEWLLSPSD 63
QY 56 NEGQKVITYSSRHVNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTCVK 114
Db 64 NQIVDQVILVSGDKIDYYPDLKGRVHFTSNDVSGSDASINVTNLQSLDICTYQCKVK 123
QY 115 NSGRYVSHVLKVLVPSKPKCELEGELTEGSDLTLCQESSSGTEPIVYVQRIREKEG 174
Db 124 KAPGVANKKFTLLVWLVKPSGTRCFVDGSEIGNDFKIKCEPKESLPLQYEWKLT-- 178
QY 175 EDERLPPKSRIDYHNHPGRVILLONLTMSYSGLYOCTAGNEAKGSCVVRV-TVQYVQSIGM 233
Db 179 SDQTMPTSLWAEMTSPVISKNASSEYSGTCTVRNRVGSQCLLRNVPPSNRAGT 238
QY 234 VAGAVTGIAGALLIFLLVWLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSSG 293
Db 239 IAGAVGTLLALVLIIGAILFCCHKRREKYEKEVH-HDIREDPVPPKSTARSYIGS 297


```

; TITLE OF INVENTION: Targeting Recombinant Virus with a Bispecific Fusion Protein Ligar
; TITLE OF INVENTION: Coupling with an Antibody to Cells for Gene Therapy
; FILE REFERENCE: RTC/DNA001
; CURRENT APPLICATION NUMBER: US/09/604,107A
; CURRENT FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens, mus and staphylococcus aureus
; US-09-604-107A-8

Query Match      17.8%; Score 340.5; DB 4; Length 466;
Best Local Similarity 27.0%; Pred. No. 4.3e-24;
Matches 99; Conservative 66; Mismatches 158; Indels 43; Gaps 10;

QY      23 IKRVAEEKVTLPCHHOLGLPEKDTLDIEWLLT--DNEGQKVITYSSRHVYNLTESQK 80
DB      104 IEKAKGETAYLPCKFTLSPEDQGLDIEWLLISPADNQVDQVILYSGDKIYDDYDPLK 163

QY      81 GRVAFASNFL-AGDASLQIEPLKPSDEGRYTCCKVNSGRYVMSHVILKVLVRPSKPCEL 139
DB      164 GRVHFTSNDLKGSDASINVTNLQSLDITGYQCKVKAFCVANKKIHLVVLKPSGARCIV 223

QY      140 EGGLETEGSLTLQCESSSGTEPIVYVQRIREKEGEDERLPPKSRIDYNHPCRVLLQNL 199
DB      224 DGSEIEGSDFKIKCPKEGSLPLQYEWQKL-----SDSQMPTSLAEMTSVIVKQNAS 278

QY      200 MSYGLYQCTAGNEAGKESCVRV-TVQYVQSIGVAGAVTGIVAGALLIFLLVWLLIRR 258
DB      279 SEYSGTYSCTVRNVGSDQCLLRNVPPSNKAGLIAAPKPTPPGSSA-----AADNK 332

QY      259 KOKER----YE-----EERPNR--EDAEAPKARLVKPPSSSSSGSRSSSSST 304
DB      333 FNKEQONAFYEILHLPNNEEQNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKVDNKEN 392

QY      305 RSTAN-----SASRSQR-----TLSTDAAPQGLATQAYSLVGPVGRSEPKVHH 350
DB      393 KEQONAFYEILHLPNNEEQNAFIQSLKDDPSQSANLLAEAKKLNDAQAPNLEQKLISE 452

QY      351 ANITKA 356
DB      453 EDLNSA 458

RESULT 13
US-09-336-536-40
; Sequence 40, Application US/09336536
; Patent No. 6408884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bosone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-336-536-40

Query Match      16.8%; Score 321; DB 4; Length 365;
Best Local Similarity 28.4%; Pred. No. 2.2e-22;
Matches 108; Conservative 57; Mismatches 153; Indels 62; Gaps 12;

QY      22 EIKRVAEEKVTLPCHHOLGLPE-----KDTLDIEWLLTDNEGQKVITYSSRHVYNLT 76
DB      12 KLEAVEGEVVLPAWYTWAREESWSHPREVPIILWFLEQEKEPNQVLSYINGVTN--- 68

; TITLE OF INVENTION: Targeting Recombinant Virus with a Bispecific Fusion Protein Ligar
; TITLE OF INVENTION: Coupling with an Antibody to Cells for Gene Therapy
; FILE REFERENCE: RTC/DNA001
; CURRENT APPLICATION NUMBER: US/09/604,107A
; CURRENT FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens, mus and staphylococcus aureus
; US-09-604-107A-8

Query Match      17.8%; Score 340.5; DB 4; Length 466;
Best Local Similarity 27.0%; Pred. No. 4.3e-24;
Matches 99; Conservative 66; Mismatches 158; Indels 43; Gaps 10;

QY      23 IKRVAEEKVTLPCHHOLGLPEKDTLDIEWLLT--DNEGQKVITYSSRHVYNLTESQK 80
DB      104 IEKAKGETAYLPCKFTLSPEDQGLDIEWLLISPADNQVDQVILYSGDKIYDDYDPLK 163

QY      81 GRVAFASNFL-AGDASLQIEPLKPSDEGRYTCCKVNSGRYVMSHVILKVLVRPSKPCEL 139
DB      164 GRVHFTSNDLKGSDASINVTNLQSLDITGYQCKVKAFCVANKKIHLVVLKPSGARCIV 223

QY      140 EGGLETEGSLTLQCESSSGTEPIVYVQRIREKEGEDERLPPKSRIDYNHPCRVLLQNL 199
DB      224 DGSEIEGSDFKIKCPKEGSLPLQYEWQKL-----SDSQMPTSLAEMTSVIVKQNAS 278

QY      200 MSYGLYQCTAGNEAGKESCVRV-TVQYVQSIGVAGAVTGIVAGALLIFLLVWLLIRR 258
DB      279 SEYSGTYSCTVRNVGSDQCLLRNVPPSNKAGLIAAPKPTPPGSSA-----AADNK 332

QY      259 KOKER----YE-----EERPNR--EDAEAPKARLVKPPSSSSSGSRSSSSST 304
DB      333 FNKEQONAFYEILHLPNNEEQNAFIQSLKDDPSQSANLLAEAKKLNDAQAPKVDNKEN 392

QY      305 RSTAN-----SASRSQR-----TLSTDAAPQGLATQAYSLVGPVGRSEPKVHH 350
DB      393 KEQONAFYEILHLPNNEEQNAFIQSLKDDPSQSANLLAEAKKLNDAQAPNLEQKLISE 452

QY      351 ANITKA 356
DB      453 EDLNSA 458

RESULT 11
US-09-899-634C-2
; Sequence 2, Application US/09899634C
; Patent No. 6794186
; GENERAL INFORMATION:
; APPLICANT: Thomas Buhler; Reto Andreas Gadiant; Reinhard Korn; Rao Movva
; TITLE OF INVENTION: pCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899,634C
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: delta porcine CAR
; US-09-899-634C-2

Query Match      19.8%; Score 378.5; DB 4; Length 261;
Best Local Similarity 34.6%; Pred. No. 3.7e-28;
Matches 91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;

QY      1 MSLLLLLLL---VSYVGTGLGHTT---IKRVAEEKVTLPCHHOLGLPEKDTLDIEWLLT 54
DB      1 MALLLCFVLLCGVADLTRSLTTPTEQMLEKAKGETAYLPCKFTLGPEDQGLDIEWLLS 60

QY      55 --DNEGQKVITYSSRHVYNLTBEQKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
DB      61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKGSDASINVTNLQSLDITGYQ 120

QY      112 KVNNSGRYVMSHVILKVLVRPSKPCELEGETEGESDLTLQCESSSGTEPIVYVQRIRE 171
DB      121 KVKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIGNDFDKCEPKEGSLPLLYEWQKL-- 178

QY      172 KEGEDERLPPKSRIDYNHPCRVLLQNLTVSYSLGYCTAGNEAGKESCVRV-TVQYVQS 230
DB      179 --SNSQKPLFLMAETSP--VISVKMASTYSGTYSCTVKNRVGSDQCLLRDVPVPSNR 235

QY      231 IGMVAGAVTGIVAGALLIFLLVW 253
DB      236 AGTIAGVIGVLLALVLIIGLIIF 258

RESULT 12
US-09-604-107A-8
; Sequence 8, Application US/09604107A
; Patent No. 6524572
; GENERAL INFORMATION:
; APPLICANT: Rainbow Therapeutic Company
; APPLICANT: Rainbow Therapeutic Company
; APPLICANT: Li, Yibing
; APPLICANT: Li, Yibing

```


Wed May 11 07:24:23 2005

us-09-978-544a-59.ra1

Page 18

Db 233 MNVALYVGIAVGWVAALIIGIIYCCCRGKDDNTEDKEDARN--REAYEPPPEQL 288

Search completed: May 6, 2005, 07:57:37
Job time : 80 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2005, 02:17:15 ; Search time 1289 Seconds
(without alignments)
96.534 Million cell updates/sec

Perfect score: 1908
Sequence: 1 MSLLLLLLLLVYVGTGLGTH.....TKAETPSMIPQSRARQTV 373

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	1908	100.0	373	9	US-09-796-858-24	Sequence 24, Appl
33	1908	100.0	373	10	US-09-997-428-503	Sequence 503, Appl
128	1908	100.0	373	14	US-10-167-749-59	Sequence 59, Appl
290	1908	100.0	373	14	US-10-223-083-64	Sequence 64, Appl
296	1908	100.0	373	14	US-10-219-065-130	Sequence 130, Appl
325	1908	100.0	373	14	US-10-223-084-64	Sequence 64, Appl
326	1908	100.0	373	14	US-10-223-088-64	Sequence 64, Appl
327	1908	100.0	373	14	US-10-223-090-64	Sequence 64, Appl
332	1908	100.0	373	14	US-10-223-087-64	Sequence 64, Appl
334	1908	100.0	373	14	US-10-223-083-64	Sequence 64, Appl
337	1908	100.0	373	14	US-10-223-089-64	Sequence 64, Appl
508	1908	100.0	373	14	US-10-223-081-64	Sequence 64, Appl
546	1908	100.0	373	14	US-10-223-082-64	Sequence 64, Appl
615	1908	100.0	373	15	US-10-170-481A-59	Sequence 59, Appl

Search completed: May 6, 2005, 07:56:30
Job time : 1315 secs

617	1908	100.0	373	15	US-10-210-028-59	Sequence 59, Appl
676	1908	100.0	373	15	US-10-162-521A-59	Sequence 59, Appl
685	1908	100.0	373	15	US-10-305-654-64	Sequence 64, Appl
700	1908	100.0	373	16	US-10-081-056-64	Sequence 64, Appl
707	1908	100.0	373	15	US-10-696-487-2	Sequence 2, Appl
709	1908	100.0	373	17	US-10-918-851-59	Sequence 59, Appl
710	1908	100.0	373	17	US-10-931-886-388	Sequence 388, Appl
711	1908	100.0	373	17	US-10-805-667-59	Sequence 59, Appl
712	1908	100.0	373	17	US-10-897-359-59	Sequence 59, Appl
714	1908	100.0	373	17	US-10-893-802-59	Sequence 59, Appl
715	1908	100.0	373	17	US-10-897-360-59	Sequence 59, Appl
716	1763.5	92.4	373	9	US-09-796-858-26	Sequence 26, Appl
717	692	36.3	141	15	US-10-243-552-499	Sequence 499, Appl
718	670	35.1	139	15	US-10-243-552-930	Sequence 930, Appl
719	471	24.7	365	9	US-09-899-634A-4	Sequence 4, Appl
720	465	24.4	365	9	US-09-971-798-2	Sequence 2, Appl
721	465	24.4	365	14	US-10-176-847-78	Sequence 78, Appl
722	465	24.4	365	17	US-10-482-029-76	Sequence 76, Appl
723	465	24.4	365	14	US-10-114-153-12	Sequence 12, Appl
750	433	22.7	352	10	US-09-997-428-505	Sequence 505, Appl
795	433	22.7	352	13	US-10-053-107-10	Sequence 10, Appl
801	433	22.7	352	14	US-10-213-145-10	Sequence 10, Appl
809	433	22.7	352	14	US-10-213-199-10	Sequence 10, Appl
840	433	22.7	352	14	US-10-223-085-280	Sequence 280, Appl
846	433	22.7	352	14	US-10-219-065-216	Sequence 216, Appl
872	433	22.7	352	14	US-10-223-084-280	Sequence 280, Appl
873	433	22.7	352	14	US-10-223-088-280	Sequence 280, Appl
874	433	22.7	352	14	US-10-223-090-280	Sequence 280, Appl
879	433	22.7	352	14	US-10-223-087-280	Sequence 280, Appl
880	433	22.7	352	14	US-10-223-083-280	Sequence 280, Appl
883	433	22.7	352	14	US-10-223-089-280	Sequence 280, Appl
885	433	22.7	352	14	US-10-223-081-280	Sequence 280, Appl
904	433	22.7	352	14	US-10-223-082-280	Sequence 280, Appl
906	433	22.7	352	15	US-10-305-654-280	Sequence 280, Appl
909	433	22.7	352	15	US-10-081-056-280	Sequence 280, Appl
913	424.5	22.2	422	14	US-10-114-153-14	Sequence 14, Appl
914	378.5	19.8	261	9	US-09-899-634A-2	Sequence 2, Appl
915	362.5	19.0	430	16	US-10-656-269-6	Sequence 6, Appl
916	361	18.9	431	14	US-10-314-395-2	Sequence 2, Appl
917	360	18.9	426	9	US-09-764-853-667	Sequence 667, Appl
918	360	18.9	431	17	US-10-916-064-2	Sequence 2, Appl
919	352.5	18.5	428	16	US-10-656-269-10	Sequence 10, Appl
920	342	17.9	323	9	US-09-971-798-31	Sequence 31, Appl
921	342	17.9	343	9	US-09-971-798-27	Sequence 27, Appl
922	335	17.6	393	14	US-10-270-555-1	Sequence 1, Appl
923	335	17.6	393	14	US-10-270-555-2	Sequence 2, Appl
924	335	17.6	474	14	US-10-270-555-3	Sequence 3, Appl
925	321	16.8	394	10	US-09-796-753-78	Sequence 78, Appl
926	315.5	16.5	326	15	US-10-443-108-4	Sequence 4, Appl
974	309.5	16.2	327	14	US-10-219-065-236	Sequence 236, Appl
1026	309.5	16.2	327	15	US-10-264-237-2730	Sequence 2730, Appl
1031	309.5	16.2	365	9	US-09-925-299-847	Sequence 847, Appl
1032	309.5	16.2	365	10	US-09-925-299-847	Sequence 847, Appl
1033	309.5	16.2	365	14	US-10-106-698-6387	Sequence 6387, Appl
1034	308.5	16.2	319	9	US-09-981-353-65	Sequence 65, Appl
1035	308.5	16.2	319	9	US-09-953-499-6	Sequence 6, Appl
1036	308.5	16.2	319	14	US-10-265-542-6	Sequence 6, Appl
1037	308.5	16.2	319	15	US-10-295-027-1165	Sequence 1165, Appl
1038	308.5	16.2	319	16	US-10-633-008-6	Sequence 6, Appl
1039	308.5	16.2	319	16	US-10-785-220-6	Sequence 6, Appl
1040	308.5	16.2	319	16	US-10-785-221-6	Sequence 6, Appl
1041	308.5	16.2	319	16	US-10-785-433-6	Sequence 6, Appl
1042	308.5	16.2	336	15	US-10-363-616-318	Sequence 318, Appl
1043	307.5	16.1	389	10	US-09-892-877-315	Sequence 315, Appl
1044	307.5	16.1	389	10	US-09-948-783-328	Sequence 328, Appl
1047	307.5	16.1	390	9	US-09-905-291A-39	Sequence 39, Appl
1406	307.5	16.1	390	14	US-10-066-269-110	Sequence 110, Appl
1422	307.5	16.1	390	14	US-10-299-976-39	Sequence 39, Appl

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2005, 07:09:37 ; Search time 52 Seconds
(without alignments)
690.170 Million cell updates/sec

Title: US-09-978-544a-59

Perfect score: 1908

Sequence: 1 MSLLLLLLVSYVGTGLTH.....TKAETTPSMTPSQSRAFTQV 373

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Query Length	ID	Description
1	474	24.8	365	JC7780	coxackie- and ade
2	196	10.3	299	S56749	junctional adhesion
3	188.5	9.9	338	JC5519	50K glycoprotein p
4	187	9.8	338	JC4776	limbic-system-asso
5	182	9.5	351	1 RWHU2	T-cell surface gly
6	178	9.3	5175	T20992	hypothetical prote
7	178	9.3	5198	T43290	hemocentin precurs
8	163.5	8.6	1323	PN0568	connectin 3B - chi
9	160	8.4	345	S03139	opioid-binding pro
10	159.5	8.4	347	S41638	T-cell surface gly
11	159	8.3	713	T50128	fibroblast growth
12	159	8.3	4162	T42633	connectin/titin -
13	158	8.3	345	JC4025	opioid-binding cel
14	158	8.3	7962	T38346	elastic titin - hu
15	156.5	8.2	526	A37821	butyrophilin - bov
16	156	8.2	344	T56551	neurotrophin - rat
17	155	8.1	1896	T08851	Down syndrome cell
18	154	8.1	1818	JC4058	fibroblast growth
19	153	8.0	1344	T14316	rig-1 protein - mo
20	152.5	8.0	526	S70587	butyrophilin precu
21	151.5	7.9	483	T17346	hypothetical prote
22	151	7.9	847	TJH0371	B-cell adhesion pr
23	151	7.9	1906	S68235	myosin-light-chain
24	149.5	7.8	799	S18209	fibroblast growth
25	148.5	7.8	344	1 RWRTC2	T-cell surface gly
26	148.5	7.8	738	T4A0056	platelet-endotheli
27	148.5	7.8	3707	S18252	heparan sulfate pr
28	147	7.8	647	A35648	B-cell adhesion pr
29	147	7.7	765	C42632	cell adhesion mole

30	147	7.7	812	2	B42632	cell adhesion mole
31	147	7.7	932	2	A42632	cell adhesion mole
32	146.5	7.7	404	1	I61596	advanced glycosyla
33	145	7.6	508	2	A33378	fasciclin iii prec
34	143	7.5	338	2	JC1238	opioid-binding pro
35	143	7.5	345	2	JC1239	opioid-binding pro
36	143	7.5	829	2	JC4583	fibroblast growth
37	142	7.4	868	2	A46512	CD22 homolog/B lym
38	141	7.4	822	2	S19947	fibroblast growth
39	141	7.4	822	2	B49151	fibroblast growth
40	140	7.3	1051	2	A39712	kinase-like protei
41	139.5	7.3	797	2	S38579	fibroblast growth
42	139.5	7.3	1197	2	T30581	neural cell adhesi
43	138.5	7.3	853	1	IJBONC	neural cell adhesi
44	138	7.2	344	2	B28967	T-cell surface gly
45	138	7.2	1091	1	IJCHNL	neural cell adhesi
46	137	7.2	802	2	TVHUF4	fibroblast growth
47	137	7.2	1612	2	T30805	du11 protein - mo
48	136.5	7.2	858	1	IJRTNC	neural cell adhesi
49	136	7.1	344	2	I49585	CD2 antigen protei
50	135.5	7.1	1070	2	JC4593	protein-tyrosine k
51	135.5	7.1	1273	2	T42405	sax-3 protein - Ca
52	135	7.1	518	2	JC4024	poliovirus recepto
53	134.5	7.0	1091	2	A58532	glial cell membran
54	134.5	7.0	1330	2	S49010	embryonic receptor
55	133.5	7.0	1033	2	S19247	cell adhesion prot
56	133	7.0	650	1	JC1450	fibroblast growth
57	133	7.0	1036	2	S22383	axonin 1 precursor
58	133	7.0	1091	2	S01998	contactin precursor
59	133	7.0	1333	2	I78875	receptor tyrosine
60	132.5	6.9	980	1	TVCTWD	macrophage colony-
61	132	6.9	862	2	I49583	differentiation an
62	132	6.9	1651	2	T14160	transmembrane rece
63	131	6.9	725	2	JE0100	neural cell adhesi
64	131	6.9	1092	1	JN0635	neural cell adhesi
65	131	6.9	4391	2	A38096	parlecan precursor
66	130.5	6.8	480	2	A56182	fibroblast growth
67	130.5	6.8	629	2	A46500	Ly-9.2 antigen - m
68	130.5	6.8	941	1	TVMVMD	protein-tyrosine k
69	130	6.8	761	1	IJHUNG	neural cell adhesi
70	129.5	6.8	423	2	T29549	hypothetical prote
71	129.5	6.8	1499	2	I50212	protein-tyrosine-p
72	129	6.8	584	2	T08678	hypothetical prote
73	129	6.8	1338	2	S09982	protein-tyrosine k
74	128.5	6.7	480	2	B56182	fibroblast growth
75	128.5	6.7	521	2	S34338	biliary glycoprote
76	128.5	6.7	813	1	A49123	neuroglian - fruit
77	128.5	6.7	1239	1	A32579	protein-tyrosine-p
78	128	6.7	1501	2	I58148	protein-tyrosine-p
79	128	6.7	1863	2	S46217	protein-tyrosine-p
80	128	6.7	1907	2	S50893	B-cell-restricted
81	127.5	6.7	288	2	A45803	advanced glycosyla
82	127.5	6.7	416	1	A42879	ecto-ATPase precu
83	127.5	6.7	772	2	T13078	protein-tyrosine k
84	127	6.7	519	2	A44783	Fit-1 tyrosine kin
85	127	6.7	806	2	A35963	neural cell adhesi
86	127	6.7	1336	2	J60598	neural cell adhesi
87	126	6.6	725	2	JE0099	fibroblast growth
88	126	6.6	750	2	S41051	fibroblast growth
89	126	6.6	800	1	TVH22F	neural adhesion pr
90	126	6.6	1018	2	JC4211	neural cell adhesi
91	126	6.6	1088	1	IJXLNL	protein-tyrosine k
92	125.5	6.6	975	1	TVMSKT	heparin-binding gr
93	125	6.6	800	2	A48991	fibroblast growth
94	125	6.6	801	2	I55363	contactin 1 precu
95	125	6.6	1018	2	A54744	FC gamma (Ig) rec
96	124.5	6.5	310	2	JL0119	neural cell adhesi
97	124.5	6.5	725	1	IJMSNG	fibroblast growth
98	124.5	6.5	816	2	A49151	macrophage colony-
99	124.5	6.5	972	1	TVHUMD	neural cell surf
100	124.5	6.5	1020	2	S05944	BIG-1 protein - ra
101	124.5	6.5	1028	2	I58164	neural cell adhesi
102	124.5	6.5	1115	1	IJMSNL	neural cell adhesi

103	123.5	6.5	821	1	TVMSBK	fibroblast growth	176	112	5.9	286	2	A28333	carcinoembryonic a
104	123	6.4	748	2	S41050	fibroblast growth	177	112	5.9	289	2	G00031	B7 protein - red-c
105	122.5	6.4	1694	2	S50065	sialoadhesin - mou	178	112	5.9	398	2	I49443	gene 284 protein -
106	122	6.4	821	1	TVHUF2	fibroblast growth	179	112	5.9	2029	1	TOPFLK	protein-tyrosine-p
107	121.5	6.4	240	2	JL0143	antigen BCM1 precu	180	111.5	5.8	309	2	I49503	B-lymphocyte activ
108	121.5	6.4	769	2	S16236	fibroblast growth	181	111.5	5.8	446	2	T45525	WSC4 homolog [impo
109	121.5	6.4	822	2	A45081	fibroblast growth	182	111.5	5.8	1241	2	T37190	nephlin - human
110	121.5	6.4	822	2	A41794	fibroblast growth	183	111.5	5.8	1880	2	T18531	tractin - medicina
111	121.5	6.4	1021	2	A57112	keratinocyte growt	184	111	5.8	248	1	MPRT0	myelin P0 protein
112	121	6.3	841	2	JCS894	contactin precursor	185	111	5.8	811	2	AP1054	fasciclin II, tran
113	120.5	6.3	707	2	A38429	killer cell inhibi	186	111	5.8	873	2	B41054	fasciclin II PI-11
114	120.5	6.3	707	2	A54846	keratinocyte growt	187	111	5.8	1437	2	T31093	probable protein-t
115	120.5	6.3	822	2	B54846	fibroblast growth	188	110.5	5.8	729	2	A49120	fibroblast growth
116	120.5	6.3	822	2	A41794	fibroblast growth	189	110.5	5.8	871	1	T48696	protein-tyrosine k
117	120	6.3	330	2	T42718	probable neural ce	190	110.5	5.8	881	1	T48697	protein-tyrosine k
118	120	6.3	521	2	JC1508	CP86 precursor - r	191	110.5	5.8	1898	2	S46216	leukocyte antigen-
119	120	6.3	702	2	A36319	biliary glycoprote	192	110	5.8	238	2	T22098	hypothetical prote
120	120	6.3	806	1	TVHUF3	carcinoembryonic a	193	110	5.8	270	2	S65739	basigin precursor
121	120	6.3	1040	1	TVHUF3	fibroblast growth	194	110	5.8	296	2	I46021	Fc gamma receptor
122	120	6.3	1040	2	A34695	transient axonal g	195	110	5.8	330	2	A40071	Fc gamma (IgG) rec
123	119.5	6.3	733	2	I49293	axonal glycoprotei	196	110	5.8	521	2	F87775	protein C24A11.8 [
124	119.5	6.3	819	1	TVCHFG	fibroblast growth	197	110	5.8	1040	2	A57638	receptor tyrosine
125	119.5	6.3	822	2	I49289	fibroblast growth	198	110	5.8	1103	2	T22889	hypothetical prote
126	119.5	6.3	822	2	S29840	fibroblast growth	199	110	5.8	1173	2	T25893	hypothetical prote
127	118.5	6.2	6642	2	T29757	fibroblast growth	200	110	5.8	2783	2	T34416	hypothetical prote
128	119	6.2	321	2	T54766	protein UNC-89 - C	201	109	5.7	407	2	T08732	hypothetical prote
129	119	6.2	823	2	B35963	B-lymphocyte activ	202	109	5.7	582	1	BNRT3S	myelin-associated
130	119	6.2	823	2	B35963	plasmacytoma-assoc	203	109	5.7	626	1	BNRT3	myelin-associated
131	118.5	6.2	1028	2	A53449	non-specific cross-	204	109	5.7	1240	2	T03097	myelin-associated
132	118.5	6.2	344	2	A27681	butyrophilin - mou	205	109	5.7	1298	2	A48999	CD0 protein - huma
133	118.5	6.2	487	2	S65133	heparin-binding gr	206	108.5	5.7	285	2	S36903	protein-tyrosine k
134	118.5	6.2	662	2	C40862	irregular chiasm C	207	108.5	5.7	462	2	I38404	Fc gamma (IgG) rec
135	118.5	6.2	764	2	A49448	hypothetical prote	208	108.5	5.7	646	2	I38049	neu differentiation
136	118.5	6.2	789	2	T28714	hypothetical prote	209	108.5	5.7	764	1	QRHUGS	cell surface glyco
137	118.5	6.2	822	1	TVHUF3	fibroblast growth	210	108.5	5.7	2222	1	QRHUGS	secretory componen
138	118.5	6.2	1328	2	T23007	hypothetical prote	211	108	5.7	2222	1	QRHUGS	sdh protein - frui
139	118	6.2	1355	2	T28007	hypothetical prote	212	108	5.7	248	1	JH0252	myelin P0 protein
140	117.5	6.2	705	2	S51635	fibroblast growth	213	108	5.7	330	2	I49660	FC-gamma-1/gamma-2
141	117.5	6.2	269	2	A46506	leukocyte activati	214	108	5.7	495	2	A55181	pregnancy-specific
142	117.5	6.2	682	2	A35969	heparin-binding gr	215	108	5.7	588	2	JH0506	adhesion molecule
143	117.5	6.2	822	1	TVHUF3	fibroblast growth	216	108	5.7	588	2	A45254	surface glycoprote
144	117.5	6.2	832	2	JH0393	fibroblast growth	217	108	5.7	637	2	B33785	myelin-associated
145	117	6.1	658	2	T13931	projectin - fruit	218	108	5.7	812	1	A36477	fibroblast growth
146	117	6.1	244	2	A40428	non-specific cross-	219	108	5.7	1459	2	T24088	hypothetical prote
147	117	6.1	467	1	HLMSP3	poliovirus recepto	220	107.5	5.6	2295	2	C98369	protein unc-52 [im
148	117	6.1	620	2	JH0593	Schwann cell myeli	221	107.5	5.6	309	2	I49522	gene B7-2 protein
149	116.5	6.1	898	1	A40114	fasciclin II precu	222	107.5	5.6	458	1	WNMSK1	biliary glycoprote
150	116.5	6.1	304	1	RWCH7	cell surface glyco	223	107.5	5.6	640	2	A43273	heregulin precursor
151	116.5	6.1	417	2	A41194	poliovirus recepto	224	107.5	5.6	814	1	A39752	probable receptor
152	115.5	6.1	729	2	A56795	fibroblast growth	225	107.5	5.6	1272	2	JC7604	neurofascin - chic
153	115.5	6.1	323	2	S06946	FC gamma (IgG) rec	226	107	5.6	275	2	JC7604	CD86 spliced varia
154	115.5	6.1	478	2	B41194	poliovirus recepto	227	107	5.6	335	2	H43354	pregnancy-specific
155	115	6.0	1262	1	I53960	PRR2 alpha - human	228	107	5.6	353	2	S14242	heparin-binding fi
156	115	6.0	1496	1	A48758	protein-tyrosine-p	229	107	5.6	599	2	T16774	hypothetical prote
157	114.5	6.0	247	1	A54662	myelin P0 protein	230	107	5.6	1011	2	T13669	neuromusculin - fr
158	114.5	6.0	530	2	A54337	poliovirus recepto	231	107	5.6	1897	1	TDHULK	leukocyte antigen-
159	114.5	6.0	1379	2	JC4954	vascular endotheli	232	107	5.6	26926	1	I38344	titin, cardiac mus
160	114	6.0	402	2	T09062	probable advanced	233	106.5	5.6	251	2	I38053	myelin protein zer
161	114	6.0	458	2	JC1509	biliary glycoprote	234	106.5	5.6	349	2	A43815	carcinoembryonic a
162	114	6.0	458	2	S68177	C-CAM2a protein is	235	106.5	5.6	351	2	B34595	pregnancy-specific
163	114	6.0	163	2	S23969	cell-adhesion mole	236	106.5	5.6	416	2	G83656	hypothetical prote
164	114	6.0	538	2	JC2457	vascular cell adhe	237	106.5	5.6	824	2	S36439	fibroblast growth
165	114	6.0	626	1	A61084	myelin-associated	238	106.5	5.6	977	2	I45877	protein-tyrosine k
166	114	6.0	820	2	S17295	fibroblast growth	239	106.5	5.6	978	1	A49814	protein-tyrosine k
167	114	6.0	946	1	A47299	ror-related recept	240	105.5	5.5	457	2	A27449	I-cell surface gly
168	114	6.0	3375	2	T19821	hypothetical prote	241	105.5	5.5	959	2	I38547	novel cellular pro
169	113.5	5.9	417	1	RWHUPA	poliovirus recepto	242	105.5	5.5	1015	2	T3186	hypothetical prote
170	113.5	5.9	2051	2	T30938	receptor tyrosine	243	105.5	5.5	1367	2	A41288	protein-tyrosine k
171	113	5.9	364	2	A30521	myeloid cell surfa	244	105.5	5.5	1894	2	C54689	protein-tyrosine-p
172	113	5.9	526	1	A32164	biliary glycoprote	245	105	5.5	329	1	A29128	myelin P0 protein
173	113	5.9	1363	2	I58375	protein-tyrosine k	246	105	5.5	406	2	E43354	B7-2 antigen - hum
174	112.5	5.9	352	1	RWHUPD	poliovirus recepto	247	105	5.5	544	2	JC5018	pregnancy-specific
175	112.5	5.9	824	2	S24108	protein-tyrosine k	248	105	5.5				intercellular adhe

249	105	5.5	562	2	T49904	hypothetical prote	322	100	5.2	790	2	A39627	protein-tyrosine k
250	104.5	5.5	241	2	S32359	glial growth facto	323	100	5.2	978	2	S16385	macrophage colony-
251	104.5	5.5	339	2	JC7509	glycoprotein VI-1	324	100	5.2	994	2	I49276	c-mer tyrosine kin
252	104.5	5.5	1268	1	A39640	neural cell adhesi	325	100	5.2	1052	2	B49120	protein-tyrosine k
253	104.5	5.5	1443	2	I50600	neogenin - chicken	326	99.5	5.2	210	2	JC4122	pregnancy-specific
254	104	5.5	283	1	FCMSG1	Fc gamma (IgG) rec	327	99.5	5.2	424	2	B36109	pregnancy-specific
255	104	5.5	341	2	JC1511	biliary glycoprote	328	99.5	5.2	540	1	OHUUR	natriuretic peptid
256	104	5.5	341	2	JC1512	biliary glycoprote	329	99.5	5.2	1021	2	T42634	connectin/titin -
257	104	5.5	426	2	C55181	pregnancy-specific	330	99	5.2	193	2	F89967	hypothetical prote
258	104	5.5	426	2	B35334	pregnancy-specific	331	99	5.2	419	2	A33258	pregnancy-specific
259	104	5.5	428	2	A7658	pregnancy-specific	332	99	5.2	419	2	A31135	pregnancy-specific
260	104	5.5	436	2	B55181	pregnancy-specific	333	99	5.2	426	2	B33258	pregnancy-specific
261	104	5.5	523	2	I50478	neurolin - goldfis	334	99	5.2	426	2	A35341	pregnancy-specific
262	104	5.5	538	2	I68093	PRR2 delta - human	335	99	5.2	584	2	I50419	s-glycerin precurs
263	104	5.5	1003	2	JH0823	FL-160-2 protein -	336	99	5.2	627	1	A43300	squalene-hopene cy
264	104	5.5	1277	2	T30532	neural cell adhesi	337	99	5.2	635	2	JC5896	killer cell inhibi
265	104	5.5	1912	2	A56178	protein-tyrosine-p	338	99	5.2	917	2	I48950	telencephalin prec
266	104	5.5	3488	2	T34418	hypothetical prote	339	99	5.2	1772	2	A45532	major mezozoite su
267	103.5	5.4	230	2	A56210	neu differentiatio	340	99	5.2	2109	2	E89086	protein H05009.1 [
268	103.5	5.4	241	2	D43273	heregulin precursor	341	99	5.2	2109	2	T33247	hypothetical prote
269	103.5	5.4	270	2	A34636	FC-gamma receptor	342	98.5	5.2	416	2	A54017	colon carcinoma-as
270	103.5	5.4	636	2	I61718	neu differentiatio	343	98	5.1	333	2	A31923	amalgam protein pr
271	103.5	5.4	637	2	C43273	heregulin precursor	344	98	5.1	421	2	T46266	hypothetical prote
272	103.5	5.4	639	2	I61719	neu differentiatio	345	98	5.1	547	1	S28904	intercellular adhe
273	103.5	5.4	645	2	B43273	heregulin, splice	346	98	5.1	1535	2	S46224	peroxidasein - frui
274	103.5	5.4	662	2	I61722	neu differentiatio	347	98	5.1	2541	2	T29340	hypothetical prote
275	103.5	5.4	1232	2	T43027	neural cell adhesi	348	97.5	5.1	272	2	I48268	biliary glycoprote
276	103.5	5.4	1375	2	I13822	frazzled gene prot	349	97.5	5.1	275	2	P90402	basigin type III -
277	103.5	5.4	1427	2	I51669	tumor suppressor -	350	97.5	5.1	317	2	JL0118	FC gamma (IgG) rec
278	103.5	5.4	1447	2	A44100	tumor suppressor p	351	97.5	5.1	413	2	S65948	hemolin - cecropia
279	103.5	5.4	1526	2	T33823	frazzled gene prot	352	97.5	5.1	413	2	A37778	hemolin precursor
280	103	5.4	372	2	C93971	Ig V-region-like B	353	97.5	5.1	414	2	C86301	arginine/serine-ri
281	103	5.4	569	2	A46462	T cell activation	354	97.5	5.1	535	2	I17212	hypothetical prote
282	103	5.4	680	2	JC5895	killer cell inhibi	355	97.5	5.1	793	2	D38992	cacharin 8 - human
283	103	5.4	739	2	J50675	vascular cell adhe	356	97.5	5.1	976	1	TVHUKT	protein-tyrosine k
284	103	5.4	1259	2	S36126	neural cell adhesi	357	97.5	5.1	1147	2	A59307	myosin-light-chain
285	103	5.4	1485	1	I82PT2	DNA topoisomerase	358	97.5	5.1	1520	2	T00273	hypothetical prote
286	102.5	5.4	426	2	S09016	pregnancy-specific	359	97	5.1	206	2	A40305	biliary glycoprote
287	102.5	5.4	429	1	E8RT	Ig epsilon chain C	360	97	5.1	274	2	T32736	hypothetical prote
288	102.5	5.4	1876	2	T28627	vitellogenin - Rip	361	97	5.1	288	2	A55737	PD-1 protein - hum
289	102.5	5.4	6831	2	A88852	protein unc-22 [im	362	97	5.1	440	2	A43519	complement recepto
290	102.5	5.4	6839	2	S72422	twitchin [similar	363	97	5.1	521	2	B86332	hypothetical prote
291	102.5	5.4	7160	2	T27935	hypothetical prote	364	97	5.1	572	2	S46529	Ig Y heavy chain (
292	102	5.3	324	2	G43354	pregnancy-specific	365	97	5.1	650	2	E82937	DNA topoisomerase,
293	102	5.3	326	2	F43354	pregnancy-specific	366	97	5.1	1026	1	A40315	maternal effect pr
294	102	5.3	333	2	A43354	pregnancy-specific	367	97	5.1	1177	2	T16594	hypothetical prote
295	102	5.3	527	2	T18232	conserved hypothet	368	97	5.1	1918	2	S43719	lactase [EC 3.2.1.
296	102	5.3	871	2	S47538	cacharin - African	369	97	5.1	1926	2	S01169	beta-glycosidase c
297	102	5.3	975	2	T30816	macrophage colony-	370	96.5	5.1	246	1	A32999	myelin P0 protein
298	102	5.3	1089	2	T21582	hypothetical prote	371	96.5	5.1	332	2	JN0067	pregnancy-specific
299	101.5	5.3	226	2	A46477	membrane-bound imm	372	96.5	5.1	783	2	I50116	N-cadherin precurs
300	101.5	5.3	240	2	JC4121	pregnancy-specific	373	96.5	5.1	883	2	S57653	brevican precursor
301	101.5	5.3	402	2	A54312	pregnancy-specific	374	96.5	5.1	946	2	S28061	SCP1 protein - rat
302	101	5.3	344	2	T29264	hypothetical prote	375	96	5.0	370	2	S29139	aggreccan - pig [fr
303	101	5.3	974	1	A49714	protein-tyrosine k	376	96	5.0	378	2	S61992	Ig V-region-like B
304	101	5.3	1176	2	JN0583	myosin-light-chain	377	96	5.0	398	2	A39371	Ig V-region-like B
305	101	5.3	1210	2	I39410	AF-4 protein, spli	378	96	5.0	662	2	T16525	hypothetical prote
306	101	5.3	1257	1	A41060	neural cell adhesi	379	96	5.0	769	1	QRRTGS	secretory componen
307	100.5	5.3	366	2	A33286	cell-surface glyco	380	96	5.0	857	2	S44883	ZC262.3 protein -
308	100.5	5.3	457	1	RWMSF4	T-cell surface gly	381	96	5.0	1007	2	C84668	probable receptor-
309	100.5	5.3	719	2	A30047	enhancer of split	382	96	5.0	1791	2	T02345	hypothetical prote
310	100.5	5.3	987	2	A88746	protein C18F3.2 [i	383	96	5.0	4930	2	B69679	polyketide synthet
311	100.5	5.3	1256	2	T30396	CDO protein - rat	384	95.5	5.0	333	1	B42053	gap junction prote
312	100.5	5.3	1287	2	T30988	hypothetical prote	385	95.5	5.0	414	2	C75461	hypothetical prote
313	100	5.2	255	2	JC7593	SH2 domain-contain	386	95.5	5.0	451	2	S71754	cellular hepatitis
314	100	5.2	305	2	JC4523	nucleic acid-bindi	387	95.5	5.0	475	2	C86663	N-acetylmuramoyl-L
315	100	5.2	395	2	D43354	pregnancy-specific	388	95.5	5.0	583	2	I39428	alcam - human
316	100	5.2	397	2	C43354	pregnancy-specific	389	95.5	5.0	587	2	JH0464	DM-GRASP precursor
317	100	5.2	417	2	A28277	pregnancy-specific	390	95.5	5.0	647	2	JQ2149	B west mating prot
318	100	5.2	424	2	A34595	pregnancy-specific	391	95.5	5.0	811	2	PN0689	connectin 1 - chic
319	100	5.2	426	2	A35964	pregnancy-specific	392	95.5	5.0	993	2	S49461	synaptonemal compl
320	100	5.2	463	2	T29671	hypothetical prote	393	95	5.0	247	2	S58394	myelin/Oligodentro
321	100	5.2	647	2	B41288	vascular cell adhe	394	95	5.0	271	2	S43512	GP42/Basigin prote

395	95	5.0	273	2	JX0107	basigin precursor	468	91.5	4.8	267	2	A38442	probable tumor sup
396	95	5.0	435	2	D33258	pregnancy-specific	469	91.5	4.8	278	2	JC1506	biliary glycoprote
397	95	5.0	906	1	IJHUCN	cadherin 2 precurs	470	91.5	4.8	278	2	JC1507	biliary glycoprote
398	95	5.0	906	1	IJHUCN	N-cadherin precurs	471	91.5	4.8	430	2	I48142	B-lymphocyte anti
399	95	5.0	1106	1	PFHUGB	platelet-derived g	472	91.5	4.8	561	1	A44128	(N-acetyl)neuraminy
400	95	5.0	1248	2	B96827	hypothetical prote	473	91.5	4.8	1008	2	T41244	SEC14 protein homo
401	94.5	5.0	299	2	VVVPB2	CD80 precursor - r	474	91.5	4.8	3507	2	T34513	hypothetical prote
402	94.5	5.0	353	1	VVVPB2	coat protein VP2 -	475	91	4.8	282	2	C28928	pregnancy-specific
403	94.5	5.0	451	2	T30603	perlecan homolog 2	476	91	4.8	304	2	G11624	refin PF80025c - m
404	94.5	5.0	495	1	A26396	T-cell surface gly	477	91	4.8	336	2	I48471	hypothetical prote
405	94.5	5.0	503	2	S63257	probable membrane	478	91	4.8	344	2	I48471	hypothetical prote
406	94.5	5.0	547	2	T45635	hypothetical prote	479	91	4.8	401	1	JC2P1L	complement regulat
407	94.5	5.0	618	2	T08685	hypothetical prote	480	91	4.8	497	2	QX2054	natriuretic peptid
408	94.5	5.0	757	2	S54620	RTS1 protein - yea	481	91	4.8	536	2	S71332	prophage pi3 prote
409	94.5	5.0	905	1	IJXLC1	N-cadherin 1 precu	482	91	4.8	874	2	G86797	hypothetical prote
410	94.5	5.0	1180	2	T20773	hypothetical prote	483	91	4.8	874	2	G86797	hypothetical prote
411	94.5	5.0	1260	1	S05479	neural cell adhesi	484	90.5	4.7	335	2	S58892	signaling lymphocy
412	94.5	5.0	1655	2	T32633	hypothetical prote	485	90.5	4.7	404	2	F71520	hypothetical prote
413	94.5	5.0	4549	2	T20771	hypothetical prote	486	90.5	4.7	610	2	A46480	FC gamma (Igg) rec
414	94.5	5.0	4867	2	T20774	hypothetical prote	487	90.5	4.7	964	2	S06028	hypothetical prote
415	94	4.9	257	2	F80401	basigin type II -	488	90.5	4.7	967	2	S66852	gene suppressor-of
416	94	4.9	276	2	S20690	31.6K hypothetical	489	90.5	4.7	1565	2	S04729	hypothetical prote
417	94	4.9	361	2	FN0020	fibroblast growth	490	90.5	4.7	1565	2	S04729	surface antigen pa
418	94	4.9	419	2	JC4123	pregnancy-specific	491	90.5	4.7	1882	1	GNVVTB	genome polyprotein
419	94	4.9	127	2	T22938	hypothetical prote	492	90.5	4.7	6805	2	S20901	titin - rabbit (fr
420	94	4.9	1374	2	T23004	hypothetical prote	493	90	4.7	142	2	S58082	transmembrane prot
421	94	4.9	1742	2	S24600	plasmalogen relate	494	90	4.7	336	2	S42632	transmembrane prot
422	94	4.9	2124	2	A28452	projectin - fruit	495	90	4.7	374	1	A39878	Fit-1S protein pre
423	94	4.9	3828	2	T13857	trithorax antigen	496	90	4.7	464	2	C30127	FC gamma (Igg) rec
424	94	4.9	243	2	A53244	trithorax antigen	497	90	4.7	556	2	S51892	transmembrane carc
425	93.5	4.9	247	2	A51717	leukocyte antigen	498	90	4.7	735	2	T15306	hypothetical prote
426	93.5	4.9	249	1	A61087	myelin/oligodendro	499	90	4.7	882	2	T38912	receptor tyrosine k
427	93.5	4.9	278	2	A39037	myelin P0 glycopro	500	90	4.7	890	1	A53743	R-cadherin precurs
428	93.5	4.9	355	2	B26883	carcinoembryonic a	501	90	4.7	913	1	A47543	C-kit-related kina
429	93.5	4.9	466	2	JC5897	neural cell adhesi	502	90	4.7	954	2	I51703	hypothetical prote
430	93.5	4.9	535	2	A54155	killer cell inhibi	503	90	4.7	962	2	T00262	hypothetical prote
431	93.5	4.9	540	2	T44683	natriuretic peptid	504	90	4.7	964	2	T15746	hypothetical prote
432	93.5	4.9	2843	1	RBUHAP	precorrin methylas	505	90	4.7	1004	2	A55142	myosin-light-chain
433	93.5	4.9	336	2	C27658	adenomatous polyo	506	90	4.7	1029	2	T30351	myosin-like protein
434	93	4.9	344	2	A41357	pregnancy-specific	507	90	4.7	1072	2	A38457	integrin alpha-6 c
435	93	4.9	769	2	B81447	FC gamma (Igg) rec	508	90	4.7	1156	2	T34326	germline RNA helic
436	93	4.9	817	2	S74283	chemotaxis histidi	509	90	4.7	1172	2	T32759	hypothetical prote
437	93	4.9	773	1	QRBBG	secretory componen	510	90	4.7	1356	2	JC1402	protein-tyrosine k
438	93	4.9	817	2	A48721	titin, muscle - ch	511	90	4.7	1575	2	S68448	synaptotagmin, 170K
439	93	4.9	915	2	S74283	probable protein k-	512	90	4.7	1659	2	JC4956	vitellogenin, 170K
440	93	4.9	976	1	TVM5MD	macrophage colony-	513	90	4.7	2090	2	S26058	probable transform
441	93	4.9	1840	2	T29091	transitin - chicke	514	90	4.7	13055	2	T16580	hypothetical prote
442	93	4.9	2132	1	A55182	aggreacan precursor	515	89.5	4.7	164	2	T16168	hypothetical prote
443	92.5	4.8	151	2	T21827	hypothetical prote	516	89.5	4.7	321	2	JH0395	biliary glycoprote
444	92.5	4.8	252	2	S33323	nonspecific cross-	517	89.5	4.7	335	2	A33514	pregnancy-specific
445	92.5	4.8	403	2	T27825	hypothetical prote	518	89.5	4.7	351	2	JH0396	pregnancy-specific
446	92.5	4.8	419	2	A36109	pregnancy-specific	519	89.5	4.7	416	2	S33473	interleukin-1 rece
447	92.5	4.8	628	2	I38000	Lutheran blood gro	520	89.5	4.7	417	2	JH0394	biliary glycoprote
448	92.5	4.8	757	2	I45956	polymERIC immunogl	521	89.5	4.7	475	2	S45116	biliary glycoprote
449	92.5	4.8	829	2	C84363	colorectal tumor's	522	89.5	4.7	536	2	A45409	natriuretic peptid
450	92.5	4.8	1087	2	C84363	transmembrane olig	523	89.5	4.7	722	2	E71403	atrial natriuretic
451	92.5	4.8	1114	2	I50222	deltaE91 - chicken	524	89.5	4.7	739	2	A41288	hypothetical prote
452	92.5	4.8	1259	2	A43425	inner cell wall ma	525	89.5	4.7	757	1	S48841	vascular cell adhe
453	92	4.8	238	2	S77699	tapasin 1 homolog,	526	89.5	4.7	808	2	G83210	secretory componen
454	92	4.8	430	2	T28143	Balbiansi ring 1 pr	527	89.5	4.7	829	2	D14485	probable adenylate
455	92	4.8	511	2	S24345	hypothetical prote	528	89.5	4.7	1450	2	D71485	probable adenylate
456	92	4.8	688	2	T32750	high molecular mas	529	89.5	4.7	1622	2	JE0378	alpha-fetoprotein
457	92	4.8	1151	2	T18535	metabotropic gluta	530	89.5	4.7	2783	1	A41948	DNA (cytosine-5-)-
458	92	4.8	1180	2	JC2132	mutator 2 - fruit	531	89.5	4.7	3924	2	S37431	alpha-fetoprotein
459	92	4.8	1261	2	T13165	versican precursor	532	89	4.7	245	2	A30154	IgE receptor alpha
460	92	4.8	1643	2	A56508	anucleate primary	533	89	4.7	335	2	C54312	pregnancy-specific
461	92	4.8	1807	2	S03124	vitellogenin A2 pr	534	89	4.7	335	2	S33251	nonspecific cross-
462	92	4.8	2397	1	A55535	versican precursor	535	89	4.7	432	2	S30133	T-cell surface gly
463	92	4.8	2409	1	A390979	aggreacan precursor	536	89	4.7	475	2	S52893	hypothetical prote
464	92	4.8	2415	1	A39085	hypothetical prote	537	89	4.7	486	2	T15001	hypothetical prote
465	92	4.8	3036	2	T18995	versican precursor	538	89	4.7	524	2	S35341	kettin - fruit fly
466	92	4.8	3381	2	T42389	versican precursor	539	89	4.7	565	2	T29718	hypothetical prote
467	92	4.8	3381	2	T42389	versican precursor	540	89	4.7	636	2	S63131	probable membrane

541	89	4.7	671	2	B54857	transcription fact	614	86.5	4.5	1125	2	B41206	microtubule-associ
542	89	4.7	1142	2	S59359	GIN4 protein - yea	615	86.5	4.5	1187	2	T19413	hypothetical prote
543	89	4.7	1560	2	T42727	proliferation pote	616	86.5	4.5	1327	2	T21268	hypothetical prote
544	89	4.7	1920	2	S43721	lactase [EC 3.2.1.	617	86.5	4.5	1329	2	C69048	cobalamin biosynth
545	88.5	4.6	152	2	S21826	T-cell receptor be	618	86.5	4.5	1426	2	T30817	homeotic protein C
546	88.5	4.6	333	1	A40548	gap junction prote	619	86.5	4.5	1469	2	T19168	hypothetical prote
547	88.5	4.6	419	2	B43112	pregnancy-specific	620	86.5	4.5	1561	1	S06839	surface antigen ap
548	88.5	4.6	495	2	T25750	hypothetical prote	621	86.5	4.5	1659	2	S79926	hypothetical prote
549	88.5	4.6	519	2	S78089	G-protein signalin	622	86.5	4.5	1955	2	T30934	myosin-like protei
550	88.5	4.6	666	2	H89581	protein dim-1 [imp	623	86.5	4.5	2139	2	S46404	vitellogenin - yel
551	88.5	4.6	1213	2	A58198	serine/proline-ric	624	86.5	4.5	2327	2	T42630	aggreccan - bovine
552	88.5	4.6	2233	2	B95075	beta-galactosidase	625	86.5	4.5	2944	2	A54849	collagen alpha 1IV
553	88.5	4.6	2845	2	I49505	adenomatous polyo	626	86	4.5	133	2	I46632	rearranged T-cell
554	88.5	4.6	3122	2	T17202	DNA-directed DNA p	627	86	4.5	366	2	I37135	MHC class I histoc
555	88.5	4.6	4436	2	E71086	hypothetical prote	628	86	4.5	448	1	VHIHBC	nucleocapsid prote
556	88	4.6	257	2	S00682	IGE Fc receptor al	629	86	4.5	535	2	T37189	hypothetical prote
557	88	4.6	383	2	T46707	proteophosphoglyc	630	86	4.5	537	1	A28111	hypothetical prote
558	88	4.6	488	2	AG0621	probable bacteriop	631	86	4.5	556	2	A44441	nauretic peptid
559	88	4.6	522	2	E91116	conserved hypothet	632	86	4.5	572	2	A57284	B-cell antigen CD1
560	88	4.6	856	2	T43631	serine/threonine k	633	86	4.5	648	2	T25438	spermatid perinocl
561	88	4.6	877	1	IJB0CN	N-cadherin precurs	634	86	4.5	712	2	T25438	hypothetical prote
562	88	4.6	884	2	D96730	unknown protein F5	635	86	4.5	740	2	T09480	hypothetical prote
563	88	4.6	1212	2	JC2131	metabotropic gluta	636	86	4.5	782	2	S50719	hypothetical prote
564	88	4.6	1451	2	S242167	190K protein - hum	637	86	4.5	791	2	E35216	FP5 protein - fow
565	88	4.6	1872	2	T30888	vitellogenin - Ath	638	86	4.5	960	1	JN0677	protein-tyrosine k
566	87.5	4.6	400	2	T34363	hypothetical prote	639	86	4.5	1028	2	B24785	hypothetical prote
567	87.5	4.6	481	2	G81089	glucose-6-phosphat	640	86	4.5	1087	2	I51552	platelet-derived g
568	87.5	4.6	534	2	T39903	serine-rich protei	641	86	4.5	1124	2	JH0588	calmodulin-binding
569	87.5	4.6	644	2	G96748	hypothetical prote	642	86	4.5	1468	2	S11515	formin - mouse
570	87.5	4.6	773	2	T46283	hypothetical prote	643	86	4.5	1852	1	VJCH2	vitellogenin II pr
571	87.5	4.6	834	2	S64498	M-sema F protein p	644	85.5	4.5	131	2	T20334	hypothetical prote
572	87.5	4.6	929	2	T38948	hypothetical colle	645	85.5	4.5	182	2	I83053	pregnancy-specific
573	87.5	4.6	937	2	S58135	hyphally regulated	646	85.5	4.5	307	2	A71602	refin PF0955w - m
574	87.5	4.6	1087	2	T22847	hypothetical prote	647	85.5	4.5	321	2	D39371	Ig V-region-like B
575	87.5	4.6	1250	2	T22845	hypothetical prote	648	85.5	4.5	339	2	I56071	MHC class I histoc
576	87.5	4.6	1319	2	A28313	glued protein - fr	649	85.5	4.5	357	2	S11139	class I histocopa
577	87.5	4.6	1436	2	S57238	forked protein 5.4	650	85.5	4.5	360	2	S69083	probable membrane
578	87.5	4.6	1449	2	T02737	forked protein 5.6	651	85.5	4.5	364	2	I46604	MHC PD14 transpla
579	87.5	4.6	1571	2	T00062	hypothetical prote	652	85.5	4.5	366	2	I46604	MHC PD14a transpla
580	87	4.6	233	2	JH0372	42K surface glycop	653	85.5	4.5	402	2	E86185	hypothetical prote
581	87	4.6	273	2	B28928	pregnancy-specific	654	85.5	4.5	457	1	A28468	chromogranin A pre
582	87	4.6	275	2	A28928	pregnancy-specific	655	85.5	4.5	671	2	A35912	homeotic protein o
583	87	4.6	391	2	T09058	butyrophilin homol	656	85.5	4.5	753	2	G02173	semaphorin III fam
584	87	4.6	408	2	S57148	hypothetical prote	657	85.5	4.5	796	2	T39962	coatamer complex b
585	87	4.6	422	2	S32357	glial growth facto	658	85.5	4.5	858	2	A57513	heat shock protein
586	87	4.6	431	2	S47538	acrosin [EC 3.4.21	659	85.5	4.5	929	2	T35683	ftsK homolog - Str
587	87	4.6	448	1	VH1N1	nucleocapsid prote	660	85.5	4.5	1089	1	S33727	platelet-derived g
588	87	4.6	482	2	T66902	dextranucrase [EC	661	85.5	4.5	1151	2	T38424	hypothetical prote
589	87	4.6	838	2	I45557	eyeless, long form	662	85.5	4.5	1265	1	A37967	neural cell adhesi
590	87	4.6	874	2	B86322	F6A14.8 protein -	663	85.5	4.5	1315	2	T50262	probable nucleopor
591	87	4.6	939	2	S28394	probable serine/th	664	85.5	4.5	1324	2	S52863	DNA-binding protei
592	87	4.6	1032	2	G99427	protein T08D2.3 [i	665	85.5	4.5	1677	2	T43021	vitellogenin precu
593	87	4.6	1054	2	S54473	TPS3 protein - yea	666	85.5	4.5	2059	2	T13858	probable DNA-direc
594	87	4.6	1102	2	S55100	hypothetical prote	667	85.5	4.5	2094	2	S33124	tpx protein - huma
595	87	4.6	1118	1	A49724	protein-tyrosine-p	668	85.5	4.5	2271	2	F90073	hypothetical prote
596	87	4.6	1215	2	I52882	autoantigen - huma	669	85	4.5	191	2	C75011	hypothetical prote
597	87	4.6	1327	2	T09402	immunoglobulin-lik	670	85	4.5	246	2	A47712	myelin/oligodendro
598	87	4.6	1369	1	JC4860	protein-tyrosine k	671	85	4.5	267	2	A35902	Fc gamma (IgG) rec
599	87	4.6	1394	2	A29637	position-specific	672	85	4.5	324	2	I49768	bone sialoprotein
600	87	4.6	1465	2	S43529	165K protein, skel	673	85	4.5	392	2	H96938	membrane permease,
601	87	4.6	1603	2	S17983	gene posterior sex	674	85	4.5	399	2	B64488	hypothetical prote
602	87	4.6	1823	2	S28974	vitellogenin precu	675	85	4.5	508	2	S12640	transposition prot
603	87	4.6	2491	1	A28372	insulin-like growt	676	85	4.5	528	2	PC4025	intercellular adhe
604	86.5	4.5	287	4	PC4402	peB leader/Ig hea	677	85	4.5	625	2	T16777	hypothetical prote
605	86.5	4.5	459	2	A46254	CD4 precursor - ra	678	85	4.5	641	2	T17278	hypothetical prote
606	86.5	4.5	520	1	S44099	brain-derived neur	679	85	4.5	647	2	T23407	hypothetical prote
607	86.5	4.5	646	2	S30180	phosphoenolpyruvat	680	85	4.5	687	2	B87318	hypothetical prote
608	86.5	4.5	654	2	PC7085	nuclear factor of	681	85	4.5	712	2	T18195	gag protein - silk
609	86.5	4.5	677	2	T00369	hypothetical prote	682	85	4.5	728	2	T51071	related to ttfA pr
610	86.5	4.5	818	1	S44098	brain-derived neur	683	85	4.5	779	2	T49717	related to BCS1 pr
611	86.5	4.5	906	1	IYXLC2	N-cadherin 2 precu	684	85	4.5	1280	2	T29021	hypothetical prote
612	86.5	4.5	935	2	A40694	cadherin-associate	685	85	4.5	1370	2	T19188	hypothetical prote
613	86.5	4.5	976	2	T29583	hypothetical prote	686	85	4.5	1442	2	S72441	protein-tyrosine-p

833	82	4.3	1589	2	T13606	hypothetical prote	906	81	4.2	1048	2	T30815	platelet-derived g
834	82	4.3	2761	2	T21064	hypothetical prote	907	81	4.2	1147	2	T35781	hypothetical prote
835	81.5	4.3	146	2	S26408	T-cell receptor be	908	81	4.2	1443	2	T31896	hypothetical prote
836	81.5	4.3	206	2	A39268	heterochromatin pr	909	81	4.2	1528	2	T06694	hypothetical prote
837	81.5	4.3	277	2	I52825	gene MAC25 protein	910	81	4.2	1684	2	TJ0057	gravin - human
838	81.5	4.3	282	2	S50031	prostacyclin-stimu	911	81	4.2	1858	2	T18273	1-phosphatidylinos
839	81.5	4.3	282	2	T17219	hypothetical prote	912	81	4.2	2526	2	T20531	hypothetical prote
840	81.5	4.3	309	2	T15747	hypothetical prote	913	81	4.2	2722	2	T20532	hypothetical prote
841	81.5	4.3	341	2	A49136	class I histocompa	914	81	4.2	2738	2	E88320	protein P07A11.6 {
842	81.5	4.3	364	2	T46926	hypothetical prote	915	81	4.2	2942	2	T42730	Bassoon protein -
843	81.5	4.3	365	2	T35620	hypothetical prote	916	81	4.2	3942	2	T13564	microtubule-associ
844	81.5	4.3	366	2	B37028	MHC class I histoc	917	80.5	4.2	5327	2	S26266	T-cell receptor be
845	81.5	4.3	366	2	D75289	hypothetical prote	918	80.5	4.2	113	2	S26266	fibroblast growth
846	81.5	4.3	420	2	T14911	bZIP DNA-binding p	919	80.5	4.2	254	2	C42651	mucln 5AC (Clone J
847	81.5	4.3	455	2	G01923	KIR (cl-5) NK rece	920	80.5	4.2	279	2	S53363	hypothetical prote
848	81.5	4.3	482	2	JC7583	basic helix-loop-h	921	80.5	4.2	299	2	T32982	acetolactate synth
849	81.5	4.3	498	2	S11246	LAG-3 protein prec	922	80.5	4.2	309	2	I51911	42K membrane glyco
850	81.5	4.3	517	2	S20248	transcription fact	923	80.5	4.2	407	2	S152703	neurexin I-beta pr
851	81.5	4.3	567	2	S29498	lymphocyte antigen	924	80.5	4.2	468	2	E40228	hypothetical prote
852	81.5	4.3	656	1	S59631	endo-1,4-beta-xyla	925	80.5	4.2	507	2	S05542	hypothetical prote
853	81.5	4.3	660	2	T02768	spike glycoprotein	926	80.5	4.2	523	2	C84753	hypothetical prote
854	81.5	4.3	661	2	T51779	non-phototropic hy	927	80.5	4.2	588	2	I37202	B-CAM protein - hu
855	81.5	4.3	699	2	A82425	helicase IV VCA071	928	80.5	4.2	598	2	A84616	hypothetical prote
856	81.5	4.3	735	2	A33369	glycogen(starch) s	929	80.5	4.2	642	2	E90767	probable terminase
857	81.5	4.3	767	2	T31558	hypothetical prote	930	80.5	4.2	642	2	G90970	hypothetical prote
858	81.5	4.3	818	2	T19120	hypothetical prote	931	80.5	4.2	654	2	A85717	hypothetical prote
859	81.5	4.3	829	1	IJHUCP	cadherin 3 precurs	932	80.5	4.2	658	2	S50831	endoglin precursor
860	81.5	4.3	860	2	JC5702	ErbB kinase activa	933	80.5	4.2	677	2	B69379	methy1-accepting c
861	81.5	4.3	868	2	JC5701	ErbB kinase activa	934	80.5	4.2	739	2	S18642	polynucleotide ade
862	81.5	4.3	876	2	I49152	protein-tyrosine k	935	80.5	4.2	905	2	IC5963	stable tubule only
863	81.5	4.3	880	2	B53743	probable membrane	936	80.5	4.2	917	2	I49699	glycoprotein 130 -
864	81.5	4.3	1027	2	A56533	chromatin remodel	937	80.5	4.2	926	2	A33271	A-alpha Y 3 protei
865	81.5	4.3	1032	2	S65341	probable membrane	938	80.5	4.2	971	1	A36376	replication licens
866	81.5	4.3	1054	2	D96519	myosin-like protei	939	80.5	4.2	1199	2	T23005	hypothetical prote
867	81.5	4.3	1184	2	T09484	cartilage intermed	940	80.5	4.2	1224	2	S28368	hypothetical prote
868	81.5	4.3	1201	2	A57359	anillin - fruit fl	941	80.5	4.2	1367	2	S51959	hypothetical prote
869	81.5	4.3	1205	2	S64819	probable membrane	942	80.5	4.2	1374	2	S69875	hypothetical prote
870	81.5	4.3	1417	2	H90670	probable adhesin [943	80.5	4.2	1460	2	D81675	polymorphic membra
871	81.5	4.3	1417	2	D85521	probable adhesin [944	80.5	4.2	1461	2	T26327	hypothetical prote
872	81.5	4.3	1462	1	B36182	protein-tyrosine-p	945	80.5	4.2	1477	2	T13797	hypothetical prote
873	81.5	4.3	1530	2	I45944	neurexin I-alpha -	946	80.5	4.2	1507	2	A40228	neurexin I-alpha p
874	81.5	4.3	1621	2	T15264	hypothetical prote	947	80.5	4.2	1522	2	T39371	transcription regu
875	81.5	4.3	2453	2	S60254	nuclear receptor c	948	80.5	4.2	1547	2	T28657	blackjack protein,
876	81	4.2	138	2	T27639	T-cell receptor ga	949	80.5	4.2	1681	2	S59693	hypothetical prote
877	81	4.2	194	2	T39060	hypothetical prote	950	80.5	4.2	1859	2	S63325	probable membrane
878	81	4.2	253	2	T15475	hypothetical prote	951	80.5	4.2	1859	2	S64633	probable membrane
879	81	4.2	313	2	H36854	hemagglutinin - va	952	80.5	4.2	1862	2	I49502	ankyrin - mouse
880	81	4.2	351	2	G38196	hypothetical prote	953	80	4.2	2274	2	T30258	adenomatous polyop
881	81	4.2	351	2	AC3090	conserved hypotet	954	80	4.2	166	2	A33402	pregnancy-specific
882	81	4.2	354	2	I54531	histocompatibility	955	80	4.2	219	2	A11534	hypothetical prote
883	81	4.2	379	2	A81678	conserved hypotet	956	80	4.2	267	2	I72882	Fc gamma receptor
884	81	4.2	414	2	A69907	cell wall-binding	957	80	4.2	313	2	JQ1862	31R protein - vari
885	81	4.2	426	2	B53580	neurexin III beta	958	80	4.2	351	2	S45305	MHC class I histoc
886	81	4.2	509	2	JC5288	SHP substrate-1 pr	959	80	4.2	359	1	HLH12	CD44 antigen precu
887	81	4.2	513	2	AC5289	SHP substrate-1 pr	960	80	4.2	368	2	A45831	MHC class I histoc
888	81	4.2	536	2	A40676	sphere organelle p	961	80	4.2	432	1	S38170	gene HLA-A-0203 pr
889	81	4.2	551	2	S64314	probable membrane	962	80	4.2	432	1	RWM074	MHC class I histoc
890	81	4.2	566	2	A49880	alpha-N-acetylglala	963	80	4.2	479	2	AP3019	pyruvate kinase li
891	81	4.2	655	2	G56524	protein T1N5.9 [i	964	80	4.2	479	2	C98265	pyruvate kinase (p
892	81	4.2	662	2	T18293	probable transcrip	965	80	4.2	499	2	A11472	heat-shock protein
893	81	4.2	662	2	G84903	probable BHLH tran	966	80	4.2	539	2	F72288	methy1-accepting c
894	81	4.2	769	2	T27550	hypothetical prote	967	80	4.2	550	2	T29919	hypothetical prote
895	81	4.2	773	2	T00502	probable receptor-	968	80	4.2	573	2	A33533	cell surface glyco
896	81	4.2	808	1	T04982	dynamitin-like prote	969	80	4.2	584	2	B25682	homeotic protein E
897	81	4.2	873	2	JC7079	homeobox protein Z	970	80	4.2	595	1	A48077	myb-related protei
898	81	4.2	883	2	S49126	brevican precursor	971	80	4.2	600	2	S07638	spore coat protein
899	81	4.2	895	2	S74225	leptin receptor, i	972	80	4.2	663	2	T37772	telomere length re
900	81	4.2	919	2	A41275	DNA ligase (ATP) {	973	80	4.2	732	2	C64972	probable Affase -
901	81	4.2	972	2	T49773	related to actin-i	974	80	4.2	743	2	B84639	transcription fact
902	81	4.2	972	2	F71608	hypothetical prote	975	80	4.2	772	2	A55004	polypeptide - Japa
903	81	4.2	1016	2	T05066	hypothetical prote	976	80	4.2	789	2	I50804	polypeptide - Japa
904	81	4.2	1021	2	T39207	leukocyte surface	977	80	4.2	791	2	A56241	aryl hydrocarbon r
905	81	4.2	1046	2	T39276	hypothetical prote	978	80	4.2	814	2	T26702	hypothetical prote

979	80	4.2	853	2	T46347	hypothetical prote	1052	79	4.1	792	2	S20554	pyruvate, water di
980	80	4.2	899	2	S51341	SGD1 protein - Yea	1053	79	4.1	792	2	T29187	hypothetical prote
981	80	4.2	1143	2	T28129	hypothetical prote	1054	79	4.1	824	2	G81748	conserved hypotet
982	80	4.2	1194	2	C59436	KIAA1391 protein [1055	79	4.1	825	1	EDBEXD	immediate-early pr
983	80	4.2	1257	2	S28764	neurocan precursor	1056	79	4.1	852	2	T06310	hypothetical prote
984	80	4.2	1471	2	B48218	neurexin iii-alpha	1057	79	4.1	860	1	QRHULD	LDL receptor precu
985	80	4.2	2468	2	A83412	hypothetical prote	1058	79	4.1	883	2	S04722	puff 74E protein -
986	80	4.2	2588	2	T14342	NSD1 protein - mou	1059	79	4.1	912	2	A54423	brevican precursor
987	80	4.2	3432	1	GNWVS	genome polyprotein	1060	79	4.1	948	2	A57640	retinoblastoma bin
988	79.5	4.2	132	1	RNWS12	T-cell receptor ga	1061	79	4.1	951	2	T26738	hypothetical prote
989	79.5	4.2	200	2	JC4357	HMG1 protein - sea	1062	79	4.1	971	2	B90835	probable tail fibe
990	79.5	4.2	213	2	S35527	heterochromatin pr	1063	79	4.1	973	2	C85693	neuronal kinesin h
991	79.5	4.2	218	2	JC7220	nuclear protein SR	1064	79	4.1	1032	2	I38510	hypothetical prote
992	79.5	4.2	299	2	T12483	hypothetical prote	1065	79	4.1	1038	2	S53522	platelet-derived g
993	79.5	4.2	303	2	H83108	hypothetical prote	1066	79	4.1	1058	1	PWMSRB	probable transcrip
994	79.5	4.2	392	2	T46418	hypothetical prote	1067	79	4.1	1098	2	T08599	probable tail fibe
995	79.5	4.2	423	2	A84483	probable protein k	1068	79	4.1	1122	2	G64887	dynein heavy chain
996	79.5	4.2	425	2	E71276	hypothetical prote	1069	79	4.1	1169	2	T30207	hypothetical prote
997	79.5	4.2	426	2	JH0518	lymphocyte homing	1070	79	4.1	1263	2	T15496	gene 62 protein -
998	79.5	4.2	475	2	A54879	pregnancy-specific	1071	79	4.1	1310	1	WZB562	glucan 1,4-alpha-g
999	79.5	4.2	577	2	T48530	clathrin binding p	1072	79	4.1	1367	1	S48478	hypothetical prote
1000	79.5	4.2	640	1	S76024	conserved hypotet	1073	79	4.1	1418	2	T15232	hypothetical prote
1001	79.5	4.2	646	2	T02398	protein phosphatas	1074	79	4.1	1461	2	E90596	hypothetical prote
1002	79.5	4.2	658	2	S68418	hypothetical prote	1075	79	4.1	1461	2	A85547	protein F6N18.13 f
1003	79.5	4.2	680	2	T30620	hypothetical prote	1076	79	4.1	1494	2	D86452	alpha-2-macroglobu
1004	79.5	4.2	688	2	A83179	conserved hypotet	1077	79	4.1	2109	1	I50421	alpha-2-macroglobu
1005	79.5	4.2	697	2	T16908	hypothetical prote	1078	79	4.1	4543	1	A53102	alpha-2-macroglobu
1006	79.5	4.2	736	2	T41259	hypothetical prote	1079	79	4.1	4544	1	S02392	gp330 protein prec
1007	79.5	4.2	819	2	A47018	lectin-like adhesi	1080	79	4.1	4545	1	S25111	alpha-2-macroglobu
1008	79.5	4.2	831	2	T49721	hypothetical prote	1081	79	4.1	4660	2	T42737	Ig heavy chain V r
1009	79.5	4.2	837	2	AD0159	outer membrane ush	1082	79	4.1	115	2	S19958	T-cell surface gly
1010	79.5	4.2	861	1	VCLJSC	env polyprotein pr	1083	78.5	4.1	115	2	A29523	protein F58A4.1 [i
1011	79.5	4.2	909	2	H86350	hypothetical prote	1084	78.5	4.1	246	2	D88560	B16R protein - vac
1012	79.5	4.2	982	2	A53253	microtubule-associ	1085	78.5	4.1	254	2	F42527	hypothetical prote
1013	79.5	4.2	1018	2	T34433	hypothetical prote	1086	78.5	4.1	290	2	F42527	hypothetical prote
1014	79.5	4.2	1032	2	A96714	hypothetical prote	1087	78.5	4.1	301	2	S40973	hypothetical prote
1015	79.5	4.2	1033	2	T51904	hypothetical prote	1088	78.5	4.1	303	2	S40973	hypothetical prote
1016	79.5	4.2	1051	2	S61918	protein kinase C (1089	78.5	4.1	334	2	H85057	probable G-box bin
1017	79.5	4.2	1139	1	S61918	cardiac myosin-bin	1090	78.5	4.1	346	2	T03373	hypothetical prote
1018	79.5	4.2	1152	2	A33183	microtubule-associ	1091	78.5	4.1	362	2	B40784	MHC class I histoc
1019	79.5	4.2	1163	2	S56126	lymphocyte fuction	1092	78.5	4.1	366	2	S42823	hypothetical prote
1020	79.5	4.2	1269	2	S35366	furin (BC 3.4.21.7	1093	78.5	4.1	420	2	T46910	serotonin receptor
1021	79.5	4.2	1284	2	S55050	unknown protein [i	1094	78.5	4.1	425	2	S03961	Ig mu chain C regi
1022	79.5	4.2	1311	2	T08986	hypothetical prote	1095	78.5	4.1	457	2	A81833	pre-mRNA splicing
1023	79.5	4.2	1311	2	T08986	hypothetical prote	1096	78.5	4.1	494	2	T40608	conserved hypotet
1024	79.5	4.2	1892	2	T18314	homeotic protein z	1097	78.5	4.1	560	2	C86400	hypothetical prote
1025	79.5	4.2	3005	2	S33642	hypothetical prote	1098	78.5	4.1	574	2	S48940	hypothetical prote
1026	79.5	4.2	6713	2	JC4788	sodium channel pro	1100	78.5	4.1	605	2	T27123	hypothetical prote
1027	79	4.1	218	2	T23555	MHC HLA-A cell sur	1101	78.5	4.1	627	2	T14765	hypothetical prote
1028	79	4.1	238	2	T68699	IgE Fc receptor al	1102	78.5	4.1	723	2	T14765	hypothetical prote
1029	79	4.1	250	2	A34342	FC gamma 2 recepto	1103	78.5	4.1	748	2	T51738	RNA helicase RH3 [
1030	79	4.1	264	2	T46030	hypothetical prote	1104	78.5	4.1	869	2	T22422	probable protein k
1031	79	4.1	268	2	T23555	hypothetical prote	1105	78.5	4.1	894	2	S25332	hypothetical prote
1032	79	4.1	270	2	B75581	probable cytochrom	1106	78.5	4.1	918	2	A44257	interleukin-6 sign
1033	79	4.1	275	2	H35216	cell wall-binding	1107	78.5	4.1	959	2	S32016	flagellum-associat
1034	79	4.1	316	1	QRHUT2	microtubule-associ	1108	78.5	4.1	969	2	H69425	modification methy
1035	79	4.1	326	2	A39953	interleukin-1 beta	1109	78.5	4.1	976	2	T51137	ionotropic glutama
1036	79	4.1	338	2	A39953	MHC class I histoc	1110	78.5	4.1	1012	2	T24384	hypothetical prote
1037	79	4.1	363	1	S42102	MHC class I histoc	1111	78.5	4.1	1013	2	T30818	hypothetical prote
1038	79	4.1	368	2	H96990	probable membrane	1112	78.5	4.1	1105	2	T18295	hadr protein - Kle
1039	79	4.1	441	1	QRHUT1	microtubule-associ	1113	78.5	4.1	1196	2	H86389	hypothetical prote
1040	79	4.1	461	2	H84099	glucose-6-phosphat	1114	78.5	4.1	1224	2	S73171	hypothetical prote
1041	79	4.1	481	2	E81854	hypothetical prote	1115	78.5	4.1	1235	2	T13710	atypical protein k
1042	79	4.1	482	2	T22981	hypothetical prote	1116	78.5	4.1	1255	2	A37488	hypothetical prote
1043	79	4.1	484	2	S66713	conserved hypotet	1117	78.5	4.1	1337	2	T13348	hypothetical prote
1044	79	4.1	488	2	AD0735	probable Na+/H+ an	1118	78.5	4.1	1358	2	S70310	hypothetical prote
1045	79	4.1	528	2	T34941	probable membrane	1119	78.5	4.1	1382	2	T49316	profilaggrin relat
1046	79	4.1	542	2	S64030	synapsin Iia - rat	1120	78.5	4.1	1386	1	GNWVJF	genome polyprotein
1047	79	4.1	586	2	C30411	probable starch sy	1121	78.5	4.1	1440	1	A60988	saliva-interacting
1048	79	4.1	610	2	T39758	proline-serine ric	1122	78.5	4.1	1556	2	T02885	peroxisome prolif
1049	79	4.1	615	2	T39758	suppressor of Yeas	1123	78.5	4.1	1560	2	T02885	protein-tyrosine-p
1050	79	4.1	741	2	I51657	phosphoenolpyruvat	1124	78.5	4.1	1615	2	B49502	
1051	79	4.1	792	2	A90930								

1125	78.5	4.1	1736	2	F86178	hypothetical prote	1198	77.5	4.1	353	2	B53250	class I histocompa
1126	78.5	4.1	1767	2	A42125	trophozoite cystei	1199	77.5	4.1	354	2	B69002	histocompatibility
1127	78.5	4.1	1767	2	A49502	protein-tyrosine-p	1200	77.5	4.1	361	2	B59099	hypothetical prote
1128	78.5	4.1	1777	2	T34369	hypothetical prote	1201	77.5	4.1	364	1	S31304	protein-tyrosine-p
1129	78.5	4.1	1796	2	S65004	probable membrane	1202	77.5	4.1	364	2	A35997	MHC class I histoc
1130	78.5	4.1	1911	2	T33048	calcium channel al	1203	77.5	4.1	365	2	T37483	HLA-A*34.2 antigen
1131	78.5	4.1	1977	2	S47771	sodium channel alp	1204	77.5	4.1	366	2	A60389	MHC class I histoc
1132	78.5	4.1	1997	1	S12050	protein-tyrosine-p	1205	77.5	4.1	401	2	A57226	mei-S332 protein -
1133	78.5	4.1	2055	2	T00093	hypothetical prote	1206	77.5	4.1	402	1	QR8072	microtubule-associ
1134	78.5	4.1	2559	2	T09144	probable guanine n	1207	77.5	4.1	440	2	S74969	hypothetical prote
1135	78.5	4.1	3078	2	T28432	variant-specific s	1208	77.5	4.1	450	2	T25542	hypothetical prote
1136	78	4.1	214	2	D26839	F23A5.5 [imported]	1209	77.5	4.1	454	1	MHY	Ig mu chain C regi
1137	78	4.1	218	2	A57334	sodium channel, vo	1210	77.5	4.1	457	2	S73774	diacylglycerol-poi
1138	78	4.1	218	2	A42737	sodium channel bet	1211	77.5	4.1	460	2	T45968	hypothetical prote
1139	78	4.1	286	2	C84857	hypothetical prote	1212	77.5	4.1	474	2	T00699	hypothetical prote
1140	78	4.1	317	2	T39869	probable lysophosp	1213	77.5	4.1	474	2	AG2269	heterocyst specifi
1141	78	4.1	332	2	H82064	conserved hypothet	1214	77.5	4.1	486	2	D70154	replication initia
1142	78	4.1	349	2	T31394	hypothetical serin	1215	77.5	4.1	495	1	FWSYC2	glycinin chain Ala
1143	78	4.1	357	2	S11133	class I histocompa	1216	77.5	4.1	499	2	T45749	hypothetical prote
1144	78	4.1	366	2	I37078	HLA-C alpha chain	1217	77.5	4.1	500	2	B44055	envelope protein -
1145	78	4.1	371	2	B84709	hypothetical prote	1218	77.5	4.1	500	2	A44055	envelope protein -
1146	78	4.1	391	2	T36321	hypothetical prote	1219	77.5	4.1	531	2	T18931	hypothetical prote
1147	78	4.1	469	2	S76891	hypothetical prote	1220	77.5	4.1	537	2	T49769	intercellular adhe
1148	78	4.1	481	2	A27626	sucrose phosphoryl	1221	77.5	4.1	537	2	A45815	intracellular recep
1149	78	4.1	487	1	BWSOGM	gtfA protein - Str	1222	77.5	4.1	570	2	A57535	interleukin 1 recep
1150	78	4.1	504	2	I56542	calmodulin-binding	1223	77.5	4.1	590	1	S55095	myb-related protei
1151	78	4.1	511	2	A97212	protein containing	1224	77.5	4.1	594	1	D55514	diacylglycerol-poi
1152	78	4.1	513	2	T34546	hypothetical prote	1225	77.5	4.1	625	2	T41603	alpha-amylase - fi
1153	78	4.1	517	2	T40129	hypothetical prote	1226	77.5	4.1	630	2	T51086	prolactin receptor
1154	78	4.1	536	2	T37544	hypothetical serin	1227	77.5	4.1	642	2	B49849	terminase large ch
1155	78	4.1	540	2	T00646	hypothetical prote	1228	77.5	4.1	646	1	S15901	chromogranin B pre
1156	78	4.1	551	1	S52657	seed biotin-contai	1229	77.5	4.1	665	1	H97093	fructose-bisphosph
1157	78	4.1	555	2	J01526	interleukin-1 rece	1230	77.5	4.1	716	2	T19355	hypothetical prote
1158	78	4.1	564	2	I53106	gene gli protein -	1231	77.5	4.1	722	2	B86583	transcription elon
1159	78	4.1	574	2	A84782	hypothetical prote	1232	77.5	4.1	722	2	C72040	transcription elon
1160	78	4.1	577	2	S84613	probable membrane	1233	77.5	4.1	735	2	T45059	hypothetical prote
1161	78	4.1	621	2	T24090	hypothetical prote	1234	77.5	4.1	888	2	S23085	conserved hypothet
1162	78	4.1	660	2	TJ0067	chitinase (EC 3.2.	1235	77.5	4.1	921	2	AE0332	fibronectin-bindin
1163	78	4.1	671	2	T12976	hypothetical prote	1236	77.5	4.1	940	2	S19702	cyclic nucleotide
1164	78	4.1	682	2	T43292	G protein-linked a	1237	77.5	4.1	1054	2	T30901	MHC class II trans
1165	78	4.1	713	2	A95942	probable bifunctio	1238	77.5	4.1	1130	2	A48843	xeroderma pigmento
1166	78	4.1	739	2	TJ00581	vascular cell adhe	1239	77.5	4.1	1293	2	S42402	transcription co-r
1167	78	4.1	753	2	F69338	pyruvate, water di	1240	77.5	4.1	1495	2	S60255	hypothetical prote
1168	78	4.1	763	2	T24367	hypothetical prote	1241	77.5	4.1	2048	2	AG2109	hypothetical prote
1169	78	4.1	765	2	T49592	neurofilament trip	1242	77.5	4.1	2109	2	T38414	transcription fact
1170	78	4.1	785	2	I50180	cadherin-7 - chick	1243	77.5	4.1	2470	2	I50726	cation-independent
1171	78	4.1	792	2	E85778	phosphoenolpyruvat	1244	77.5	4.1	3212	2	T24692	hypothetical prote
1172	78	4.1	831	2	T49758	related to cytochr	1245	77	4.0	162	2	T51668	tumor suppressor -
1173	78	4.1	841	1	I78885	serine/threonine-s	1246	77	4.0	186	2	T61783	sodium channel bet
1174	78	4.1	915	2	T09575	smoothelin - human	1247	77	4.0	203	2	C87801	protein C10G11.9 l
1175	78	4.1	919	2	T32541	unc-5 protein - Ca	1248	77	4.0	203	2	T25916	hypothetical prote
1176	78	4.1	941	2	T51135	ligand-gated chann	1249	77	4.0	214	2	H96842	F23A5.34 [imported
1177	78	4.1	942	2	T32551	protein-tyrosine k	1250	77	4.0	287	2	B96717	unknown protein, 3
1178	78	4.1	947	1	B44294	unc-5 protein, lon	1251	77	4.0	316	2	C37028	MHC class I histoc
1179	78	4.1	966	2	S25365	CYC8 protein - yea	1252	77	4.0	326	2	JC4112	pregnancy-specific
1180	78	4.1	1038	2	H90053	hypothetical prote	1253	77	4.0	357	2	S11137	class I histocompa
1181	78	4.1	1047	2	A59246	HIRA protein - fru	1254	77	4.0	364	2	T72217	class I histocompa
1182	78	4.1	1095	2	T20528	hypothetical prote	1255	77	4.0	365	2	T61902	MHC class I histoc
1183	78	4.1	1137	2	JC5950	integrin alpha-7 c	1256	77	4.0	393	2	S63379	probable membrane
1184	78	4.1	1158	2	S73348	nuclear factor R1P	1257	77	4.0	432	1	RWC214	T-cell surface gly
1185	78	4.1	1174	2	A40853	potassium channel	1258	77	4.0	435	2	S75346	hypothetical prote
1186	78	4.1	1191	2	T14154	serine/threonine p	1259	77	4.0	450	2	AD1710	phosphoglucutase
1187	78	4.1	1289	2	T31344	GP80 precursor - s	1260	77	4.0	452	2	T40769	hypothetical prote
1188	78	4.1	1389	2	T03273	embryogenesis tran	1261	77	4.0	484	2	T25731	hypothetical prote
1189	78	4.1	1650	2	S3457	dominant autoantig	1262	77	4.0	511	2	T23189	hypothetical prote
1190	78	4.1	2165	2	T1371	hypothetical prote	1263	77	4.0	521	2	T21440	hypothetical prote
1191	78	4.1	2228	1	ZLNZSV	genome polyprotein	1264	77	4.0	527	2	F89240	protein K01D2.6 l
1192	78	4.1	2938	2	T42761	Basoon protein -	1265	77	4.0	530	2	S46589	UTR1 protein - yea
1193	78	4.1	5170	2	T15348	hypothetical prote	1266	77	4.0	571	2	A11094	probable peptidogl
1194	77.5	4.1	202	2	A42410	ryudocan precursor	1267	77	4.0	607	2	C75432	dihydroxy-acid deh
1195	77.5	4.1	214	2	B97143	hypothetical secre	1268	77	4.0	644	2	S39356	transcription fact
1196	77.5	4.1	319	2	E96715	protein F4N2.12 l	1269	77	4.0	646	2	JQ2150	B west mating prot
1197	77.5	4.1	345	2	T29786	hypothetical prote	1270	77	4.0	662	2	D40228	neurexin II-beta p

1271	77	4.0	721	2	F82198	probable toxin sec	1344	76.5	4.0	1466	2	T32422	hypothetical prote
1272	77	4.0	810	2	S69652	hypothetical prote	1345	76.5	4.0	1567	2	T03730	antigen containing
1273	77	4.0	875	2	S62177	HIR2 protein - Yea	1346	76.5	4.0	1679	2	S49802	probable membrane
1274	77	4.0	884	2	S77031	hypothetical prote	1347	76.5	4.0	2228	2	S97942	beta-galactosidase
1275	77	4.0	886	2	S29605	glycoprotein 350/2	1348	76.5	4.0	2488	2	T42739	guanine nucleotide
1276	77	4.0	887	2	T20941	hypothetical prote	1349	76.5	4.0	3432	1	GNWUJE	guanine nucleotide
1277	77	4.0	913	1	IJCHCR	R-cadherin precurs	1350	76	4.0	198	2	JC1457	genomic polyprotein
1278	77	4.0	920	2	T52426	dynamitin-like prote	1351	76	4.0	218	2	B47712	ryudocan precursor
1279	77	4.0	940	2	T01854	hypothetical prote	1352	76	4.0	235	2	168700	myelin/oligodendro
1280	77	4.0	947	2	T20512	hypothetical prote	1353	76	4.0	247	2	S74912	MHC HLA-A cell sur
1281	77	4.0	1023	2	G82213	hypothetical prote	1354	76	4.0	267	2	T52381	hypothetical prote
1282	77	4.0	1048	2	H87721	hypothetical prote	1355	76	4.0	273	2	F91083	zinc finger protein
1283	77	4.0	1055	2	T43275	hypothetical prote	1356	76	4.0	283	2	T11644	hypothetical membr
1284	77	4.0	1106	2	S38783	probable purine nu	1357	76	4.0	313	2	E70951	hypothetical prote
1285	77	4.0	1199	2	T29145	hypothetical prote	1358	76	4.0	318	2	D71441	hypothetical prote
1286	77	4.0	1518	2	S37928	hypothetical prote	1359	76	4.0	329	2	A40730	hypothetical prote
1287	77	4.0	1534	2	A85962	probable membrane	1360	76	4.0	331	2	T35100	class I histocompa
1288	77	4.0	1534	2	G91017	hypothetical prote	1361	76	4.0	336	2	T30757	probable secreted
1289	77	4.0	1549	2	T21809	hypothetical prote	1362	76	4.0	348	2	150107	hypothetical prote
1290	77	4.0	1715	2	C40228	neurexin II-alpha	1363	76	4.0	355	2	B40730	MHC class I histoc
1291	77	4.0	1812	2	I49350	breast/ovarian can	1364	76	4.0	356	2	A27797	class I histocompa
1292	77	4.0	1912	2	T29088	vitellogenin I pre	1365	76	4.0	356	2	JH0289	class I histocompa
1293	77	4.0	2237	2	T45115	vitellogenin I	1366	76	4.0	361	2	B82533	translation releas
1294	77	4.0	3562	2	A47171	N-type calcium cha	1367	76	4.0	365	2	T37470	HLA-A*0210 - hum
1295	76.5	4.0	116	2	C27390	chondroitin sulfat	1368	76	4.0	403	2	T49603	hypothetical prote
1296	76.5	4.0	127	2	T30102	Ig lambda chain pr	1369	76	4.0	409	2	E64456	hypothetical prote
1297	76.5	4.0	139	2	C27639	hypothetical prote	1370	76	4.0	426	2	A39621	homeotic protein H
1298	76.5	4.0	202	2	I53137	T-cell receptor ga	1371	76	4.0	490	2	T26067	hypothetical prote
1299	76.5	4.0	235	2	S20000	fibroglycan (synde	1372	76	4.0	500	2	T37488	hypothetical prote
1300	76.5	4.0	237	2	T13649	Ig light chain pre	1373	76	4.0	523	2	T37488	hypothetical prote
1301	76.5	4.0	242	2	T48519	hypothetical prote	1374	76	4.0	535	2	S66148	actin-like protein
1302	76.5	4.0	242	2	S71527	hypothetical prote	1375	76	4.0	535	2	A75481	gene pipsaqueak pr
1303	76.5	4.0	274	2	C36464	outer surface prot	1376	76	4.0	568	2	A75481	sensor histidine k
1304	76.5	4.0	302	2	S46760	fibroblast growth	1377	76	4.0	602	2	139411	AF-9 protein - hum
1305	76.5	4.0	325	2	A21507	hypothetical prote	1378	76	4.0	616	2	T32753	hypothetical prote
1306	76.5	4.0	341	2	S24240	hypothetical prote	1379	76	4.0	635	2	F75477	hypothetical prote
1307	76.5	4.0	359	2	T47588	lymphocyte surface	1380	76	4.0	640	1	Q0BEU2	UL35 protein - hum
1308	76.5	4.0	363	2	S47588	hypothetical prote	1381	76	4.0	653	2	A49722	endoglin precursor
1309	76.5	4.0	380	2	G69604	spore coat protein	1382	76	4.0	655	2	T28885	hypothetical prote
1310	76.5	4.0	400	2	S22733	hypothetical prote	1383	76	4.0	670	2	E86164	probable gtpase ac
1311	76.5	4.0	445	2	AF0033	Ha-transferring tw	1384	76	4.0	695	2	T39954	nucleolus-cytoplas
1312	76.5	4.0	474	1	OMHULB	alpha-1-B-glycopro	1385	76	4.0	734	2	B42680	splicing regulator
1313	76.5	4.0	475	2	I76668	pregnancy-specific	1386	76	4.0	749	2	S50095	splicing regulator
1314	76.5	4.0	493	2	S13530	CD4E protein, epi	1387	76	4.0	757	2	T05688	hypothetical prote
1315	76.5	4.0	497	2	S47890	exuperantia 1 - fr	1388	76	4.0	775	1	EDBE11	hypothetical prote
1316	76.5	4.0	500	2	B98260	hypothetical prote	1389	76	4.0	776	2	T33543	immediate-early pr
1317	76.5	4.0	500	2	A30324	histidase huth [im	1390	76	4.0	822	2	T51049	related to nucleol
1318	76.5	4.0	508	2	A29605	protein A precursor	1391	76	4.0	839	2	F75518	hypothetical prote
1319	76.5	4.0	523	2	S67271	hypothetical prote	1392	76	4.0	853	2	A71339	probable outer mem
1320	76.5	4.0	524	2	S47143	A mating type prot	1393	76	4.0	860	2	F71000	hypothetical prote
1321	76.5	4.0	539	2	B27207	hypothetical prote	1394	76	4.0	887	1	IJCHCL	E-cadherin precurs
1322	76.5	4.0	545	2	A45769	intercellular adhe	1395	76	4.0	944	2	H64650	translation initia
1323	76.5	4.0	607	2	A43776	acetylcholine rece	1396	76	4.0	960	2	T17297	hypothetical prote
1324	76.5	4.0	690	2	I51298	drebrin E2 - chick	1397	76	4.0	966	2	S43878	hypothetical prote
1325	76.5	4.0	709	2	C28821	transforming prote	1398	76	4.0	995	2	S50358	hypothetical prote
1326	76.5	4.0	761	2	T26955	1-phosphatidylinos	1399	76	4.0	1002	2	T09438	trwC protein - Esc
1327	76.5	4.0	786	2	T16509	hypothetical prote	1400	76	4.0	1029	2	T02576	hypothetical prote
1328	76.5	4.0	789	2	C83949	hypothetical prote	1401	76	4.0	1032	2	B82276	ToxR-activated lip
1329	76.5	4.0	812	2	A81096	hypothetical prote	1402	76	4.0	1054	2	T43226	hypothetical prote
1330	76.5	4.0	815	2	T49744	cell division prot	1403	76	4.0	1057	2	H83273	translation initia
1331	76.5	4.0	865	2	T46651	probable ubiquitin	1404	76	4.0	1085	2	S66149	ribonuclease E PA2
1332	76.5	4.0	891	2	A46203	transcription acti	1405	76	4.0	1192	2	T18611	gene pipsaqueak pr
1333	76.5	4.0	896	2	S48761	mating type A-alph	1406	76	4.0	1230	2	T18259	probable serine/th
1334	76.5	4.0	899	2	A35895	trehalose-phosphat	1407	76	4.0	1237	2	A34598	serine/threonine p
1335	76.5	4.0	928	2	A87749	androgen receptor	1408	76	4.0	1280	2	T00365	hypothetical prote
1336	76.5	4.0	987	2	B71617	protein F55C7.7c [1409	76	4.0	1355	2	S40022	spalt protein - fr
1337	76.5	4.0	1184	2	S50832	SERA antigen/papal	1410	76	4.0	1357	2	T29285	hypothetical prote
1338	76.5	4.0	1184	2	G01763	atrophin-1 - human	1411	76	4.0	1374	2	D72593	hypothetical prote
1339	76.5	4.0	1192	2	F88062	atrophin-1 - human	1412	76	4.0	1394	2	B34598	hypothetical prote
1340	76.5	4.0	1234	2	T31623	protein ZK250.10 [1413	76	4.0	1403	2	T11583	ecdysone-induced p
1341	76.5	4.0	1268	2	S52781	hypothetical prote	1414	76	4.0	1457	2	D81019	probable translati
1342	76.5	4.0	1361	2	T30884	neurocan - mouse	1415	76	4.0	1578	2	148216	adhesion and penet
1343	76.5	4.0	1366	2	B86292	neural specific DN	1416	76	4.0	1578	2	148216	neurexin III-alpha
					F7H2.12 protein -								

1417 76 4.0 1579 2 T30271 surface protein -
1418 76 4.0 1726 2 T30810 chromatin structur
1419 76 4.0 1737 2 A59235 unconventional myo
1420 76 4.0 1804 2 T34518 nestin - golden ha
1421 76 4.0 1810 1 A32230 tenascin precursor
1422 76 4.0 1931 2 A59234 slow myosin heavy
1423 76 4.0 2124 2 T01526 hypothetical prote
1424 76 4.0 2167 2 AF1489 cell wall-associat
1425 76 4.0 2447 2 T16870 hypothetical prote
1426 76 4.0 3624 2 AD0835 large repetitive p
1427 76 4.0 4006 2 T09070 probable tenascin
1428 75.5 4.0 102 2 C32530 Ig heavy chain v r
1429 75.5 4.0 116 2 S22553 Ig heavy chain v r
1430 75.5 4.0 131 2 A27472 Ig heavy chain pre
1431 75.5 4.0 178 2 T20599 hypothetical prote
1432 75.5 4.0 196 2 S50487 hypothetical prote
1433 75.5 4.0 202 2 B87342 hypothetical prote
1434 75.5 4.0 212 2 T10923 3C3, 14c protein -
1435 75.5 4.0 254 2 B31790 Ig heavy chain v r
1436 75.5 4.0 261 2 C85681 hypothetical prote
1437 75.5 4.0 280 1 B64235 fibronectin-bindin
1438 75.5 4.0 290 2 I68750 MHC class I lympho
1439 75.5 4.0 296 2 S74253 homeotic protein s
1440 75.5 4.0 311 2 T04801 hypothetical prote
1441 75.5 4.0 317 2 S55316 mucin (clone FGM-2
1442 75.5 4.0 324 2 A81364 protein gp49 [Bact
1443 75.5 4.0 341 2 C86307 F20D23.17 protein
1444 75.5 4.0 344 2 S50474 hypothetical prote
1445 75.5 4.0 346 1 D64811 aldose 1-epimerase
1446 75.5 4.0 353 2 G02922 MHC class I lero-G
1447 75.5 4.0 356 2 T51376 plant adhesion mol
1448 75.5 4.0 357 2 S11141 class I histocompa
1449 75.5 4.0 424 1 A29830 benzene 1,2-dioxvg
1450 75.5 4.0 448 2 T29257 hypothetical prote
1451 75.5 4.0 465 2 T29257 hypothetical prote
1452 75.5 4.0 467 2 G59849 endo-1,4-beta-xyla
1453 75.5 4.0 473 2 F70031 cell wall-binding
1454 75.5 4.0 497 2 T51195 hypothetical prote
1455 75.5 4.0 503 2 JC5287 SHP substrate-1 pr
1456 75.5 4.0 510 2 H94824 En/Spm-like transp
1457 75.5 4.0 511 2 I50114 early growth respo
1458 75.5 4.0 519 2 S3796 modifier-3 protein
1459 75.5 4.0 519 2 A54590 GAGA transcription
1460 75.5 4.0 531 2 S20900 titin - mouse (fra
1461 75.5 4.0 593 2 JC7829 metal-responsive t
1462 75.5 4.0 608 2 T37864 hypothetical prote
1463 75.5 4.0 653 2 I48341 endoglin - mouse
1464 75.5 4.0 671 2 A01666 DNA ligase homolog
1465 75.5 4.0 699 2 I37369 epican - human
1466 75.5 4.0 706 2 S33035 probable lysophosp
1467 75.5 4.0 753 2 A52009 cation-transportin
1468 75.5 4.0 756 2 JC5886 signaling mediator
1469 75.5 4.0 781 2 T51433 probable cation tr
1470 75.5 4.0 816 2 S05548 gap protein hunchb
1471 75.5 4.0 851 2 T38648 hypothetical prote
1472 75.5 4.0 878 2 T21621 hypothetical prote
1473 75.5 4.0 880 1 JC4166 protein-tyrosine k
1474 75.5 4.0 910 2 C59456 subtilisin sendai
1475 75.5 4.0 929 2 I51027 type XII collagen
1476 75.5 4.0 935 2 T19011 hypothetical prote
1477 75.5 4.0 962 2 D86186 hypothetical prote
1478 75.5 4.0 1013 2 T46442 hypothetical prote
1479 75.5 4.0 1033 2 A12359 hypothetical prote
1480 75.5 4.0 1064 2 B86465 probable Protein k
1481 75.5 4.0 1093 2 I38533 AF17 protein - hum
1482 75.5 4.0 1121 2 T38127 phosphoprotein pho
1483 75.5 4.0 1171 2 T042916 metabotropic gluta
1484 75.5 4.0 1240 2 T04833 hypothetical prote
1485 75.5 4.0 1332 2 S41552 probable transcrip
1486 75.5 4.0 1343 2 AF0611 cell division prot
1487 75.5 4.0 1404 2 E85509 hypothetical prote
1488 75.5 4.0 1404 2 E90658 RING core protein
1489 75.5 4.0 1447 2 S02160 DNA topoisomerase

1490 75.5 4.0 1557 2 T18412 lipid-binding prot
1491 75.5 4.0 1711 2 C71625 variant-specific s
1492 75.5 4.0 1753 2 S30855 hypothetical prote
1493 75.5 4.0 1807 2 JC6319 integrin beta-4 ch
1494 75.5 4.0 2015 2 B11989 hypothetical prote
1495 75.5 4.0 2610 2 T20968 hypothetical prote
1496 75.5 4.0 2774 2 A43359 microtubule-associ
1497 75.5 4.0 3869 2 A48205 All-1 protein +GRE
1498 75.5 4.0 4377 2 A55575 ankyrin 3, long sp
1499 75 3.9 107 2 D72598 hypothetical prote
1500 75 3.9 138 2 A27639 T-cell receptor ga

ALIGNMENTS

RESULT 1

JC7780

coxackie- and adenovirus receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004

C:Accession: JC7780

R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.

Biochem. Biophys. Res. Commun. 288, 805-808, 2001

A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor

A:Reference number: JC7780

A:Contents: Liver

A:Accession: JC7780

A:Molecule type: mRNA

A:Residues: 1-365 <THO>

A:Cross-references: UNIPROT:Q8MWV3; GB:AY033651

C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells.

Query Match 24.8%; Score 474; DB 2; Length 365;

Best Local Similarity 33.6%; Pred. No. 1.1e-26;

Matches 128; Conservative 66; Mismatches 153; Indels 34; Gaps 11;

Qy 1 MSLLLLLL---VSYYVGTLTGHT---IKRVAEEKVTLPCHHQLGPKDTLDIEWLLT 54

Db 1 MELLRLFLLCGVADFTRGSLITTPQWIEKAKGETAYLPCKFTLGPEDQGLDIEWLLS 60

Qy 55 --DNEGQKVITYSSRHVNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYC 111

Db 61 PADNQKVDVILYSGDKIYDDYQDLKGRVHFVFTSNDLKSGDASINVTNLQSLDITGYQC 120

Qy 112 KVKNSGRYVWSHVTLKVLVRSPKCELEGTSGSDTLQCESSSGTEPIVYVQRIRE 171

Db 121 KVKAPGVGNKKIQTLVLRPSGIRCYDVGSEIIGNDFPKLCEPKESLPURYEQKL-- 178

Qy 172 KEGDERLPPKSRIDYDHPGRVLLQNLTMSSGLYQCTAGNAGKESCVRV-TVQYVQS 230

Db 179 --SDSKLPTSLPMTSP-VISVKASAEYSGYTCTVRNRVSGDQCLRLDVVPPSNR 235

Qy 231 IGWAGAVTGIVAGALLIFLLVLLIRKRYEERPEERNEIREDAEAPKARLVKPPSS 290

Db 236 AGTTAGAVIGTLLALVLIALIVFCCHKRREKEVEVH-HDIREVPPPKSRSTARSY 294

Qy 291 SSGSRSSRSSSTPRSTANSASRSQRTLSLT--AAPO-PGLATQAYSLVGVSEPKK 347

Db 295 IGSNHSLSGMSPSNMEGYKTNQVPSDELRAPOSPTL-----PPAK 339

Qy 348 VHANLTKAETTPSMIPSQSR 368

Db 340 VAAPNLRMGAVPVMIPAQSK 360

RESULT 2

S56749

junctional adhesion molecule precursor - human

N:Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11

C:Species: Homo sapiens (man)

C>Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A59406; S56749

Db 115 TQHPKTSQVLLIVQPPKISNISDVTVNNGSNVLLVCMANGREPVI-TWRHLTPGTR 173
Qy 171 EKEGEDERLPKSRIDYNHNGRVLQNLMTSYSGLYOCTAGNEAKESC-VYRVTVQVQ 229
Db 174 EFGEESEYLE-----ILGITRQSGKYCKEKAANEVSSADVQVKVTVNYP 219
Qy 230 SI--GMVAGVTG-----IVAGALLFLVLLWLRKDKERYEERPNREDAEAPK 281
Db 220 TITESKNEATYTGQASLKCSASA-----VPAPDFEYRDDTRIN----- 259
Qy 282 ARLVKPSSSSSGSSRSSTSTANSASRSQRTSLTDAPOPLATOAYSILVGP-EV 340
Db 260 -----SANGLEIKSTEGQSSLLTVNTEHYGNTVCVAANKLVGNASLVLFREGSV 311
Qy 341 RG 342
Db 312 RG 313

RESULT 5

RWHUC2
T-cell surface glycoprotein CD2 precursor - human
N;Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
A;Accession: A28967
A;Molecule type: DNA
A;Residues: 1-351 <DIA>
A;Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670
A;Accession: A26486
A;Molecule type: mRNA
A;Residues: 1-338, 'M', 340, 'QKQTHCPPLIKDORNCILFQ' <SE1>
A;Accession: B26486
A;Molecule type: protein
A;Residues: 25-46, 'X', 50 <SE2>
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
A;Contents: revision
A;Accession: A28416
A;Molecule type: mRNA
A;Residues: 333-351 <SE3>
R;Seed, B.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap
A;Reference number: A28023; MUID:87204137; PMID:2437578
A;Accession: A28023
A;Molecule type: mRNA
A;Residues: 1-265, 'O', 267-351 <SEE>
A;Cross-references: GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:g178669
R;Sayre, P.H.; Chang, H.C.; Husey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure
A;Reference number: S02292; MUID:87204243; PMID:2883656
A;Accession: S02292
A;Molecule type: mRNA
A;Residues: 1-338, 'M', 340, 'QKQTHCPPLIKDORNCILFQ' <SA1>
A;Cross-references: GB:M16336; NID:g180093; PIDN:AAA51946.1; PID:g180094
A;Accession: A30430
A;Molecule type: protein
A;Residues: 25-43, 152-163 <SA2>
R;Lang, G.; Worton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.
EMBO J. 7, 1675-1682, 1988
A;Title: The structure of the human CD2 gene and its expression in transgenic mice.

A;Reference number: S00829; MUID:89005055; PMID:2901953
A;Accession: S00829
A;Molecule type: DNA
A;Residues: 1-351 <LAN>
A;Cross-references: EMBL:X07871
C;Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appears
or is closely associated with, the erythrocyte receptor.
C;Genetics:
A;Gene: GDB:CD2
A;Cross-references: GDB:118735; OMIM:186990
A;Map position: 1p13.1-1p13.1
A;Introns: 21/1; 128/1; 205/1; 246/1
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;25-206/Domain: extracellular #status predicted <EXT>
F;210-234/Domain: transmembrane #status predicted <TMM>
F;237-351/Domain: intracellular #status predicted <INT>
F;89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 182; DB 1; Length 351;
Best Local Similarity 25.1%; Pred. No. 1.1e-05;
Matches 89; Conservative 51; Mismatches 128; Indels 86; Gaps 17;
Qy 45 DTLDIEWLLTDNEG-----QKVITYSSRVHNNLTBEQGRVAFASNFLAGDASLQIEP 100
Db 53 DIDDIKWEKTSKKKIAQFRKXETFEKDYK-----LFGKNTLKKH 96
Qy 101 LKPSDEGRYCKVKNK-GRVWVSHV-LKVLVPSKPK-----CELEGELTEGSLTLOCE 154
Db 97 LKTDQDIYKYVSYDTKGNVLEKIFDLKIQERVSKPKISWTC-----INTLTCE 147
Qy 155 SSGTEPIVYVQRIREKEGEDERLPKSRIDYNHNGRVLQNLMTSYSGLYOCTAGNEA 214
Db 148 VMNGTDEPLNLYQ-----DGKHLKLSQ-----RVITHKWTLSAKFKCTAGNKV 192
Qy 215 GKSCVVRVTQVQVSGVGMVAGVTGIVAGALLFLVLLI-----RRKDKERYEER 269
Db 193 SKSSSEVPVS---CPEKGLDIYLIIGCGGSLLMVFPVALLVYITRKQKQSRNDEEL 249
Qy 270 PNEIREDAEAPKARLVKPPSSSSSGSSRSSTSTANSASRSQRTSLTDAAPQPC-- 327
Db 250 --ETRAHRAVATEERGRKPHQIPAS--TPQNPATSQHPHPPPPGHRSQ--APSHRPPPPGHR 303
Qy 328 -----LATQAYSLVGPEVRGS--EPKKVHANLTAKETTPSMIPSQS 367
Db 304 VQHQPQKPPAPSGTQVHQKGPPLPRPVQPKPPHGA-----AEN--SLSPSSN 351

RESULT 6

T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20992; T24733
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20992
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F11
A;Experimental source: clone F15G9
R;Kishaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-5175 <W12>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A:Molecule type: mRNA
A:Residues: 1-526 <JAC>
A:Cross-references: UNIPROT:P18892; GB:M35551; NID:g1763685; PIDN:AAB39766.1; PID:g16277
C:Superfamily: rfp transforming protein
C:Keywords: transmembrane protein

Query Match 8.2%; Score 156.5; DB 2; Length 526;
Best Local Similarity 24.0%; Pred. No. 0.0012;
Matches 70; Conservative 54; Mismatches 149; Indels 19; Gaps 12;

Qy	3	LLLLLLVSYVVGTLGTHTEIKRVAEEKVTLPCHQLGLPEKDTLDIEMLLTONEGNQKV	62
Db	18	LLQLPKLSAPFDVIGPOEPILAVVGEDAELPCRLSPNVSAG-MELRWF--REKVSFAV	74
Qy	63	VITYSSRHVYNNLTTEEQKGRVAFASNFLA-GDASLQIEPLKPSDEGRYTCKVQNSGRYVW	121
Db	75	FVSRGQEQEGEEMAEYGRVSLVEDHIAEGSVAVRIQEVKASDDGEYRCFFRQDENYEE	134
Qy	122	SHVILKVLVRPSKPCKELEGETEGSDLTLOCESSG-TEPIVYVWQRIREKE---GEDE	177
Db	135	AIVHLKVAALGSDPHISM--KVQESGETQLECTSVGWYPEPQV-QWRTHRGEEFFPSMSES	191
Qy	178	RLPPKSRIDYNNHPGRVLLQNLTMYSGLYQCTAGNEAKESCV-VRVTVOYVQSI--GMV	234
Db	192	RNPDEEGL-FTVRASVIRDSM--KNVSCCIRNLLGQEKDVEVSIPASFFPRLTPMWV	248
Qy	235	AGAVTGIVAGALLI--FLLVLLIRKDKERYEEERNEIREDAEAPKARL	284
Db	249	AVAVILVVLGLLTIGSIFFTWRLYKERSQRQRNEFSKESKELLELKWKRAVL	300

Search completed: May 6, 2005, 08:06:05
Job time : 90 secs

THIS PAGE IS BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2005, 07:15:07 ; Search time 127 Seconds
(without alignment)
1503.981 Million cell updates/sec

Title: US-09-978-544A-59

Perfect score: 1908

Sequence: 1 MSLLLLLLVSYVGTGLGTH.....TKAETTPSMIPQSRAFQTV 373

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1908	100.0	373	2 Q9H6B4	Q9H6B4 homo sapien
2	1781	93.3	372	2 Q8K1G0	Q8K1G0 rattus norv
3	1763.5	92.4	373	2 Q8R373	Q8R373 mus musculus
4	1759.5	92.2	373	2 Q920S5	Q920S5 mus musculus
5	1787.5	41.3	332	2 Q640U3	Q640U3 xenopus tro
6	592.5	31.1	160	2 Q8C1H8	Q8C1H8 mus musculus
7	487.5	25.6	372	2 Q90Y50	Q90Y50 brachydanio
8	474	24.8	365	2 Q8WV3	Q8WV3 bos taurus
9	465	24.4	365	1 CXAR_HUMAN	P78310 homo sapien
10	463	24.3	358	2 Q9R056	Q9R056 rattus norv
11	457.5	24.0	365	1 CXAR_MOUSE	P97792 mus musculus
12	457.5	24.0	365	2 Q9DBJ8	Q9DBJ8 mus musculus
13	443	23.2	319	2 Q9TU79	Q9TU79 sus scrofa
14	434.5	22.8	344	2 Q9UKV4	Q9UKV4 homo sapien
15	433.5	22.7	344	2 Q9R067	Q9R067 rattus norv
16	433	22.7	319	2 Q9TU80	Q9TU80 canis famil
17	422.5	22.1	352	2 Q9IW66	Q9IW66 mus musculus
18	407.5	21.4	298	2 Q804R4	Q804R4 brachydanio
19	362.5	19.0	430	2 Q8N4F1	Q8N4F1 homo sapien
20	336	17.6	237	2 Q6DQX5	Q6DQX5 oryctolagus
21	335	17.6	394	2 Q6AYD4	Q6AYD4 rattus norv
22	321.5	16.9	390	2 Q9SK13	Q9SK13 macaca fasc
23	321	16.8	394	2 Q925F2	Q925F2 mus musculus
24	320.5	16.8	323	2 Q8NDD2	Q8NDD2 homo sapien
25	317.5	16.6	407	2 Q9D2J4	Q9D2J4 mus musculus
26	314.5	16.5	325	2 Q95791	Q95791 homo sapien
27	309.5	16.2	327	2 Q96IQ7	Q96IQ7 homo sapien
28	308.5	16.1	319	1 A33_HUMAN	Q96AP7 homo sapien
29	307.5	16.1	390	2 Q96AP7	Q96AP7 homo sapien
30	305.5	16.0	390	2 Q96T50	Q96T50 homo sapien
31	300.5	15.7	304	2 Q9CVA4	Q9CVA4 mus musculus

32	299.5	15.7	248	2 Q9D0T4	Q9D0T4 mus musculus
33	296.5	15.5	406	2 Q8N7T8	Q8N7T8 homo sapien
34	295	15.5	387	2 Q86XK7	Q86XK7 homo sapien
35	295	15.5	412	2 Q6MZS4	Q6MZS4 homo sapien
36	283	14.8	335	2 Q9PWR4	Q9PWR4 gallus gall
37	282	14.8	284	2 Q9NX42	Q9NX42 homo sapien
38	280.5	14.7	259	2 Q7Z2Q1	Q7Z2Q1 homo sapien
39	278.5	14.6	252	2 Q8W7T6	Q8W7T6 homo sapien
40	278.5	14.6	319	1 A33_MOUSE	Q9JKA5 mus musculus
41	277	14.5	335	2 Q9YGH1	Q9YGH1 gallus gall
42	275.5	14.4	338	2 Q9YGV5	Q9YGV5 gallus gall
43	273.5	14.3	325	2 Q9Z109	Q9Z109 mus musculus
44	269.5	14.1	300	2 Q9D9J0	Q9D9J0 mus musculus
45	267	14.0	318	2 Q9I684	Q9I684 xenopus lae
46	266.5	14.0	300	2 Q9DA22	Q9DA22 mus musculus
47	265	13.9	432	2 Q6DDE7	Q6DDE7 xenopus lae
48	263.5	13.8	442	2 Q6NWX8	Q6NWX8 brachydanio
49	261.5	13.7	332	2 Q6P359	Q6P359 xenopus tro
50	256	13.4	305	2 Q6P3A4	Q6P3A4 mus musculus
51	214.5	11.2	390	2 Q6P500	Q6P500 rattus norv
52	205.5	10.8	292	2 Q66I72	Q66I72 brachydanio
53	200.5	10.5	300	2 Q9JHY1	Q9JHY1 rattus norv
54	196	10.3	299	1 JAM1_HUMAN	Q9Y624 homo sapien
55	195.5	10.2	300	2 Q8VC39	Q8VC39 mus musculus
56	193.5	10.1	298	1 JAM1_BOVIN	Q8X256 bos taurus
57	193.5	10.1	309	2 Q86FL1	Q86FL1 homo sapien
58	193.5	10.1	310	1 JAM3_HUMAN	Q9BX67 homo sapien
59	193	10.1	181	2 Q91665	Q91665 xenopus lae
60	190	10.0	300	1 JAM1_MOUSE	Q8H792 mus musculus
61	189.5	9.9	338	1 LAMP_CHICK	Q98919 gallus gall
62	188	9.9	280	2 Q737I6	Q737I6 grus americ
63	188	9.9	338	1 LAMP_RAT	Q62813 rattus norv
64	187	9.8	338	1 LAMP_HUMAN	Q13449 homo sapien
65	186	9.7	350	2 Q02869	Q02869 gallus gall
66	185	9.7	200	2 Q8WMT7	Q8WMT7 homo sapien
67	185	9.7	334	2 Q02870	Q02870 gallus gall
68	185	9.7	337	2 Q6GLZ7	Q6GLZ7 xenopus lae
69	184.5	9.7	341	1 LAMP_MOUSE	Q8B1K3 mus musculus
70	184	9.6	164	2 Q99KG0	Q99KG0 mus musculus
71	183	9.6	351	1 CD2_HUMAN	P06729 homo sapien
72	181	9.5	345	2 Q6S263	Q6S263 pan troglod
73	181	9.5	510	2 Q96K15	Q96K15 homo sapien
74	180.5	9.5	289	2 Q7ZWT0	Q7ZWT0 xenopus lae
75	180.5	9.5	344	2 Q6SZ62	Q6SZ62 papio anubi
76	180	9.4	350	2 Q6SZ59	Q6SZ59 cercocebus
77	178	9.3	508	2 Q8CED8	Q8CED8 mus musculus
78	178	9.3	508	2 Q8R007	Q8R007 mus musculus
79	178	9.3	5175	2 Q8I0L3	Q8I0L3 caenorhabdi
80	178	9.3	5198	2 Q76518	Q76518 caenorhabdi
81	177.5	9.3	334	2 Q6S256	Q6S256 macaca neme
82	177.5	9.3	341	2 Q6S257	Q6S257 macaca arct
83	176.5	9.3	351	2 Q6S261	Q6S261 macaca fasc
84	175.5	9.2	484	2 Q26475	Q26475 schistocerc
85	175	9.2	340	2 Q764N3	Q764N3 sus scrofa
86	174.5	9.1	345	2 Q6S258	Q6S258 macaca asia
87	174	9.1	483	2 Q9DBP8	Q9DBP8 mus musculus
88	173	9.1	510	2 Q96NY8	Q96NY8 homo sapien
89	171.5	9.0	298	2 Q8C5K9	Q8C5K9 mus musculus
90	171	9.0	3410	2 Q7TN00	Q7TN00 rattus norv
91	169.5	8.9	585	2 Q6UY09	Q6UY09 homo sapien
92	169	8.9	413	2 Q7QBV2	Q7QBV2 anopheles g
93	168.5	8.8	351	2 Q6S260	Q6S260 macaca mula
94	167.5	8.8	291	2 Q66J15	Q66J15 xenopus tro
95	167.5	8.8	298	1 JAM2_HUMAN	P57087 homo sapien
96	167.5	8.8	310	2 Q68FQ2	Q68FQ2 rattus norv
97	166	8.7	495	2 Q9HCY1	Q9HCY1 homo sapien
98	165.5	8.7	298	2 Q9J159	Q9J159 m vasculen
99	164.5	8.6	662	2 Q60926	Q60926 homo sapien
100	164	8.6	438	2 Q920C3	Q920C3 mus musculus
101	164	8.6	509	2 Q920C2	Q920C2 mus musculus
102	164	8.6	529	2 Q91V87	Q91V87 mus musculus
103	163.5	8.6	298	2 Q5YNC1	Q5YNC1 homo sapien
104	163.5	8.6	312	2 Q6UXG6	Q6UXG6 homo sapien

105	163.5	8.6	1323	2	Q08476	Q08476 gallus gall	178	150	7.9	765	2	Q9BKQ1	Q9bkql aplysia cal
106	163	8.5	3950	2	Q7YR55	Q7yrf5 canis famil	179	150	7.9	812	2	Q9BKQ0	Q9bkq0 aplysia cal
107	162.5	8.5	298	2	Q8CE95	Q8ce95 mus musculu	180	149.5	7.8	545	2	Q9VCT4	Q9vct4 drosophila
108	162	8.5	584	2	Q00478	Q00478 homo sapien	181	149.5	7.8	727	1	PEC1_MOUSE	Q08481 mus musculu
109	161.5	8.5	310	2	Q9D1W9	Q9dlm9 mus musculu	182	149.5	7.8	808	1	FGR4_MOUSE	Q03142 mus musculu
110	161.5	8.5	310	2	Q9D8B7	Q9d8b7 mus musculu	183	149.5	7.8	1235	2	Q86BD5	Q86bd5 drosophila
111	161.5	8.5	310	2	Q9EPK4	Q9epk4 m junctiona	184	149.5	7.8	1235	2	Q9V787	Q9v787 drosophila
112	161	8.4	577	2	Q80Y42	Q80y42 mus musculu	185	148.5	7.8	286	2	Q46535	Q46535 bos taurus
113	161	8.4	577	2	Q8D221	Q8d221 m mus muscu	186	148.5	7.8	344	1	CD2_RAT	Q46535 bos taurus
114	160.5	8.4	1431	2	Q80U60	Q80u60 mus musculu	187	148.5	7.8	533	2	Q8NCB6	Q8ncb6 homo sapien
115	160	8.4	345	1	OPCM_BOVIN	P11834 bos taurus	188	148.5	7.8	535	2	Q6UXG8	Q6uxg8 homo sapien
116	159.5	8.4	347	1	CD2_HORSE	P37998 equus cabal	189	148.5	7.8	738	1	PEC1_HUMAN	P16284 homo sapien
117	159	8.3	438	2	Q9JLB7	Q9jlb7 mus musculu	190	148.5	7.8	799	2	Q8C3V5	Q8c3v5 mus musculu
118	159	8.3	513	2	Q9JLB8	Q9jlb8 mus musculu	191	148.5	7.8	799	2	Q8CIB8	Q8cib8 mus musculu
119	159	8.3	713	2	Q90330	Q90330 coturnix co	192	148.5	7.8	2623	2	Q6WR10	Q6wri0 homo sapien
120	159	8.3	4162	2	Q88918	Q88918 gallus gall	193	148.5	7.8	3707	1	PGBM_MOUSE	Q05793 mus musculu
121	158.5	8.3	296	2	Q640C0	Q640c0 xenopus lae	194	148	7.8	329	2	Q8N2Z5	Q8n2z5 homo sapien
122	158.5	8.3	300	2	Q7SYQ7	Q7syq7 xenopus lae	195	148	7.8	344	2	Q9N242	Q9n242 gallus gall
123	158.5	8.3	399	2	Q9Y279	Q9y279 homo sapien	196	148	7.8	363	2	Q6NV41	Q6nv41 brachydanio
124	158.5	8.3	1496	2	Q92626	Q92626 homo sapien	197	148	7.8	847	1	CD22_HUMAN	P20273 homo sapien
125	158	8.3	338	2	Q7Z3W6	Q7z3w6 homo sapien	198	148	7.8	5636	2	Q96RW7	Q96rw7 homo sapien
126	158	8.3	345	1	OPCM_HUMAN	Q44982 homo sapien	199	147.5	7.7	344	2	Q6B0I4	Q6b0i4 homo sapien
127	158	8.3	394	2	Q86Y79	Q86yt9 homo sapien	200	147.5	7.7	344	2	Q6P660	Q6p660 homo sapien
128	158	8.3	7962	2	Q10465	Q10465 homo sapien	201	147.5	7.7	353	1	CEPU_CHICK	Q90773 gallus gall
129	157	8.2	639	2	Q96P30	Q96p30 homo sapien	202	147	7.7	313	2	Q57596	Q57596 gallus gall
130	157	8.2	734	2	Q96LA4	Q96la4 homo sapien	203	147	7.7	315	2	Q9DGI5	Q9dgi5 gallus gall
131	157	8.2	734	2	Q96P31	Q96p31 homo sapien	204	147	7.7	348	1	NEGR_MOUSE	Q80z24 mus musculu
132	157	8.2	740	2	Q96P29	Q96p29 homo sapien	205	147	7.7	394	2	Q7ZXX1	Q7zxx1 xenopus lae
133	157	8.2	742	2	Q8N6S2	Q8n6s2 homo sapien	206	147	7.7	765	2	Q9TWA4	Q9twa4 aplysia cal
134	157	8.2	807	2	Q6NY23	Q6ny23 brachydanio	207	147	7.7	812	2	Q9TWA5	Q9twa5 aplysia cal
135	156.5	8.2	544	2	Q6UXI8	Q6uxi8 homo sapien	208	147	7.7	932	2	Q9BKP9	Q9bkp9 aplysia cal
136	156	8.2	344	1	NTRI_MOUSE	Q99pj0 mus musculu	209	147	7.7	932	2	Q9TWA6	Q9twa6 aplysia cal
137	156	8.2	344	1	NTRI_RAT	Q62718 rattus norv	210	147	7.7	1598	2	Q9P214	Q9p214 homo sapien
138	156	8.2	344	2	Q8BG33	Q8bg33 m mus muscu	211	147	7.7	2013	2	Q8VHZ8	Q8vhz8 rattus norv
139	156	8.2	697	2	Q8NC72	Q8nc72 homo sapien	212	147	7.7	2013	2	Q9ERC8	Q9erc8 mus musculu
140	156	8.2	1059	2	Q6UXM1	Q6uxm1 homo sapien	213	146.5	7.7	404	1	RAGE_HUMAN	P15109 homo sapien
141	156	8.2	1119	2	Q6UXM1	Q6uxm1 homo sapien	214	146.5	7.7	484	2	Q6BE00	Q6be00 xenopus lae
142	156	8.2	34350	2	Q8WZ42	Q8wz42 homo sapien	215	146.5	7.7	497	2	Q9BXN7	Q9bxn7 homo sapien
143	155.5	8.1	332	2	Q8BU81	Q8bu81 homo sapien	216	146.5	7.7	1194	2	Q7TPV3	Q7tpv3 mus musculu
144	155.5	8.1	334	2	Q76PA0	Q76pa0 homo sapien	217	146.5	7.7	1214	2	Q6ZQA6	Q6zqa6 mus musculu
145	155.5	8.1	359	2	Q78410	P78410 homo sapien	218	146	7.7	362	2	Q9JHQ1	Q9jhq1 rattus norv
146	155.5	8.1	413	2	Q7QBV1	Q7qbv1 anopheles g	219	145	7.6	508	1	FAS3_DROME	P15278 drosophila
147	155.5	8.1	526	1	BUTY_BOVIN	P18892 bos taurus	220	145	7.6	528	2	P91670	P91670 drosophila
148	155	8.1	316	2	Q8VE98	Q8ve98 mus musculu	221	144.5	7.6	592	2	Q9JLN5	Q9jln5 mus musculu
149	155	8.1	344	1	NTRI_HUMAN	Q9p121 homo sapien	222	144.5	7.6	697	1	SILA_HUMAN	Q961c7 homo sapien
150	155	8.1	2012	1	DISCA_HUMAN	Q60469 homo sapien	223	144.5	7.6	858	2	O18466	O18466 hirudo medi
151	154	8.1	259	2	Q9Y582	Q9y582 homo sapien	224	144	7.5	294	2	Q8BH36	Q8bh36 mesocricetu
152	154	8.1	394	2	Q7Z499	Q7z499 homo sapien	225	144	7.5	348	1	NEGR_RAT	Q9z0j8 rattus norv
153	154	8.1	403	2	Q9VP08	Q9vp08 drosophila	226	144	7.5	384	2	Q8N9I7	Q8n9i7 homo sapien
154	154	8.1	529	2	Q7TQM3	Q7tqm3 rattus norv	227	144	7.5	474	2	Q7PKB3	Q7pke3 anopheles g
155	154	8.1	807	2	Q6DD66	Q6dd66 xenopus lae	228	144	7.5	940	2	Q8NFA7	Q8nfa7 homo sapien
156	154	8.1	818	2	Q91742	Q91742 xenopus lae	229	144	7.5	4071	2	Q6KDZ1	Q6kdz1 gallus gall
157	154	8.1	818	2	Q9P5V9	Q9psv9 xenopus lae	230	143.5	7.5	731	2	P78409	P78409 homo sapien
158	153.5	8.0	321	2	Q6UXI4	Q6uxi4 homo sapien	231	143.5	7.5	802	2	Q95M13	Q95ml3 bos taurus
159	153	8.0	1340	2	Q8ND42	Q8nda2 homo sapien	232	143.5	7.5	838	2	Q90YM1	Q90ym1 brachydanio
160	153	8.0	1366	1	ROB3_MOUSE	Q9z2i4 mus musculu	233	143	7.5	336	2	Q8WVV5	Q8wvv5 homo sapien
161	152.5	8.0	526	1	BUTY_HUMAN	Q13410 homo sapien	234	143	7.5	345	1	OPCM_RAT	P32736 rattus norv
162	152.5	8.0	526	2	Q9H458	Q9h458 homo sapien	235	143	7.5	523	2	O00480	Q00480 homo sapien
163	152	8.0	315	2	Q96DM5	Q96dm5 homo sapien	236	143	7.5	582	2	Q80WN2	Q80wn2 mus musculu
164	151.5	7.9	738	2	P79390	P79390 bos primige	237	143	7.5	595	2	Q68SN8	Q68sn8 mus musculu
165	151.5	7.9	1093	1	L1G1_HUMAN	Q96jal homo sapien	238	143	7.5	739	1	PEC1_BOVIN	P51866 bos taurus
166	151.5	7.9	1249	2	Q90Z04	Q90z04 xenopus lae	239	143	7.5	802	2	Q8TDA0	Q8tda0 homo sapien
167	151	7.9	1228	2	Q8MRA3	Q8mra3 drosophila	240	143	7.5	802	2	Q8TDA0	Q8tda0 homo sapien
168	151	7.9	1675	2	Q98SW4	Q98sw4 brachydanio	241	143	7.5	828	2	Q91743	Q91743 xenopus lae
169	151	7.9	1906	1	KMLS_CHICK	P11799 gallus gall	242	143	7.5	1252	2	Q96DN3	Q96dn3 homo sapien
170	150.5	7.9	334	2	Q9NR44	Q9nr44 homo sapien	243	142.5	7.5	308	2	Q68EV1	Q68ev1 xenopus lae
171	150.5	7.9	508	2	Q96LA5	Q96la5 homo sapien	244	142.5	7.5	316	2	Q6UXI2	Q6uxi2 homo sapien
172	150.5	7.9	655	1	LY9_HUMAN	Q9hbg7 homo sapien	245	142.5	7.5	351	2	Q8JFU3	Q8jfu3 brachydanio
173	150	7.9	315	2	Q7TBE4	Q7tpb4 rattus norv	246	142.5	7.5	351	2	Q7SY58	Q7sy58 brachydanio
174	150	7.9	319	2	O00477	Q00477 homo sapien	247	142.5	7.5	379	2	Q80UL9	Q80ul9 mus musculu
175	150	7.9	357	2	Q15338	Q15338 homo sapien	248	142.5	7.5	388	2	Q8NC34	Q8nc34 homo sapien
176	150	7.9	513	2	O00481	Q00481 homo sapien	249	142.5	7.5	534	2	Q8NB18	Q8nb18 homo sapien
177	150	7.9	732	2	Q8CAW4	Q8caw4 mus musculu	250	142	7.4	329	2	Q9TTF2	Q9ttf2 canis famil

251	142	7.4	350	2	Q6PJN1	Q6pjni homo sapien	324	135.5	7.1	1273	2	O44928	O44928 caenorhabdi
252	142	7.4	504	2	Q8N441	Q8n441 homo sapien	325	135.5	7.1	1327	2	Q8QHL3	Q8qhl3 gallus gall
253	142	7.4	504	2	Q9H4D7	Q9h4d7 homo sapien	326	135.5	7.1	1386	1	ROB3_HUMAN	RObml3 homo sapien
254	142	7.4	828	2	Q9DGK3	Q9dgk3 xenopus lae	327	135.5	7.1	1428	2	Q8AY67	Q8ay67 brachydanio
255	142	7.4	829	2	Q9SPV8	Q9spv8 xenopus lae	328	135.5	7.1	1662	2	Q7QIV4	Q7qiv4 anopheles g
256	142	7.4	1470	1	ROB2_MOUSE	Q7tpd3 mus musculus	329	135.5	7.1	2133	2	Q7PQG9	Q7pqg9 anopheles g
257	141.5	7.4	316	2	Q9BXR1	Q9bxr1 homo sapien	330	135.5	7.1	4736	2	Q7YTP9	Q7ytp9 mytilus gal
258	141.5	7.4	509	2	Q9EQY5	Q9eqy5 m mman-g pr	331	135	7.1	292	2	Q8OW97	Q8ow97 meriones un
259	141.5	7.4	512	2	Q96DN8	Q96dn8 homo sapien	332	135	7.1	370	2	Q7TSN7	Q7tsn7 mus musculus
260	141.5	7.4	1031	2	Q90YM2	Q90ym2 brachydanio	333	135	7.1	590	1	LIB5_HUMAN	LIB5023 homo sapien
261	141	7.4	334	2	Q96AV7	Q96av7 homo sapien	334	135	7.1	621	2	Q811T7	Q811t7 mus musculus
262	141	7.4	352	1	NEGR_HUMAN	Q7z3b1 homo sapien	335	135	7.1	837	1	NCM2_HUMAN	O15394 homo sapien
263	141	7.4	377	2	Q8OV04	Q8ov04 mus musculus	336	135	7.1	1214	2	O75054	O75054 homo sapien
264	141	7.4	527	2	O00475	O00475 homo sapien	337	134.5	7.0	304	2	Q9BE26	Q9be26 macaca fasc
265	141	7.4	536	2	Q8BJE2	Q8bje2 mus musculus	338	134.5	7.0	605	2	Q921P2	Q921p2 mus musculus
266	141	7.4	771	2	Q7QEV8	Q7qev8 anopheles g	339	134.5	7.0	789	1	KIR1_MOUSE	Q80w68 mus musculus
267	141	7.4	822	2	Q91288	Q91288 pleurodeles	340	134.5	7.0	838	2	O8BO96	Q8bq96 mus musculus
268	141	7.4	998	2	Q95R27	Q95r27 drosophila	341	134.5	7.0	838	2	O8C482	O8c4b2 mus musculus
269	141	7.4	998	2	Q9W4Y6	Q9w4y6 drosophila	342	134.5	7.0	1060	2	Q9QZ13	Q9qzi3 rattus norv
270	140.5	7.4	337	2	Q6DFY2	Q6dfy2 mus musculus	343	134.5	7.0	1091	1	LIG1_MOUSE	P70193 mus musculus
271	140	7.3	376	2	Q9OZ71	Q9oz71 brachydanio	344	134	7.0	291	2	O86FD7	Q86fd7 schistosoma
272	140	7.3	440	2	Q6ZMD4	Q6zmd4 homo sapien	345	134	7.0	297	2	P78408	P78408 homo sapien
273	140	7.3	515	1	PVR1_MOUSE	Q9ikf6 mus musculus	346	134	7.0	367	2	O6ZWL4	O6zwl4 homo sapien
274	140	7.3	1051	1	PRK7_CHICK	Q91048 gallus gall	347	134	7.0	529	2	O7KYR7	O7kyr7 homo sapien
275	140	7.3	3198	2	Q9U8G8	Q9u8g8 manduca sex	348	134	7.0	795	2	Q90TMO	Q90ymo brachydanio
276	139.5	7.3	796	2	Q91287	Q91287 pleurodeles	349	134	7.0	846	2	O57577	O57577 cynops pyrr
277	139.5	7.3	1045	2	Q86T37	Q86t37 homo sapien	350	134	7.0	1100	2	O57576	O57576 cynops pyrr
278	139.5	7.3	1197	1	CAM1_BRARE	Q90478 brachydanio	351	134	7.0	2597	2	O6WRH9	Q6wrh9 rattus norv
279	139.5	7.3	1320	2	Q96KE5	Q96ke5 homo sapien	352	133.5	7.0	285	2	Q9D780	Q9d780 mus musculus
280	139.5	7.3	1320	2	Q86TC9	Q86tc9 homo sapien	353	133.5	7.0	433	2	Q9V644	Q9v644 drosophila
281	139	7.3	515	2	Q6P9M9	Q6p9m9 mus musculus	354	133.5	7.0	569	1	SILP_MOUSE	Q920g3 mus musculus
282	138.5	7.3	337	1	OPCM_CHICK	Q98892 gallus gall	355	133.5	7.0	1033	2	Q24327	Q24327 drosophila
283	138.5	7.3	344	2	Q9DF61	Q9df61 gallus gall	356	133.5	7.0	1033	2	Q9V643	Q9v643 drosophila
284	138.5	7.3	345	2	O6GM08	Q6gm08 xenopus lae	357	133.5	7.0	1746	2	O8WV19	Q8wv19 homo sapien
285	138.5	7.3	853	1	NCAL_BOVIN	P18136 bos taurus	358	133	7.0	289	2	O8K3J3	O8k3j3 meriones un
286	138	7.2	344	2	Q9R201	Q9r201 mus musculus	359	133	7.0	650	2	O63709	O63709 rattus ep
287	138	7.2	592	2	Q96KE5	Q96ke5 homo sapien	360	133	7.0	977	2	Q96RD9	Q96rd9 homo sapien
288	138	7.2	1091	1	NCAL_CHICK	P13590 gallus gall	361	133	7.0	1010	1	CONT_CHICK	P14781 gallus gall
289	138	7.2	1099	2	P97527	P97527 rattus norv	362	133	7.0	1036	1	AXOI_CHICK	P28685 gallus gall
290	137.5	7.2	263	2	Q7TPW5	Q7tpw5 mus musculus	363	133	7.0	1333	1	VGR1_MOUSE	P35969 mus musculus
291	137.5	7.2	509	2	Q91YK7	Q91yk7 mus musculus	364	133	7.0	1378	1	ROB2_HUMAN	Q9hck4 homo sapien
292	137.5	7.2	582	2	Q95N25	Q95n25 bos taurus	365	132.5	6.9	980	1	KFMS_FELCA	P13369 felis silve
293	137.5	7.2	697	2	Q922E0	Q922e0 mus musculus	366	132.5	6.9	1994	2	Q6ZPF2	Q6zpp2 mus musculus
294	137.5	7.2	757	1	KIR1_HUMAN	Q96j84 homo sapien	367	132.5	6.9	2176	2	O6V4S5	Q6v4s5 mus musculus
295	137.5	7.2	789	1	KIR1_RAT	Q6x936 rattus norv	368	132	6.9	296	2	O42404	O42404 gallus gall
296	137.5	7.2	2673	2	Q96SE3	Q96sec3 homo sapien	369	132	6.9	398	2	O9Y640	Q9y640 homo sapien
297	137	7.2	209	2	Q6DDH9	Q6ddh9 xenopus lae	370	132	6.9	413	2	O699P0	O699p0 antherea p
298	137	7.2	283	2	Q8NF70	Q8nf70 homo sapien	371	132	6.9	472	2	Q811T8	Q811t8 mus musculus
299	137	7.2	344	1	CD2_MOUSE	P08920 mus musculus	372	132	6.9	515	2	Q96FU5	Q96pj5 homo sapien
300	137	7.2	358	2	Q90490	Q90490 brachydanio	373	132	6.9	515	2	Q96RE0	Q96re0 homo sapien
301	137	7.2	421	2	Q7PV30	Q7pv30 anopheles g	374	132	6.9	549	2	Q9NQS3	Q9nqs3 homo sapien
302	137	7.2	1612	1	ROB1_MOUSE	O89026 mus musculus	375	132	6.9	858	2	O86X47	Q86x47 homo sapien
303	137	7.2	1730	2	Q7YRQ7	Q7yrq7 sus scrofa	376	132	6.9	862	1	CD22_MOUSE	P35329 mus musculus
304	136.5	7.2	336	1	C226_HUMAN	Q15762 homo sapien	377	132	6.9	1026	2	O94780	O94780 homo sapien
305	136.5	7.2	350	2	Q99430	Q99420 homo sapien	378	132	6.9	1030	2	Q8NFA8	Q8nfa8 homo sapien
306	136.5	7.2	858	1	NCAL_RAT	P13596 rattus norv	379	132	6.9	1100	2	O94779	O94779 homo sapien
307	136.5	7.2	1391	2	Q8N314	Q8n314 homo sapien	380	132	6.9	1107	2	Q9W0B0	Q9w0b0 drosophila
308	136.5	7.2	1409	2	O8J127	O8j127 brachydanio	381	132	6.9	1264	2	P91767	P91767 manduca sex
309	136.5	7.2	1409	2	Q801W2	Q801m2 brachydanio	382	132	6.9	1651	1	ROB1_RAT	O55005 rattus norv
310	136.5	7.2	1614	2	Q8UVD7	Q8uud7 xenopus lae	383	131.5	6.9	416	2	Q8N7I3	Q8n7i3 homo sapien
311	136	7.1	421	1	PVR1_PIG	Q7qlk4 anopheles g	384	131.5	6.9	416	2	Q67IP8	Q67ip8 homo sapien
312	136	7.1	515	1	Q9D076	Q9d006 mus musculus	385	131.5	6.9	510	2	O6EHI2	Q6ehi2 rattus norv
313	136	7.1	549	2	Q9JLB9	Q9jlb9 mus musculus	386	131.5	6.9	779	2	O97136	O97136 manduca sex
314	136	7.1	549	2	Q8NFA5	Q8nfas homo sapien	387	131.5	6.9	837	2	O97137	O97137 manduca sex
315	136	7.1	816	2	Q8NFA5	Q8nfas homo sapien	388	131.5	6.9	1269	2	O6U7I5	O6u7i5 brachydanio
316	136	7.1	1062	2	Q8BKG3	Q8bk93 mus musculus	389	131.5	6.9	1643	2	Q7QGT8	Q7qgt8 anopheles g
317	135.5	7.1	487	2	Q7T2H2	Q7t2h2 gallus gall	390	131	6.9	288	2	Q28499	Q28499 macaca mula
318	135.5	7.1	517	1	PVR1_HUMAN	Q15223 homo sapien	391	131	6.9	450	2	O6UXI0	O6uxi0 homo sapien
319	135.5	7.1	590	2	O6P4T5	Q6p4t5 mus musculus	392	131	6.9	725	2	O73634	O73634 xenopus lae
320	135.5	7.1	878	2	Q8GV22	Q8gv22 mytilus gal	393	131	6.9	922	2	Q90413	Q90413 brachydanio
321	135.5	7.1	1070	1	PRK7_HUMAN	Q13308 homo sapien	394	131	6.9	1028	1	O6INB5	O6inb5 xenopus lae
322	135.5	7.1	1070	2	Q6IQ54	Q6iq54 homo sapien	395	131	6.9	1092	1	NCA2_XENLA	P36335 xenopus lae
323	135.5	7.1	1269	2	O01632	O01632 caenorhabdi	396	131	6.9	1254	2	O674V1	O674v1 podocoryne

397	131	6.9	1476	2	Q7QJ29	Q7qj29 anopheles g	470	127	6.7	519	1	ECTO RAT	P16573 rattus norv
398	131	6.9	4391	1	PGBM HUMAN	P98160 homo sapien	471	127	6.7	591	2	O6NP04	O6np04 drosophila
399	130.5	6.8	390	2	G66KX2	G66kx2 xenopus lae	472	127	6.7	595	2	G6ZRS5	G6zrs5 homo sapien
400	130.5	6.8	395	2	Q9PSD0	Q9psd0 xenopus. fi	473	127	6.7	784	2	Q8I063	Q8i063 drosophila
401	130.5	6.8	437	2	Q9NFS6	Q9nfs6 homo sapien	474	127	6.7	806	1	CEK2 CHICK	P18460 gallus gall
402	130.5	6.8	480	2	Q9PSD1	Q9psd1 xenopus. fi	475	127	6.7	1027	2	Q90W79	Q90w79 gallus gall
403	130.5	6.8	482	2	Q90WB5	Q90wb5 anas platyr	476	127	6.7	1316	2	Q7QE16	Q7qe16 anopheles g
404	130.5	6.8	978	1	KFMS FSVMD	P00545 feline sarc	477	127	6.7	1336	1	VGR1 RAT	P53767 rattus norv
405	130.5	6.8	1125	2	Q7QEC1	Q7qec1 anopheles g	478	127	6.7	1342	2	Q9GPE6	Q9gpe6 drosophila
406	130.5	6.8	2174	2	Q9GOR0	Q9gor0 drosophila	479	127	6.7	1342	2	Q9VPZ7	Q9vpz7 drosophila
407	130	6.8	321	2	Q5S202	Q5s202 rattus norv	480	127	6.7	1377	1	NEO1 RAT	P97603 rattus norv
408	130	6.8	336	1	C226 MACMU	P18906 macaca mula	481	127	6.7	1461	1	NEO1 HUMAN	Q92859 homo sapien
409	130	6.8	761	1	NCA2 HUMAN	P13592 homo sapien	482	127	6.7	1461	1	ROB1 HUMAN	Q9y6n7 homo sapien
410	130	6.8	848	1	NCA1 HUMAN	P13591 homo sapien	483	126.5	6.6	325	2	Q8UWL3	Q8uwl3 ictalurus p
411	130	6.8	877	2	Q9GSH3	Q9gsh3 halocynthia	484	126.5	6.6	413	2	Q640R3	Q640r3 mus musculus
412	130	6.8	1946	2	Q8JH72	Q8jh72 apis mellif	485	126.5	6.6	645	2	Q6NZB6	Q6nzb6 mus musculus
413	129.5	6.8	305	2	Q6DJ75	Q6dj75 xenopus tro	486	126.5	6.6	649	2	Q7TMP7	Q7tmp7 mus musculus
414	129.5	6.8	336	2	Q46551	Q46551 hylobates s	487	126.5	6.6	654	1	LY9 MOUSE	Q01965 mus musculus
415	129.5	6.8	422	2	Q96PZ3	Q96pj3 homo sapien	488	126.5	6.6	733	2	Q8SQ83	Q8sq83 trichosurus
416	129.5	6.8	1499	2	Q90815	Q90815 gallus gall	489	126.5	6.6	1006	2	Q6IDB9	Q6ide9 drosophila
417	129.5	6.8	2217	2	Q8AV57	Q8av57 gallus gall	490	126.5	6.6	2008	2	Q9VRJ5	Q9vrs5 drosophila
418	129.5	6.8	5516	2	Q7ZZ48	Q7zz48 brachydanio	491	126.5	6.6	2046	2	Q7KSE9	Q7kse9 drosophila
419	129	6.8	262	2	Q80T70	Q80t70 mus musculus	492	126	6.6	498	2	Q9UBF9	Q9ubf9 homo sapien
420	129	6.8	388	2	Q8R464	Q8r464 mus musculus	493	126	6.6	719	2	Q66IV0	Q66iv0 xenopus lae
421	129	6.8	463	2	Q66J72	Q66j72 xenopus lae	494	126	6.6	725	2	Q73633	Q73633 xenopus lae
422	129	6.8	584	2	Q9Y3Y8	Q9y3y8 homo sapien	495	126	6.6	800	2	Q99052	Q99052 mus musculus
423	129	6.8	714	2	Q6ZPB6	Q6zpe6 mus musculus	496	126	6.6	1018	2	Q28106	Q28106 bos taurus
424	129	6.8	1056	2	Q7ZW34	Q7zw34 brachydanio	497	126	6.6	1088	1	NCA1 XENLA	P16170 xenopus lae
425	129	6.8	1117	2	Q6P1C6	Q6plc6 mus musculus	498	126	6.6	1624	2	Q63ZG4	Q63zg4 xenopus lae
426	129	6.8	1338	1	VGR1 HUMAN	P17948 h vascular	499	125.5	6.6	342	2	Q95MM9	Q95mm9 canis famil
427	129	6.8	2828	2	Q9NR39	Q9nr99 homo sapien	500	125.5	6.6	442	2	Q6KAT6	Q6kat6 mus musculus
428	128.5	6.7	280	2	Q9TTF1	Q9ttf1 canis famil	501	125.5	6.6	493	2	Q6P5Y4	Q6p5y4 homo sapien
429	128.5	6.7	285	2	Q8VE93	Q8ve93 mus musculus	502	125.5	6.6	525	2	Q7PZS8	Q7pzs8 anopheles g
430	128.5	6.7	332	1	SLF6 HUMAN	Q96du3 homo sapien	503	125.5	6.6	975	1	KIT_MOUSE	P05532 mus musculus
431	128.5	6.7	452	2	Q70355	Q70355 mus musculus	504	125.5	6.6	975	2	Q6QJB7	Q6qjb7 mus musculus
432	128.5	6.7	480	2	Q9PSC9	Q9psc9 xenopus. fi	505	125.5	6.6	975	2	Q6QJB8	Q6qjb8 mus musculus
433	128.5	6.7	508	2	Q8BJA5	Q8bja5 mus musculus	506	125	6.6	402	1	RAGE RAT	Q63495 rattus norv
434	128.5	6.7	521	2	Q61352	Q61352 mus musculus	507	125	6.6	402	2	Q6MG86	Q6mg86 rattus norv
435	128.5	6.7	727	2	Q6RK32	Q6rkb2 rattus norv	508	125	6.6	898	2	Q8NCE6	Q8nce6 homo sapien
436	128.5	6.7	813	1	QGR2 XENLA	Q03364 xenopus lae	509	125	6.6	627	2	Q8N466	Q8n466 homo sapien
437	128.5	6.7	814	2	Q6GNF8	Q6gnp8 xenopus lae	510	125	6.6	705	2	Q8CBD3	Q8cbd3 mus musculus
438	128.5	6.7	837	2	Q8RK38	Q8rk38 rattus norv	511	125	6.6	782	2	Q61563	Q61563 mus musculus
439	128.5	6.7	1302	1	NKG DROME	P20241 drosophila	512	125	6.6	800	2	Q7TSI8	Q7tsi8 mus musculus
440	128.5	6.7	17903	2	Q7RTI4	Q7rti4 drosophila	513	125	6.6	801	1	FGR3 MOUSE	Q69226 mus musculus
441	128	6.7	285	2	Q8BTK0	Q8btk0 mus musculus	514	125	6.6	898	2	Q69226	Q69226 mus musculus
442	128	6.7	288	2	Q77684	Q77684 macaca neme	515	125	6.6	1018	1	CONT HUMAN	Q12860 homo sapien
443	128	6.7	316	2	Q8AW77	Q8aw77 brachydanio	516	125	6.6	2772	2	Q9VAV4	Q9vav4 drosophila
444	128	6.7	381	2	Q9Y4A4	Q9y4a4 homo sapien	517	125	6.6	2894	2	Q7KRX2	Q7kxr2 drosophila
445	128	6.7	454	2	Q8MG97	Q8mg97 rattus norv	518	124.5	6.5	303	2	Q7ZXR4	Q7zxr4 xenopus lae
446	128	6.7	643	1	LIB5_PANTR	Q8mjz7 pan troglod	519	124.5	6.5	310	1	FCGB HUMAN	P31994 homo sapien
447	128	6.7	762	2	Q71TW8	Q71tw8 homo sapien	520	124.5	6.5	331	2	Q6INF0	Q6info xenopus lae
448	128	6.7	800	2	Q9JHX9	Q9jhx9 rattus norv	521	124.5	6.5	342	2	P97635	P97635 rattus norv
449	128	6.7	837	2	Q7Z7F2	Q7z7f2 homo sapien	522	124.5	6.5	332	2	Q7PSN2	Q7psn2 anopheles g
450	128	6.7	1501	2	Q7TTI7	Q7tti7 mus musculus	523	124.5	6.5	632	2	Q6ZRS5	Q6zrs5 homo sapien
451	128	6.7	1501	2	Q9QW00	Q9qw00 rattus sp.	524	124.5	6.5	662	2	Q8MQZ9	Q8mqz9 drosophila
452	128	6.7	1863	2	Q64605	Q64605 rattus norv	525	124.5	6.5	662	2	Q9VGD0	Q9vgd0 drosophila
453	128	6.7	1904	2	Q64699	Q64699 mus musculus	526	124.5	6.5	671	2	Q63711	Q63711 rattus ratt
454	128	6.7	2213	2	Q7Z5N4	Q7z5n4 homo sapien	527	124.5	6.5	725	1	NCA2 MOUSE	P13594 mus musculus
455	127.5	6.7	91	2	Q91667	Q91667 xenopus lae	528	124.5	6.5	764	2	Q8MQQ1	Q8mqq1 drosophila
456	127.5	6.7	232	2	Q7PJ18	Q7pj18 anopheles g	529	124.5	6.5	764	2	Q9W4U1	Q9w4u1 drosophila
457	127.5	6.7	288	1	CD80 HUMAN	P33681 homo sapien	530	124.5	6.5	815	2	Q8AYP3	Q8ayp3 brachydanio
458	127.5	6.7	385	2	Q9UQF5	Q9uqf5 homo sapien	531	124.5	6.5	972	1	KFMS HUMAN	P07333 homo sapien
459	127.5	6.7	398	2	Q8N126	Q8n126 homo sapien	532	124.5	6.5	975	2	Q7TS86	Q7ts86 mus musculus
460	127.5	6.7	404	2	Q9Y3B9	Q9y3b9 homo sapien	533	124.5	6.5	1020	1	CONT MOUSE	P12960 mus musculus
461	127.5	6.7	416	1	RAGE_BOVIN	Q28173 bos taurus	534	124.5	6.5	1020	2	Q6NXV7	Q6nxv7 mus musculus
462	127.5	6.7	432	2	Q9UUF1	Q9ujp1 homo sapien	535	124.5	6.5	1028	2	Q62682	Q62682 rattus norv
463	127.5	6.7	455	2	Q9UIK0	P59901 homo sapien	536	124.5	6.5	1115	1	NCA1 MOUSE	P13595 mus musculus
464	127.5	6.7	499	1	L1A4 HUMAN	Q921k7 mus sapien	537	124	6.5	1193	2	Q7QGT6	Q7qgt6 anopheles g
465	127.5	6.7	510	2	Q7L3E0	Q7l3e0 homo sapien	538	124	6.5	367	2	Q9D4M0	Q9d4m0 mus musculus
466	127.5	6.7	524	2	Q921K7	Q921k7 mus musculus	539	124	6.5	372	2	Q8C257	Q8c257 mus musculus
467	127.5	6.7	772	2	P9Y2J6	P9y2j6 homo sapien	540	124	6.5	467	1	SIL5 MOUSE	Q91y57 mus musculus
468	127.5	6.7	1028	2	P97528	P97528 rattus norv	541	124	6.5	498	2	Q8BRT6	Q8brt6 mus musculus
469	127	6.7	464	2	Q6GLZ5	Q6glz5 xenopus tro	542	124	6.5	537	1	IR18_MOUSE	Q61098 mus musculus

543	124	6.5	731	2	Q91150	Q91150 notophthalm	616	121	6.3	173	2	Q9JKD5	Q9jkd5 rattus norv
544	124	6.5	817	2	Q8UG38	Q8jg38 brachydanio	617	121	6.3	304	2	Q9TQX1	Q9tcx1 canis famli
545	124	6.5	837	1	NCM2_MOUSE	Q85136 mus musculus	618	121	6.3	305	2	Q98261	Q98261 homo sapien
546	124	6.5	880	2	Q7KPK8	Q7kpk8 drosophila	619	121	6.3	328	2	Q6FHA8	Q6fha8 homo sapien
547	124	6.5	1026	2	Q62845	Q62845 rattus norv	620	121	6.3	365	2	Q8AXL6	Q8axl6 oncorhynch
548	124	6.5	1395	2	Q7KVK3	Q7kvk3 drosophila	621	121	6.3	523	2	Q8K2H7	Q8k2h7 mus musculus
549	124	6.5	1429	2	Q9W213	Q9w213 drosophila	622	121	6.3	537	2	Q7PSJ8	Q7psj8 anopheles g
550	124	6.5	2776	2	Q869A0	Q869a0 drosophila	623	121	6.3	601	2	Q96CJ3	Q96cj3 homo sapien
551	124	6.5	2898	2	Q868Z9	Q868z9 drosophila	624	121	6.3	740	1	PEC1_PIG	Q95242 sus scrofa
552	124	6.5	4001	2	Q9N2P7	Q9n2p7 drosophila	625	121	6.3	841	2	Q8R221	Q8r221 mus musculus
553	123.5	6.5	325	2	Q8HW98	Q8hw98 mus musculus	626	121	6.3	965	2	Q86BP9	Q86bp9 drosophila
554	123.5	6.5	396	2	Q9N928	Q9n928 m nectin-li	627	121	6.3	1009	2	Q93250	Q93250 xenopus lae
555	123.5	6.5	461	2	Q13854	Q13854 homo sapien	628	121	6.3	1062	2	Q960C4	Q960c4 drosophila
556	123.5	6.5	531	2	Q7QBY7	Q7qey7 anopheles g	629	121	6.3	1062	2	Q9Y299	Q9y299 drosophila
557	123.5	6.5	979	2	Q8C8K9	Q8c8k9 mus musculus	630	121	6.3	1252	2	Q9YJL1	Q9yjl1 mus musculus
558	123.5	6.5	1513	2	Q90Z70	Q90z70 brachydanio	631	121	6.3	1389	2	Q90Z69	Q90z69 brachydanio
559	123.5	6.5	1860	2	Q7PQF4	Q7pqf4 anopheles g	632	121	6.3	1419	2	Q98SW3	Q98sw3 brachydanio
560	123.5	6.5	1948	1	PTNS_HUMAN	Q13332 homo sapien	633	121	6.3	1914	2	Q7Z4J0	Q7z4j0 homo sapien
561	123	6.4	282	2	Q9Y639	Q9y639 homo sapien	634	121	6.3	6620	2	Q96AA2	Q96aa2 homo sapien
562	123	6.4	366	2	Q6NV23	Q6nv23 homo sapien	635	120.5	6.3	281	2	P97300	P97300 mus musculus
563	123	6.4	403	2	Q8HY15	Q8hy15 lemur catta	636	120.5	6.3	395	2	Q8BXJ7	Q8bxj7 m mus muscu
564	123	6.4	417	2	Q7TNL1	Q7tnl1 mus musculus	637	120.5	6.3	395	2	Q8BZP4	Q8bzb4 mus musculus
565	123	6.4	496	2	Q9JIF9	Q9jif9 mus musculus	638	120.5	6.3	404	2	Q8BLO9	Q8blq9 mus musculus
566	123	6.4	520	2	Q925P2	Q925p2 mus musculus	639	120.5	6.3	404	2	Q8BYP1	Q8byp1 mus musculus
567	123	6.4	729	2	Q91147	Q91147 notophthalm	640	120.5	6.3	822	2	Q9QVW7	Q9qv7 rattus sp.
568	123	6.4	800	2	Q86LF9	Q86lf9 drosophila	641	120.5	6.3	1052	2	Q7PMY4	Q7pm4 anopheles g
569	123	6.4	801	2	Q86LF8	Q86lf8 drosophila	642	120.5	6.3	1150	2	Q8BS24	Q8bs24 mus musculus
570	123	6.4	1028	2	Q9C6X1	Q9c6x1 mus musculus	643	120.5	6.3	1209	2	P70232	P70232 mus musculus
571	123	6.4	1028	2	Q9JMB8	Q9jmb8 mus musculus	644	120.5	6.3	1276	2	Q90X32	Q90x22 brachydanio
572	123	6.4	1395	2	Q44924	Q44924 drosophila	645	120	6.3	288	2	Q9TT70	Q9tt70 sus scrofa
573	123	6.4	1596	2	Q9HCL6	Q9hcl6 homo sapien	646	120	6.3	297	2	Q9BE99	Q9be99 sus scrofa
574	123	6.4	2212	2	Q9NHN3	Q9nhn3 homo sapien	647	120	6.3	321	2	Q35187	Q35187 rattus norv
575	123	6.4	4796	2	Q9W053	Q9w055 drosophila	648	120	6.3	330	1	CD86_RABIT	CD86 rabbit
576	123	6.4	4796	2	Q9W053	Q9nfs3 drosophila	649	120	6.3	388	2	Q8NF28	Q8nf28 homo sapien
577	123	6.4	16215	2	Q9NFS3	Q9nfs3 drosophila	650	120	6.3	420	2	Q68DM9	Q68dm9 homo sapien
578	122.5	6.4	18074	2	Q9I7U4	Q9i7u4 drosophila	651	120	6.3	442	2	Q9H8B3	Q9h8b3 homo sapien
579	122.5	6.4	305	2	Q9VIM2	Q9vim2 mus musculus	652	120	6.3	521	1	CEA1_MOUSE	CEA1 mouse
580	122.5	6.4	342	2	Q95LJ9	Q95l99 canis famli	653	120	6.3	521	2	Q925P3	Q925p3 mus musculus
581	122.5	6.4	481	2	Q9MJ22	Q9mj22 pan troglod	654	120	6.3	702	1	CEAS_HUMAN	CEAS human
582	122.5	6.4	499	1	SIL8_HUMAN	Q9nyz4 homo sapien	655	120	6.3	702	2	Q8N4D0	Q8n4d0 homo sapien
583	122.5	6.4	538	2	Q9NM07	Q9nmq7 homo sapien	656	120	6.3	769	2	Q8N115	Q8n115 homo sapien
584	122.5	6.4	821	1	Q9R2_MOUSE	P21803 mus musculus	657	120	6.3	806	1	Q9R3_HUMAN	Q9r3 human
585	122.5	6.4	1028	2	Q9UQ52	Q9uq52 homo sapien	658	120	6.3	841	2	P97484	P97484 mus musculus
586	122.5	6.4	1040	2	Q9W675	Q9w675 brachydanio	659	120	6.3	1040	1	AXOI_HUMAN	AXOI human
587	122	6.4	1694	1	SN_MOUSE	Q62230 mus musculus	660	120	6.3	1040	1	AXOI_RAT	AXOI rat
588	122	6.4	352	2	Q9W6V2	Q9w6v2 gallus gall	661	120	6.3	1043	2	Q6PA07	Q6pa07 xenopus lae
589	122	6.4	496	2	Q7Z075	Q7z075 caenorhabdi	662	120	6.3	1388	2	Q7OKD0	Q7okd0 anopheles g
590	122	6.4	540	2	Q8N029	Q8n029 homo sapien	663	120	6.3	1388	1	KWLS_HUMAN	KWLS human
591	122	6.4	697	2	Q9TC35	Q9tc35 homo sapien	664	120	6.3	1914	1	Q640S5	Q640s5 xenopus tro
592	122	6.4	821	1	Q9R2_MOUSE	P21802 homo sapien	665	119.5	6.3	276	2	C226_MOUSE	C226 mouse
593	122	6.4	972	2	Q86VW7	Q86vw7 homo sapien	666	119.5	6.3	333	1	BASI_CHICK	BASI chick
594	122	6.4	1026	2	Q9IWV2	Q9i1wv2 homo sapien	667	119.5	6.3	388	1	Q6MG94	Q6mg94 rattus norv
595	122	6.4	1086	2	Q7QH02	Q7qh02 anopheles g	668	119.5	6.3	399	2	Q6F3J3	Q6f3j3 mus musculus
596	122	6.4	1187	2	Q8MR45	Q8mr45 caenorhabdi	669	119.5	6.3	428	2	Q6F3J3	Q6f3j3 mus musculus
597	121.5	6.4	4796	2	Q9NL88	Q9nl88 drosophila	670	119.5	6.3	631	1	LI1B3_HUMAN	LI1B3 human
598	121.5	6.4	240	1	Q4D8_MOUSE	P18181 mus musculus	671	119.5	6.3	707	2	Q9TT07	Q9tt07 canis famli
599	121.5	6.4	240	2	Q6P905	Q6p905 mus musculus	672	119.5	6.3	733	2	Q60830	Q60830 mus musculus
600	121.5	6.4	278	2	Q9QYL3	Q9qyl3 mus musculus	673	119.5	6.3	733	2	Q9QZM7	Q9qzm7 mus musculus
601	121.5	6.4	291	2	Q8UVA7	Q8uva7 brachydanio	674	119.5	6.3	782	2	Q9TT23	Q9tt23 oryctolagus
602	121.5	6.4	336	2	Q8MNV8	Q8mnv8 felis silve	675	119.5	6.3	819	1	FGRI_CHICK	FGRI chick
603	121.5	6.4	390	2	Q9H1X9	Q9hlx9 homo sapien	676	119.5	6.3	822	1	FGRI_RAT	FGRI rat
604	121.5	6.4	393	2	P97547	P97547 rattus norv	677	119.5	6.3	822	2	Q60818	Q60818 mus musculus
605	121.5	6.4	468	2	Q6PJ50	Q6pj50 mus musculus	678	119.5	6.3	1406	2	Q9GPP7	Q9gpp7 drosophila
606	121.5	6.4	499	2	Q7Z728	Q7z728 homo sapien	679	119.5	6.3	1463	2	Q9VQ08	Q9vq08 drosophila
607	121.5	6.4	524	1	BUTY_MOUSE	Q62556 mus musculus	680	119.5	6.3	6632	1	UN9_CABEL	UN9 caenorhabdi
608	121.5	6.4	544	2	Q8C2D4	Q8c2d4 mus musculus	681	119	6.2	8081	2	Q7Z120	Q7z120 caenorhabdi
609	121.5	6.4	611	2	Q70W32	Q70w32 oncorhynch	682	119	6.2	290	2	Q62680	Q62680 rattus norv
610	121.5	6.4	827	2	Q6GN85	Q6gn85 xenopus lae	683	119	6.2	321	2	Q62624	Q62624 rattus norv
611	121.5	6.4	948	2	Q9TTD7	Q9tttd7 trichosurus	684	119	6.2	328	2	O15430	O15430 homo sapien
612	121.5	6.4	1021	1	Q9MT32	Q63198 rattus norv	685	119	6.2	401	2	Q7PSS8	Q7ps88 anopheles g
613	121.5	6.4	1443	2	Q8MT52	Q8mtb2 drosophila	686	119	6.2	550	2	Q9VMN9	Q9vmn9 drosophila
614	121.5	6.4	1765	2	Q9VS30	Q9vs30 drosophila	687	119	6.2	640	2	Q8BSM2	Q8bsm2 mus musculus
615	121.5	6.4	1770	2	Q9VS29	Q9vs29 drosophila	688	119	6.2	675	2	Q7T0V5	Q7t0v5 xenopus lae
			1827	2	Q9VSG5	Q9vsg5 drosophila	689	119	6.2	749	2	Q967D9	Q967d9 drosophila

689	119	6.2	823	1	CEK3_CHICK	P18461 gallus gall	762	117	6.1	898	1	FAS2_SCHAM	P22648 schistocerc
690	119	6.2	902	2	Q81Q17	Q81q17 drosophila	763	117	6.1	907	2	Q9NEG0	Q9neg0 drosophila
691	119	6.2	903	2	Q967D8	Q967d8 drosophila	764	117	6.1	939	2	Q967X6	Q967x6 drosophila
692	119	6.2	903	2	Q9VQV1	Q9vqy1 drosophila	765	117	6.1	939	2	Q9VB35	Q9vb35 drosophila
693	119	6.2	1028	2	Q97409	Q97409 mus musculus	766	117	6.1	1040	1	AXO1_MOUSE	Q61330 mus musculus
694	119	6.2	1106	2	Q8WX93	Q8wx93 homo sapien	767	117	6.1	1155	2	Q7Q3K8	Q7q3k8 anopheles g
695	119	6.2	1508	2	Q6NR34	Q6nr34 drosophila	768	117	6.1	3215	2	Q8IRV7	Q8irv7 drosophila
696	119	6.2	1508	2	Q9VQY2	Q9vqy2 drosophila	769	117	6.1	4117	2	Q8IRV9	Q8irv9 drosophila
697	119	6.2	1531	2	Q967D7	Q967d7 drosophila	770	117	6.1	4179	2	Q9W4Y4	Q9w4y4 drosophila
698	118.5	6.2	281	2	P97546	P97546 rattus norv	771	117	6.1	4223	2	Q8MPN3	Q8mpn3 drosophila
699	118.5	6.2	306	2	Q9R129	Q9r129 mus musculus	772	117	6.1	4228	2	Q8IRV8	Q8irv8 drosophila
700	118.5	6.2	330	2	Q6QP58	Q6qp58 canis famil	773	117	6.1	18412	2	Q7ZZ61	Q7zz61 brachydanio
701	118.5	6.2	344	1	CEA6_HUMAN	P40199 homo sapien	774	116.5	6.1	280	2	Q8UV51	Q8uv51 brachydanio
702	118.5	6.2	344	2	Q13774	Q13774 homo sapien	775	116.5	6.1	324	2	Q8UV72	Q8uv72 brachydanio
703	118.5	6.2	379	2	Q9CWM1	Q9cwm1 mus musculus	776	116.5	6.1	339	2	Q8WMI8	Q8wmi8 homo sapien
704	118.5	6.2	487	2	Q6Q4G2	Q6q4g2 gallus gall	777	116.5	6.1	417	1	PVR_CERAE	P32506 cercopithe
705	118.5	6.2	492	2	Q9ET54	Q9et54 mus musculus	778	116.5	6.1	729	2	Q63827	Q63827 rattus norv
706	118.5	6.2	731	2	Q8CFR8	Q8cfr8 mus musculus	779	116.5	6.1	761	2	Q95LQ2	Q95lq2 macaca fasc
707	118.5	6.2	733	2	Q8OT10	Q8ot10 mus musculus	780	116.5	6.1	816	2	Q7PUH1	Q7puh1 anopheles g
708	118.5	6.2	737	2	Q965M3	Q965m3 caenorhabdi	781	116.5	6.1	1465	2	Q91285	Q91285 pleurodeles
709	118.5	6.2	764	1	ICCR_DROME	Q8180 drosophila	782	116.5	6.1	2022	2	Q7KQ55	Q7kq55 mus musculus
710	118.5	6.2	820	2	Q8CTN9	Q8ctn9 mus musculus	783	116.5	6.1	2995	2	Q6K6M0	Q6kq60 drosophila
711	118.5	6.2	822	1	FGRI_HUMAN	P11362 homo sapien	784	116.5	6.1	241	2	Q6SYC2	Q6sy60 brachydanio
712	118.5	6.2	822	1	FGRI_MOUSE	P16092 mus musculus	785	116	6.1	312	2	Q66KV0	Q66kv0 xenopus lae
713	118.5	6.2	853	2	Q6DFX7	Q6dfx7 mus musculus	786	116	6.1	328	2	Q6ZMC9	Q6zmc9 homo sapien
714	118.5	6.2	881	2	Q965M2	Q965m2 caenorhabdi	787	116	6.1	370	1	C244_HUMAN	Q9b2w8 homo sapien
715	118.5	6.2	1081	2	Q692T7	Q692t7 mus musculus	788	116	6.1	391	2	Q7T1J4	Q7t1j4 brachydanio
716	118.5	6.2	1328	2	Q21043	Q21043 caenorhabdi	789	116	6.1	458	2	Q61351	Q61351 mus musculus
717	118.5	6.2	1415	2	Q94155	Q94155 caenorhabdi	790	116	6.1	538	2	Q8C9E4	Q8c9e4 mus musculus
718	118.5	6.2	1447	2	Q16779	Q16779 caenorhabdi	791	116	6.1	551	2	Q8MSN7	Q8msn7 drosophila
719	118.5	6.2	1493	1	NEO1_MOUSE	P97798 mus musculus	792	116	6.1	620	2	Q7HNC6	Q7hnc6 homo sapien
720	118.5	6.2	8625	2	Q86G56	Q86g56 procambatus	793	116	6.1	785	2	Q7TNP4	Q7tnp4 mus musculus
721	118	6.2	423	2	Q8BU57	Q8bu57 mus musculus	794	116	6.1	956	2	Q9W4T9	Q9w4t9 drosophila
722	118	6.2	510	2	Q801V8	Q801v8 brachydanio	795	116	6.1	975	2	Q9N9Y9	Q9n9y9 drosophila
723	118	6.2	705	2	Q63710	Q63710 rattus ratt	796	116	6.1	1026	2	Q7O651	Q7o651 anopheles g
724	118	6.2	723	2	Q86Y14	Q86y14 homo sapien	797	116	6.1	1109	2	Q6P5H3	Q6p5h3 mus musculus
725	118	6.2	802	2	Q42127	Q42127 xenopus lae	798	116	6.1	1109	2	Q6AZB0	Q6azb0 mus musculus
726	118	6.2	815	2	Q805B9	Q805b9 brachydanio	799	116	6.1	1109	2	Q8T103	Q8t103 bombyx mori
727	118	6.2	1109	2	Q8CE91	Q8ce91 mus musculus	800	116	6.1	1292	2	Q8T103	Q8t103 bombyx mori
728	118	6.2	1110	2	Q8CE73	Q8ce73 mus musculus	801	116	6.1	323	1	FCGC_HUMAN	Q6uy47 homo sapien
729	118	6.2	1283	2	Q8LIM4	Q8liw4 oryza sativ	802	116	6.1	345	2	Q9UIB8	Q9uib8 homo sapien
730	118	6.2	1502	2	Q9JIM81	Q9jim81 homo sapien	803	115.5	6.1	492	2	Q8C0U8	Q8c0u8 mus musculus
731	118	6.2	19066	2	Q801W8	Q801w8 brachydanio	804	115.5	6.1	634	2	Q7RWB0	Q7rwb0 neurospora
732	117.5	6.2	327	2	Q8UJ63	Q8u63 h basigin p	805	115.5	6.1	834	2	Q6DCD2	Q6dcd2 xenopus lae
733	117.5	6.2	385	1	BASI_HUMAN	Q8u63 brachydanio	806	115.5	6.1	1114	2	Q9BWW1	Q9bww1 homo sapien
734	117.5	6.2	533	2	Q9DEE1	Q9dee1 gallus gall	807	115.5	6.1	1253	2	Q6UXJ5	Q6uxj5 homo sapien
735	117.5	6.2	533	2	Q9DEE5	Q9dee5 gallus gall	808	115.5	6.1	1253	2	Q9EQS8	Q9eqs8 mus musculus
736	117.5	6.2	600	2	Q8N7W7	Q8n7w7 homo sapien	809	115.5	6.1	275	2	Q9JK39	Q9jk39 mus musculus
737	117.5	6.2	707	2	Q7PWJ1	Q7pwj1 anopheles g	810	115.5	6.1	335	2	Q9NY08	Q9ny08 homo sapien
738	117.5	6.2	1225	2	Q6QP61	Q6qp61 xenopus lae	811	115.5	6.1	377	2	Q9VQY0	Q9vqy0 drosophila
739	117.5	6.2	1234	1	NPIN_RAT	Q9r044 rattus norv	812	115.5	6.1	606	2	Q82D70	Q82d70 streptomyce
740	117.5	6.2	1252	2	Q9JIX2	Q9jix2 rattus norv	813	115	6.1	619	2	Q9VMN6	Q9vmn6 drosophila
741	117.5	6.2	1721	2	Q961U1	Q961u1 drosophila	814	115	6.1	1066	2	Q7PXI0	Q7pxi0 anopheles g
742	117.5	6.2	2403	2	Q8MLD5	Q8mld5 drosophila	815	115	6.1	1479	2	Q8MSR5	Q8msr5 drosophila
743	117.5	6.2	4463	2	Q8MLD8	Q8mld8 drosophila	816	115	6.1	1933	2	Q7KOT5	Q7kct5 drosophila
744	117.5	6.2	6658	2	Q76281	Q76281 drosophila	817	115	6.1	2159	2	Q6PAL2	Q6pal2 mus musculus
745	117.5	6.2	7210	2	Q9V7G8	Q9v7g8 drosophila	818	115	6.0	321	2	Q8UV49	Q8uv49 brachydanio
746	117.5	6.2	8647	2	Q7KQ55	Q7kq55 drosophila	819	115	6.0	412	2	Q8HY14	Q8hy14 oryctolagus
747	117.5	6.2	8648	2	Q7KQ55	Q7kq55 drosophila	820	115	6.0	475	2	Q96PL5	Q96pl5 homo sapien
748	117.5	6.2	8930	2	Q7KQ55	Q7kq55 drosophila	821	115	6.0	521	2	Q8BHA1	Q8bha1 m mus muscu
749	117.5	6.2	8943	2	Q9V4F7	Q9v4f7 drosophila	822	115	6.0	530	1	PVR2_MOUSE	P32501 mus musculus
750	117.5	6.2	9270	2	Q8MLD9	Q8mld9 drosophila	823	114.5	6.0	530	2	Q8XJ35	Q8oxj35 mus musculus
751	117	6.1	244	2	Q758D71	Q758d71 homo sapien	824	114.5	6.0	562	2	Q6TNR7	Q6tnr7 brachydanio
752	117	6.1	244	2	Q03715	Q03715 homo sapien	825	114.5	6.0	626	1	MAG_HUMAN	Q8mjz3 pan troglod
753	117	6.1	261	2	Q9W6V1	Q9w6v1 gallus gall	826	114.5	6.0	719	2	Q9U4G1	Q9u4g1 drosophila
754	117	6.1	285	2	Q8IFG9	Q8ifg9 drosophila	827	114.5	6.0				
755	117	6.1	289	2	Q9QYL5	Q9qyl5 mus musculus	828	114.5	6.0				
756	117	6.1	298	2	Q96114	Q96114 drosophila	829	114.5	6.0				
757	117	6.1	360	2	Q8MBE6	Q8mbe6 drosophila	830	114.5	6.0				
758	117	6.1	399	2	Q7QC77	Q7qch7 anopheles g	831	114.5	6.0				
759	117	6.1	467	2	Q8CFE2	Q8cfe2 mus musculus	832	114.5	6.0				
760	117	6.1	620	1	SMS_CORJA	Q92154 coturnix co	833	114.5	6.0				
761	117	6.1	800	2	Q918X3	Q918x3 brachydanio	834	114.5	6.0				

835	114.5	6.0	956	1	MDC1_HUMAN	Q72553 homo sapien	908	112.5	5.9	3347	2	Q8MMJ9	Q8mmj9 bombyx mori
836	114.5	6.0	978	1	KIT_FELCA	Q28889 felis silve	909	112.5	5.9	3354	2	Q8T101	Q8t101 bombyx mori
837	114.5	6.0	1056	2	Q90Z03	Q90z03 xenopus lae	910	112	5.9	248	1	MYPO_MOUSE	P27573 mus musculus
838	114.5	6.0	1073	2	Q9TXI8	Q9txi8 caenorhabdi	911	112	5.9	275	2	Q6PH44	Q6ph44 brachydanio
839	114.5	6.0	1379	2	P79701	P79701 coturnix co	912	112	5.9	282	2	Q8VIM1	Q8vim1 mus musculus
840	114.5	6.0	2224	2	Q9ULM1	Q9ulm1 drosophila	913	112	5.9	283	2	Q8K091	Q8k091 mus musculus
841	114.5	6.0	4824	2	Q95YM1	Q95ym1 procambarus	914	112	5.9	287	2	Q13984	Q13984 homo sapien
842	114.5	6.0	17352	2	Q95YM2	Q95ym2 procambarus	915	112	5.9	288	2	Q9BDN6	Q9bdn6 cercocebus
843	114	6.0	378	2	Q66MN4	Q66mn4 petromyzon	916	112	5.9	289	2	Q28347	Q28347 cercocebus
844	114	6.0	402	2	Q35444	Q35444 mus musculus	917	112	5.9	295	2	Q922H8	Q922h8 mus musculus
845	114	6.0	424	2	Q8C6W0	Q8c6w0 mus musculus	918	112	5.9	340	2	Q61349	Q61349 mus musculus
846	114	6.0	458	2	Q63093	Q63093 rattus norv	919	112	5.9	445	2	Q8R4L1	Q8r4l1 mus musculus
847	114	6.0	468	2	Q9BX59	Q9bx59 homo sapien	920	112	5.9	476	2	Q6AYP5	Q6ayp5 rattus norv
848	114	6.0	468	2	Q9NWB8	Q9nwb8 homo sapien	921	112	5.9	1092	2	Q91ZT0	Q91zt0 rattus norv
849	114	6.0	538	2	Q28939	Q28939 sus scrofa	922	112	5.9	1343	1	VGR2_RAT	Q80775 rattus norv
850	114	6.0	538	2	Q29123	Q29123 sus scrofa	923	112	5.9	1363	2	Q91ZT1	Q91zt1 rattus norv
851	114	6.0	826	2	Q7Q1P7	Q7q1p7 anopheles g	924	112	5.9	1395	2	Q7QBG0	Q7qbg0 anopheles g
852	114	6.0	946	2	Q07153	Q07153 torpedo cal	925	112	5.9	2029	1	LAR_DROME	P16621 drosophila
853	114	6.0	953	2	Q8F6Y9	Q8f6y9 xenopus lae	926	111.5	5.8	215	1	CIB3_MACFA	Q8hxj7 macaca fasc
854	114	6.0	1482	2	Q9V4Y0	Q9v4y0 drosophila	927	111.5	5.8	235	2	Q9N0T0	Q9n0t0 canis fami
855	114	6.0	2222	2	Q7QEG7	Q7qeg7 anopheles g	928	111.5	5.8	235	2	Q9TQ88	Q9tq88 canis fami
856	114	6.0	3375	1	UN52_CAERL	Q06561 caenorhabdi	929	111.5	5.8	285	2	Q7ZY30	Q7zy30 xenopus lae
857	113.5	5.9	163	2	Q9NVJ5	Q9nvj5 homo sapien	930	111.5	5.8	306	1	CD80_MOUSE	Q00609 mus musculus
858	113.5	5.9	307	2	Q54947	Q54947 rattus norv	931	111.5	5.8	309	2	Q91YV7	Q91yv7 mus musculus
859	113.5	5.9	382	2	Q7PSH7	Q7psh7 anopheles g	932	111.5	5.8	317	2	Q9ESA3	Q9esa3 rattus norv
860	113.5	5.9	465	2	Q640U0	Q640j0 xenopus lae	933	111.5	5.8	331	2	Q9IB01	Q9ib01 spherooides
861	113.5	5.9	487	2	Q6Q4G0	Q6q4g0 gallus gall	934	111.5	5.8	342	2	Q9ESA1	Q9esa1 rattus norv
862	113.5	5.9	487	2	Q6Q4G1	Q6q4g1 gallus gall	935	111.5	5.8	400	2	Q8HY16	Q8hy16 cebus apell
863	113.5	5.9	487	2	Q9M6V7	Q9m6v7 gallus gall	936	111.5	5.8	401	2	Q08835	Q08835 cercopithec
864	113.5	5.9	576	2	Q8MYR8	Q8myr8 drosophila	937	111.5	5.8	403	1	RAGE_MOUSE	Q62151 mus musculus
865	113.5	5.9	743	2	Q8R6B2	Q8r6b2 vibratophaga	938	111.5	5.8	417	1	PVR_HUMAN	P15151 homo sapien
866	113.5	5.9	803	2	Q80ZP5	Q80zf5 rattus norv	939	111.5	5.8	446	2	Q6CQ08	Q6cq08 kluyveromyc
867	113.5	5.9	920	2	Q9P232	Q9p232 homo sapien	940	111.5	5.8	446	2	Q9Y849	Q9y849 kluyveromyc
868	113.5	5.9	1098	2	Q961D6	Q961d6 drosophila	941	111.5	5.8	541	2	Q95XJ7	Q95xj7 caenorhabdi
869	113.5	5.9	1332	2	Q9BN17	Q9bn17 drosophila	942	111.5	5.8	650	1	L1B1_HUMAN	Q8nh16 h leukocyte
870	113.5	5.9	1332	2	Q9VQW7	Q9vqw7 drosophila	943	111.5	5.8	731	2	Q8SPI6	Q8spi6 macropus eu
871	113.5	5.9	1506	2	Q9V7G6	Q9v7g6 drosophila	944	111.5	5.8	782	2	Q9ESA5	Q9esa5 rattus norv
872	113.5	5.9	2051	2	Q44328	Q44328 hirudo medi	945	111.5	5.8	865	2	Q68DA2	Q68da2 homo sapien
873	113	5.9	202	2	Q91406	Q91406 salmo sp. i	946	111.5	5.8	945	2	Q77589	Q77589 equus cabal
874	113	5.9	260	2	Q7Q411	Q7q411 anopheles g	947	111.5	5.8	949	1	MDC1_MOUSE	P60755 mus musculus
875	113	5.9	295	2	Q9QYL6	Q9qyl6 mus musculus	948	111.5	5.8	949	1	MDC1_RAT	P60756 rattus norv
876	113	5.9	308	2	Q9UV55	Q9uv55 brachydanio	949	111.5	5.8	1036	2	Q8SWF3	Q8swf3 drosophila
877	113	5.9	335	2	Q9NQ25	Q9nq25 homo sapien	950	111.5	5.8	1241	1	NPHN_HUMAN	Q60500 homo sapien
878	113	5.9	342	2	Q9IB00	Q9ib00 spherooides	951	111.5	5.8	1390	2	Q9VNI4	Q9vni4 drosophila
879	113	5.9	350	2	Q9VFU7	Q9vfu7 drosophila	952	111.5	5.8	1788	2	Q9IAJ0	Q9iaj0 xenopus lae
880	113	5.9	364	1	CD33_HUMAN	P20138 homo sapien	953	111.5	5.8	1880	2	O18465	O18465 hirudo medi
881	113	5.9	474	2	P79355	P79355 felis silve	954	111.5	5.8	1889	2	Q7Q0X2	Q7q0x2 anopheles g
882	113	5.9	526	1	CEA1_HUMAN	P13688 homo sapien	955	111.5	5.8	3262	2	Q9EQJ5	Q9eqj5 mus musculus
883	113	5.9	842	1	UNSA_HUMAN	Q61006 mus musculus	956	111	5.8	248	1	MYPO_RAT	P06907 rattus norv
884	113	5.9	868	1	MUSK_MOUSE	P35917 mus musculus	957	111	5.8	290	2	Q7MSD4	Q7msd4 avian adeno
885	113	5.9	1363	1	VGR3_MOUSE	Q9eq17 mus musculus	958	111	5.8	300	2	Q8CJ63	Q8cj63 mus musculus
886	113	5.9	1898	2	Q9EQ17	Q9eq17 mus musculus	959	111	5.8	337	2	Q6SJO7	Q6sj07 mus musculus
887	112.5	5.9	275	2	Q8AVV1	Q8avv1 xenopus lae	960	111	5.8	358	2	Q22780	Q22780 caenorhabdi
888	112.5	5.9	291	2	Q858Q7	Q858q7 homo sapien	961	111	5.8	445	2	Q8KJ76	Q8kjt6 mus musculus
889	112.5	5.9	321	2	Q9HCN7	Q9hcn7 homo sapien	962	111	5.8	451	2	Q8VD31	Q8vd31 mus musculus
890	112.5	5.9	399	2	Q8N772	Q8n772 homo sapien	963	111	5.8	641	2	Q86SD2	Q86sd2 ciona intes
891	112.5	5.9	410	2	Q6R319	Q6r319 bombyx mand	964	111	5.8	702	2	Q69ZY8	Q69zy8 mus musculus
892	112.5	5.9	410	2	Q6R3M0	Q6r3m0 bombyx mori	965	111	5.8	789	2	Q7PME2	Q7pme2 anopheles g
893	112.5	5.9	410	2	Q6R3M2	Q6r3m2 bombyx mori	966	111	5.8	873	1	FAS2_DROME	P34082 drosophila
894	112.5	5.9	430	2	Q7Q2X8	Q7qg58 anopheles g	967	111	5.8	980	2	Q917J1	Q917j1 drosophila
895	112.5	5.9	461	2	Q6C288	Q6c2x8 yarrowia li	968	111	5.8	1437	2	Q44329	Q44329 hirudo medi
896	112.5	5.9	567	2	Q96KV6	Q96kv6 homo sapien	969	111	5.8	2029	2	Q9VIS8	Q9vis8 drosophila
897	112.5	5.9	602	2	Q86YJ9	Q86yj9 homo sapien	970	110.5	5.8	277	2	Q8C6H8	Q8c6h8 mus musculus
898	112.5	5.9	650	2	Q8NA84	Q8na84 homo sapien	971	110.5	5.8	307	2	Q94431	Q94431 ciona intes
899	112.5	5.9	662	2	Q8MJ26	Q8mj26 pan troglod	972	110.5	5.8	320	2	Q8IWO0	Q8iwo0 homo sapien
900	112.5	5.9	793	2	Q70246	Q70246 mus musculus	973	110.5	5.8	356	2	Q8AXL7	Q8axl7 oncorhynch
901	112.5	5.9	813	2	Q8BQC3	Q8bqc3 mus musculus	974	110.5	5.8	504	2	Q6NNA1	Q6nnal drosophila
902	112.5	5.9	824	2	Q90749	Q90749 gallus gall	975	110.5	5.8	508	2	Q9VGD2	Q9vgd2 drosophila
903	112.5	5.9	1032	2	Q8AXZ4	Q8axz4 brachydanio	976	110.5	5.8	551	1	SIL5_HUMAN	O15389 homo sapien
904	112.5	5.9	1065	1	L1G2_HUMAN	Q94898 homo sapien	977	110.5	5.8	664	2	Q9VGF3	Q9vgf3 drosophila
905	112.5	5.9	1561	2	Q224D2	Q224d2 mus musculus	978	110.5	5.8	868	1	MUSK_RAT	Q52838 rattus norv
906	112.5	5.9	1940	2	Q6PDN3	Q6pdn3 mus musculus	979	110.5	5.8	907	2	Q98850	Q98850 carassius a
907	112.5	5.9	1950	2	Q80YN8	Q80yn8 mus musculus	980	110.5	5.8	1023	2	Q9ULI7	Q9uli7 homo sapien

Wed May 11 07:24:24 2005

981	110.5	5.8	1185	2	Q7PRK4	Q7prk4 anopheles g	1054	109	5.7	2169	2	Q8AV58	Q8av58 gallus gall
982	110.5	5.8	1248	2	Q9XT41	Q9xt41 cercopithe	1055	108.5	5.7	215	1	CTB3_HUMAN	Q9ny72 homo sapien
983	110.5	5.8	1898	2	Q64604	Q64604 r protein-c	1056	108.5	5.7	277	2	Q6IRE8	Q6ire8 rattus norv
984	110	5.8	1898	2	Q6NVX7	Q6nvx7 homo sapien	1057	108.5	5.7	283	2	Q7QGI4	Q7ggt4 anopheles g
985	110	5.8	238	2	Q20339	Q20339 caenorhabdi	1058	108.5	5.7	285	1	FCG2_RAT	Q63203 rattus norv
986	110	5.8	270	1	BASI_RABIT	Q28740 oryctolagus	1059	108.5	5.7	306	2	Q9QYL4	Q9qyl4 mus musculu
987	110	5.8	282	2	Q7TFU2	Q7tpu2 mus musculu	1060	108.5	5.7	313	2	O65801	O65801 ceratopteri
988	110	5.8	296	1	FCG2_BOVIN	Q28110 bos taurus	1061	108.5	5.7	325	1	NCT1_RAT	Q920h5 rattus norv
989	110	5.8	301	2	Q7THW2	Q7tmh2 mus musculu	1062	108.5	5.7	357	2	O8RI12	Q8rll2 mus musculu
990	110	5.8	324	2	Q6K94	Q6k94 homo sapien	1063	108.5	5.7	394	2	Q67GK9	Q6tgk9 oryctolagus
991	110	5.8	330	1	FCG2_MOUSE	P08101 mus musculu	1064	108.5	5.7	462	2	Q7RTW1	Q7rtw1 homo sapien
992	110	5.8	422	1	K3LI_RAT	P83556 rattus norv	1065	108.5	5.7	483	2	Q7SX76	Q7sx76 brachydanio
993	110	5.8	428	2	Q96P06	Q96p06 homo sapien	1066	108.5	5.7	537	2	Q9MZU5	Q9mzu5 sus scrofa
994	110	5.8	429	2	Q96LA6	Q96la6 homo sapien	1067	108.5	5.7	552	2	Q7QFF0	Q7qff0 anopheles g
995	110	5.8	459	2	Q9JHL6	Q9jhl6 homo sapien	1068	108.5	5.7	570	2	Q6GLY1	Q6gly1 xenopus lae
996	110	5.8	467	2	Q91V79	Q91vt9 mus musculu	1069	108.5	5.7	639	1	NRG1_HUMAN	Q92297 h pro-neure
997	110	5.8	525	2	Q8KJ01	Q8xjq1 rattus norv	1070	108.5	5.7	640	2	Q7RTV8	Q7rtv8 homo sapien
998	110	5.8	536	2	Q8GV82	P91092 caenorhabdi	1071	108.5	5.7	653	1	MU18_HUMAN	P43121 homo sapien
999	110	5.8	635	2	Q91092	Q95q79 caenorhabdi	1072	108.5	5.7	764	1	PIGR_HUMAN	P01833 homo sapien
1000	110	5.8	643	2	Q9XYS4	Q9xys4 hydra atten	1073	108.5	5.7	974	2	Q63702	Q63702 rattus ratt
1001	110	5.8	752	2	Q9XYS4	Q9xys4 asterina pe	1074	108.5	5.7	2016	2	O8MKM6	O8kmk6 drosophila
1002	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1075	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1003	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1076	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1004	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1077	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1005	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1078	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1006	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1079	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1007	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1080	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1008	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1081	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1009	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1082	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1010	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1083	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1011	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1084	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1012	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1085	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1013	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1086	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1014	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1087	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1015	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1088	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1016	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1089	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1017	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1090	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1018	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1091	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1019	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1092	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1020	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1093	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1021	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1094	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1022	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1095	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1023	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1096	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1024	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1097	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1025	110	5.8	761	2	Q9XYS4	Q9xys4 asterina pe	1098	108.5	5.7	2016	2	O8MKM7	O8kmk7 drosophila
1026	109.5	5.7	336	2	Q8UV75	Q8uv75 brachydanio	1100	108	5.7	757	2	Q7QCU0	Q7qcu0 anopheles g
1027	109.5	5.7	336	2	Q8UV75	Q8uv73 brachydanio	1101	108	5.7	812	1	FGRI_XENLA	FGri12 xenopus lae
1028	109.5	5.7	341	2	Q8YV73	Q8yvf3 mus musculu	1102	108	5.7	997	2	Q7PXX0	Q7pxx0 anopheles g
1029	109.5	5.7	341	2	Q8YV73	Q8yvf3 mus musculu	1103	108	5.7	1035	2	Q9NEG1	Q9neg1 drosophila
1030	109.5	5.7	422	2	Q8YV73	Q8yvf3 mus musculu	1104	108	5.7	1459	1	YF1M_CABEL	Yf1m4 caenorhabdi
1031	109.5	5.7	527	1	E4LB_MOUSE	Q9jmc8 mus musculu	1105	108	5.7	1555	2	Q7PPH8	Q7pph8 anopheles g
1032	109.5	5.7	527	1	E4LB_MOUSE	Q9jmc8 mus musculu	1106	108	5.7	1608	2	Q7PR41	Q7pr41 anopheles g
1033	109.5	5.7	686	1	IFL2_MOUSE	Q9rs6 mus musculu	1107	108	5.7	1887	2	Q9QW67	Q9qw67 rattus sp.
1034	109.5	5.7	729	1	FGRI_DROME	Q9rcf4 drosophila	1108	108	5.7	2389	2	Q8BE06	Q8be06 caenorhabdi
1035	109.5	5.7	741	2	Q6RCF4	Q6rcf4 vibrionphage	1109	108	5.7	283	2	Q8FG31	Q8fg31 brachydanio
1036	109.5	5.7	1014	2	Q6NFA6	Q6nfa6 homo sapien	1110	107.5	5.6	309	1	CD86_MOUSE	CD86 mus musculu
1037	109.5	5.7	1026	2	Q6ZOD0	Q6zod0 mus musculu	1111	107.5	5.6	314	2	O61238	O61238 mus musculu
1038	109	5.7	1242	1	NPHN_MOUSE	Q9qzs7 mus musculu	1112	107.5	5.6	323	2	Q9ES42	Q9esa2 mus musculu
1039	109	5.7	203	2	Q61FG6	Q61fg6 brachydanio	1113	107.5	5.6	329	2	Q9IAY6	Q9iay6 spherooides
1040	109	5.7	240	2	Q61FG6	Q61fg6 brachydanio	1114	107.5	5.6	356	2	Q64381	Q64381 mus musculu
1041	109	5.7	248	2	Q6WEB5	Q6web5 equus cabal	1115	107.5	5.6	370	2	Q800Y8	Q800y8 brachydanio
1042	109	5.7	270	2	Q6AYT8	Q6ayt8 rattus norv	1116	107.5	5.6	454	2	Q91WE4	Q91we4 mus musculu
1043	109	5.7	272	2	Q9UIB7	Q9uib7 homo sapien	1117	107.5	5.6	455	2	Q7IQE2	Q7iqe2 turslops tr
1044	109	5.7	280	2	Q95660	Q95660 homo sapien	1118	107.5	5.6	467	1	SIL7_HUMAN	Sil7 homo sapien
1045	109	5.7	283	2	Q7TSP5	Q7tsp5 mus musculu	1119	107.5	5.6	489	1	L1A1_HUMAN	L1a1 homo sapien
1046	109	5.7	333	2	Q91B04	Q91b04 spherooides	1120	107.5	5.6	538	2	Q8L7B6	Q8l7b6 arabidopsis
1047	109	5.7	407	2	Q9Y412	Q9y412 homo sapien	1121	107.5	5.6	622	2	Q9ES55	Q9ess5 mus musculu
1048	109	5.7	500	2	Q9WZ60	Q9wz60 drosophila	1122	107.5	5.6	622	2	Q9JKB2	Q9jkb2 mus musculu
1049	109	5.7	500	2	Q9XZB7	Q9xzb7 drosophila	1123	107.5	5.6	622	2	Q9JKB2	Q9jkb2 mus musculu
1050	109	5.7	626	1	MAG_RAT	P07722 rattus norv	1124	107.5	5.6	645	2	Q9R069	Q9r069 mus musculu
1051	109	5.7	869	1	MUSK_HUMAN	O15146 homo sapien	1125	107.5	5.6	650	2	O22701	O22701 arabidopsis
1052	109	5.7	1264	2	O14631	O14631 homo sapien	1126	107.5	5.6	650	2	Q99K86	Q99k86 mus musculu
1053	109	5.7	1298	1	VGR3_HUMAN	P35916 homo sapien							

1127	107.5	5.6	652	2	Q84MA9	Q84ma9 arabidopsis	1200	105.5	5.5	301	2	Q7Q864	Q7q864 anopheles g
1128	107.5	5.6	697	2	Q7PMJ7	Q7pmj7 anopheles g	1201	105.5	5.5	307	2	Q7PCU3	Q7pcu3 anopheles g
1129	107.5	5.6	697	2	Q8K4V6	Q8k4v6 mus musculus	1202	105.5	5.5	320	2	Q9IAZ9	Q9iaaz9 spheroidees
1130	107.5	5.6	814	2	Q91897	Q91897 xenopus lae	1203	105.5	5.5	324	2	Q8NBY8	Q8ncb8 homo sapien
1131	107.5	5.6	1029	2	Q9W3D9	Q9w3d9 drosophila	1204	105.5	5.5	326	2	Q8NC17	Q8nc17 homo sapien
1132	107.5	5.6	1256	2	Q9JIX1	Q9jix1 mus musculus	1205	105.5	5.5	330	2	Q9OZ42	Q9oz42 gallus gall
1133	107.5	5.6	1304	1	NRCA_HUMAN	Q92823 homo sapien	1206	105.5	5.5	403	2	Q8NZV3	Q8nzv3 brachydanio
1134	107.5	5.6	1369	1	NRAS_CHICK	Q42414 gallus gall	1207	105.5	5.5	433	2	Q00002	Q00002 altermaria
1135	107	5.6	202	2	Q9ERP6	Q9erp6 rattus norv	1208	105.5	5.5	441	2	Q9DDC4	Q9ddc4 oncorhynch
1136	107	5.6	320	2	Q7QOP8	Q7qop8 anopheles g	1209	105.5	5.5	455	2	Q9XS78	Q9xs78 delphinapte
1137	107	5.6	330	2	Q63241	Q63241 rattus norv	1210	105.5	5.5	457	1	CD4_RAT	P05540 rattus norv
1138	107	5.6	335	2	Q75237	Q75237 homo sapien	1211	105.5	5.5	474	2	Q8KJ78	Q8kl78 mus musculus
1139	107	5.6	353	2	Q63242	Q63242 rattus norv	1212	105.5	5.5	645	2	Q6DR98	Q6dr98 mus musculus
1140	107	5.6	446	2	Q63237	Q63237 rattus norv	1213	105.5	5.5	694	2	Q8SWT7	Q8swt7 drosophila
1141	107	5.6	743	2	Q6P1M7	Q6p1m7 homo sapien	1214	105.5	5.5	740	2	Q9UPP2	Q9upp2 homo sapien
1142	107	5.6	771	2	Q8N1L6	Q8n1l6 homo sapien	1215	105.5	5.5	843	1	CYP1_BRUMA	Q27450 brugia mala
1143	107	5.6	1011	2	Q24273	Q24273 drosophila	1216	105.5	5.5	997	2	O44087	O44087 caenorhabdi
1144	107	5.6	1164	2	Q66MN5	Q66mn5 drosophila	1217	105.5	5.5	999	1	MERK_HUMAN	Q12866 homo sapien
1145	107	5.6	1265	2	Q9P274	Q9p274 homo sapien	1218	105.5	5.5	1345	2	Q8VCD0	Q8vcd0 mus musculus
1146	107	5.6	1817	2	Q7S2F6	Q7szf6 xenopus lae	1219	105.5	5.5	1367	1	VGR2_MOUSE	P35918 mus musculus
1147	107	5.6	1897	1	PTPF_HUMAN	P10586 homo sapien	1220	105.5	5.5	1894	2	Q64487	Q64487 mus musculus
1148	107	5.6	1898	2	Q86WS0	Q86ws0 homo sapien	1221	105.5	5.5	4203	2	Q965G2	Q965g2 caenorhabdi
1149	107	5.6	5604	2	Q8WZ53	Q8wz53 homo sapien	1222	105.5	5.5	4219	2	Q9NL87	Q9nl87 caenorhabdi
1150	107	5.6	26926	2	Q10466	Q10466 homo sapien	1223	105.5	5.5	4447	2	Q8MXD8	Q8mxd8 caenorhabdi
1151	107	5.6	26926	2	Q8WZB3	Q8wzb3 homo sapien	1224	105.5	5.5	4488	2	Q9TXK2	Q9txk2 caenorhabdi
1152	106.5	5.6	163	2	Q8K1H8	Q8klh8 mus musculus	1225	105	5.5	219	1	MYP0_BOVIN	P10522 bos taurus
1153	106.5	5.6	251	2	Q14902	Q14902 homo sapien	1226	105	5.5	229	2	Q9TT71	Q9tt71 sus scrofa
1154	106.5	5.6	338	2	Q12811	Q12811 homo sapien	1227	105	5.5	278	2	Q9N2I3	Q9n2i3 sus scrofa
1155	106.5	5.6	337	2	Q9IAZ4	Q9iaza4 spheroidees	1228	105	5.5	278	2	O6UM59	O6uw59 homo sapien
1156	106.5	5.6	349	1	CSA8_HUMAN	P31997 homo sapien	1229	105	5.5	283	2	Q7TPH5	Q7tp5 mus musculus
1157	106.5	5.6	351	2	Q15225	Q15225 homo sapien	1230	105	5.5	329	1	CD86_HUMAN	P42081 homo sapien
1158	106.5	5.6	364	2	Q7L6L0	Q7l6l0 coturnix co	1231	105	5.5	330	2	P97269	P97269 cavia porce
1159	106.5	5.6	416	2	Q9KGK6	Q9kgk6 bacillus ha	1232	105	5.5	336	2	Q9OZ89	Q9oz89 brachydanio
1160	106.5	5.6	440	2	Q8MK39	Q8mk39 macaca mula	1233	105	5.5	360	2	Q8N732	Q8n732 homo sapien
1161	106.5	5.6	456	2	Q8R5M8	Q8r5m8 mus musculus	1234	105	5.5	426	2	O6LEU7	O6leu7 homo sapien
1162	106.5	5.6	475	2	Q8NCW2	Q8ncw2 homo sapien	1235	105	5.5	544	1	ICA3_BOVIN	Q28125 bos taurus
1163	106.5	5.6	475	2	Q8NCW3	Q8ncw3 homo sapien	1236	105	5.5	562	2	Q9LXU9	Q9lxx9 arabidopsis
1164	106.5	5.6	724	2	Q9MYN0	Q9myn0 bos taurus	1237	105	5.5	637	2	Q7RTW3	Q7rtw3 homo sapien
1165	106.5	5.6	764	2	Q8IZY7	Q8izy7 homo sapien	1238	105	5.5	676	2	Q6ZFB7	Q6zfb7 oryza sativ
1166	106.5	5.6	806	2	Q9OZ00	Q9oz00 brachydanio	1239	105	5.5	788	2	Q80ZB3	Q8ozb3 mus musculus
1167	106.5	5.6	824	2	Q91286	Q91286 pleurodeles	1240	105	5.5	789	2	Q9BE71	Q9be71 macaca faec
1168	106.5	5.6	972	2	Q76110	Q76110 callithrix	1241	105	5.5	1182	2	Q9Y7C1	Q9y7c1 magnaportie
1169	106.5	5.6	975	1	KIT_CANFA	Q97799 canis famil	1242	105	5.5	1709	1	SN_HUMAN	Q9bz22 homo sapien
1170	106.5	5.6	975	2	Q7YRV7	Q7yrv7 canis famil	1243	104.5	5.5	215	1	CIB3_RAT	Q91k00 rattus norv
1171	106.5	5.6	977	1	KIT_BOVIN	P43481 bos taurus	1244	104.5	5.5	241	2	Q07112	Q07112 bos taurus
1172	106.5	5.6	978	2	O6J1L6	Q63116 rattus norv	1245	104.5	5.5	283	2	Q6NZV7	Q6nzv7 brachydanio
1173	106.5	5.6	1196	2	Q96VNA	Q96vna coccidioides	1246	104.5	5.5	334	2	Q819N0	Q819n0 branchiosco
1174	106.5	5.6	1250	2	Q8TDY8	Q8tdy8 homo sapien	1247	104.5	5.5	339	2	Q9UIF2	Q9uif2 homo sapien
1175	106.5	5.6	1331	2	Q7Q623	Q7q623 anopheles g	1248	104.5	5.5	430	2	Q76LJ8	Q76lj8 coturnix co
1176	106	5.6	187	2	Q7KA82	Q7ka82 drosophila	1249	104.5	5.5	460	2	Q8MJZ4	Q8mjz4 pan troglod
1177	106	5.6	292	2	O02758	O02758 felis silve	1250	104.5	5.5	542	2	Q8NH5	Q8nh5 homo sapien
1178	106	5.6	292	2	Q8GMZ8	Q8gmz8 felis silve	1251	104.5	5.5	602	2	Q7TMW0	Q7tmw0 mus musculus
1179	106	5.6	296	2	O46405	O46405 bos taurus	1252	104.5	5.5	686	1	TPL2_HUMAN	Q9mp60 h x-linked
1180	106	5.6	336	2	Q80VG4	Q80vg4 bos musculus	1253	104.5	5.5	775	2	Q6PF50	Q6pf50 xenopus lae
1181	106	5.6	336	2	Q9D6E7	Q9d6e7 mus musculus	1254	104.5	5.5	810	2	Q9PS96	Q9ps96 xenopus lae
1182	106	5.6	337	2	Q8UV29	Q8uv29 brachydanio	1255	104.5	5.5	813	2	Q80TK8	Q80tk8 mus musculus
1183	106	5.6	340	2	Q9W3N2	Q9w3n2 drosophila	1256	104.5	5.5	955	1	MDG1_HUMAN	Q8nfp4 homo sapien
1184	106	5.6	341	2	Q61354	Q61354 mus musculus	1257	104.5	5.5	978	1	KIT_CAPI	Q28317 capra hircu
1185	106	5.6	361	2	Q8BWL2	Q8bwl2 debaryomyce	1258	104.5	5.5	978	2	Q9XS93	Q9xs93 canis famil
1186	106	5.6	466	2	Q6UXE8	Q6uxe8 homo sapien	1259	104.5	5.5	979	2	Q8WNZ3	Q8wnz3 canis famil
1187	106	5.6	554	2	Q9W4R3	Q9w4r3 drosophila	1260	104.5	5.5	986	2	Q8UVR9	Q8uvr9 figu rubrip
1188	106	5.6	555	1	C166_CARAU	Q90304 carassius a	1261	104.5	5.5	1184	2	Q8C1B1	Q8c1b1 mus musculus
1189	106	5.6	558	2	Q6PDB1	Q6pdb1 homo sapien	1262	104.5	5.5	1284	1	NRCA_CHICK	P35331 gallus gall
1190	106	5.6	637	2	Q6NSG0	Q6nsg0 homo sapien	1263	104.5	5.5	1443	1	NEO1_CHICK	Q90610 gallus gall
1191	106	5.6	686	1	SILB_HUMAN	Q96rl6 homo sapien	1264	104.5	5.5	1686	2	Q7RZE6	Q7rze6 neurospora
1192	106	5.6	719	1	LRF5_MOUSE	Q8bxa0 mus musculus	1265	104.5	5.5	7105	2	Q7PXW9	Q7pxw9 anopheles g
1193	106	5.6	719	2	Q84VG3	Q84vg3 oryza sativ	1266	104	5.5	133	2	Q860H6	Q860h6 gallus gall
1194	106	5.6	841	2	O54999	O54999 mus musculus	1267	104	5.5	242	2	O46604	O46604 sus scrofa
1195	106	5.6	2558	2	Q6NR91	Q6nr91 drosophila	1268	104	5.5	268	2	O46603	O46603 sus scrofa
1196	105.5	5.5	211	2	Q8BK18	Q8bki8 mus musculus	1269	104	5.5	282	2	Q96BF3	Q96bf3 homo sapien
1197	105.5	5.5	215	1	CIB3_MOUSE	Q8bkh2 mus musculus	1270	104	5.5	316	2	Q8WFB3	Q8wfb3 drosophila
1198	105.5	5.5	268	2	Q9ZQZ3	Q9zqz3 mus musculus	1271	104	5.5	337	2	Q8UVB1	Q8uvb1 brachydanio
1199	105.5	5.5	287	2	Q9UD97	Q9ud97 homo sapien	1272	104	5.5	357	2	O18872	O18872 sus scrofa

1273	104	5.5	370	2	Q6MZQ3	Q6mzg3 homo sapien	1346	103	5.4	1485	1	TOP2_SCHPO	P08096 schizosacch
1274	104	5.5	426	1	PSG9_HUMAN	Q00887 homo sapien	1347	103	5.4	16223	2	Q8IR22	P81r22 drosophila
1275	104	5.5	431	2	Q9H8V1	Q9h8v1 homo sapien	1348	102.5	5.4	241	2	Q6PK61	Q6pk61 homo sapien
1276	104	5.5	439	2	Q6GTU4	Q6gtu4 homo sapien	1349	102.5	5.4	281	2	Q8VIM0	Q8vim0 mus musculus
1277	104	5.5	463	2	SLI9_HUMAN	Q9y336 homo sapien	1350	102.5	5.4	302	1	ICOL_HUMAN	O75144 homo sapien
1278	104	5.5	499	2	Q7SFB6	Q7sfb6 neurospora	1351	102.5	5.4	310	2	Q8SPW4	Q8spw4 macaca fasc
1279	104	5.5	538	1	PVR2_HUMAN	Q92692 homo sapien	1352	102.5	5.4	318	2	Q90Z81	Q90z81 brachydanio
1280	104	5.5	646	2	Q95812	Q95812 homo sapien	1353	102.5	5.4	324	2	Q8UV37	O8uv37 brachydanio
1281	104	5.5	716	2	Q8IYV5	Q8iyy5 homo sapien	1354	102.5	5.4	325	2	O02838	O02838 sus scrofa
1282	104	5.5	716	2	Q6UXK5	Q6uxk5 homo sapien	1355	102.5	5.4	341	1	FCG2_CAVPO	FCG2 cavia porce
1283	104	5.5	718	2	Q73675	Q73675 xenopus lae	1356	102.5	5.4	429	1	ERC_FAT	P01855 rattus norv
1284	104	5.5	718	2	Q6PCK4	Q6pck4 xenopus lae	1357	102.5	5.4	521	1	LAG3_MOUSE	P01790 mus musculu
1285	104	5.5	730	2	Q9P231	Q9p231 homo sapien	1358	102.5	5.4	570	2	Q6GMZ9	Q6gmz9 xenopus lae
1286	104	5.5	832	2	Q9ULH4	Q9ulh4 homo sapien	1359	102.5	5.4	640	1	DIM1_CABEL	Q18066 caenorhabdi
1287	104	5.5	976	2	Q8JFR5	Q8jfr5 brachydanio	1360	102.5	5.4	798	2	Q86K66	Q86k66 dictyosteli
1288	104	5.5	1003	2	Q90960	Q90960 trypanosoma	1361	102.5	5.4	885	2	Q8HYV1	Q8hyv1 sus scrofa
1289	104	5.5	1134	2	Q71805	Q71805 brachydanio	1362	102.5	5.4	886	2	Q8HYV2	Q8hyv2 sus scrofa
1290	104	5.5	1144	2	Q18100	Q18100 caenorhabdi	1363	102.5	5.4	1151	2	Q8HYV2	Q8hyv2 sus scrofa
1291	104	5.5	1224	2	Q00533	Q00533 homo sapien	1364	102.5	5.4	1155	2	Q82RF1	Q82rf1 streptomyce
1292	104	5.5	1235	2	Q7QUS7	Q7q087 anopheles g	1365	102.5	5.4	1240	1	NFAS_MOUSE	Q810u3 mus musculu
1293	104	5.5	1250	2	Q08971	Q08971 mus musculu	1366	102.5	5.4	1735	2	Q7Q9I6	P97685 rattus norv
1294	104	5.5	1251	2	Q6ZQ54	Q6zq54 mus musculu	1367	102.5	5.4	1735	2	Q7Q9I6	Q7q916 anopheles g
1295	104	5.5	1277	1	CAML_FUGRU	Q98302 fugu rubrip	1368	102.5	5.4	1876	2	O02024	O02024 riportus c
1296	104	5.5	1447	1	DCC_MOUSE	P70211 mus musculu	1369	102.5	5.4	6839	2	Q23550	Q23550 caenorhabdi
1297	104	5.5	1779	2	Q74B68	Q74b68 geobacter s	1370	102.5	5.4	7158	2	Q23551	Q23551 caenorhabdi
1298	104	5.5	1912	1	PTPD_HUMAN	P23468 homo sapien	1371	102	5.3	192	2	Q9ERP7	Q9erp7 rattus norv
1299	103.5	5.4	211	2	Q7RTW5	Q7rtw5 homo sapien	1372	102	5.3	295	2	Q9ERF5	Q9erf5 mesocricetu
1300	103.5	5.4	239	2	O44730	O44730 caenorhabdi	1373	102	5.3	324	2	Q9UPK9	Q9upk9 homo sapien
1301	103.5	5.4	241	2	Q7RTW0	Q7rtw0 homo sapien	1374	102	5.3	326	2	Q9UPK8	Q9upk8 homo sapien
1302	103.5	5.4	336	2	O8UV41	O8uv41 brachydanio	1375	102	5.3	333	2	Q75238	Q75238 homo sapien
1303	103.5	5.4	360	2	Q8BJ10	Q8bj10 mus musculu	1376	102	5.3	340	2	Q9IAZ6	Q9iaz6 spherooides
1304	103.5	5.4	410	2	Q7YZA7	Q7yza7 bombyx mori	1377	102	5.3	353	2	Q9BCW3	Q9bcw3 gallus gall
1305	103.5	5.4	457	2	Q8HZT8	Q8hzt8 callithrix	1378	102	5.3	437	2	Q90W14	Q90w14 gallus gall
1306	103.5	5.4	662	1	NRG1_RAT	P43322 r pro-neure	1379	102	5.3	442	2	Q7PT04	Q7pt04 anopheles g
1307	103.5	5.4	717	2	Q7FUQ1	Q7fuq1 anopheles g	1380	102	5.3	571	2	Q8QFN4	Q8qfn4 salmo salar
1308	103.5	5.4	1007	1	ROB4_HUMAN	O8wz75 homo sapien	1381	102	5.3	595	1	SILL_HUMAN	Q96pq1 homo sapien
1309	103.5	5.4	1232	2	Q90284	Q90284 carassius a	1382	102	5.3	638	2	Q70766	Q7q766 anopheles g
1310	103.5	5.4	1256	2	Q92585	Q92585 mus musculu	1383	102	5.3	670	2	Q7Z247	Q7zz47 brachydanio
1311	103.5	5.4	1356	2	Q9BT59	Q9bt59 mus musculu	1384	102	5.3	709	2	Q8IXC7	Q8ixc7 homo sapien
1312	103.5	5.4	1375	2	Q8ML47	Q8ml47 drosophila	1385	102	5.3	718	2	Q6P6Z7	Q6p6z7 anopheles lae
1313	103.5	5.4	1375	2	Q94537	Q94537 drosophila	1386	102	5.3	808	2	Q7PVZ3	Q7pvz3 anopheles g
1314	103.5	5.4	1427	2	Q91562	Q91562 xenopus lae	1387	102	5.3	814	2	Q8IVU1	Q8ivu1 homo sapien
1315	103.5	5.4	1447	1	DCC_HUMAN	P43146 homo sapien	1388	102	5.3	848	2	Q25198	Q25198 hydra atten
1316	103.5	5.4	1526	2	Q94538	Q94538 drosophila	1389	102	5.3	975	2	P79750	P79750 fugu rubrip
1317	103.5	5.4	1526	2	Q9V6D5	Q9v6d5 drosophila	1390	102	5.3	1044	2	Q96IM3	Q96im3 homo sapien
1318	103.5	5.4	3094	2	Q695L1	Q695l1 homo sapien	1391	102	5.3	1089	2	Q19927	Q19927 caenorhabdi
1319	103	5.4	295	2	Q9GL75	Q9gl75 bos taurus	1392	102	5.3	1173	2	Q6NR54	Q6nr54 drosophila
1320	103	5.4	296	2	Q8WMZ2	Q8wmz2 sus scrofa	1393	102	5.3	1298	2	Q86W08	Q86w08 homo sapien
1321	103	5.4	310	2	Q7QK35	Q7qk35 anopheles g	1394	102	5.3	1301	2	Q9VZ81	Q9vz81 drosophila
1322	103	5.4	316	2	Q7Q0P9	Q7q0p9 anopheles g	1395	102	5.3	1363	2	Q86W07	Q86w07 drosophila
1323	103	5.4	331	2	Q63239	Q63239 rattus norv	1396	102	5.3	1377	2	Q9VJ42	Q9vj42 drosophila
1324	103	5.4	357	2	Q63238	Q63238 rattus norv	1397	102	5.3	226	1	C79A_HUMAN	C79a42 drosophila
1325	103	5.4	446	2	Q63236	Q63236 rattus norv	1398	102	5.3	240	2	Q13178	Q13178 homo sapien
1326	103	5.4	484	2	Q99J08	Q99jq8 mus musculu	1399	101.5	5.3	240	2	Q7PRJ5	Q7prj5 anopheles g
1327	103	5.4	504	2	Q8MIS3	Q8mis3 didelphis m	1400	101.5	5.3	303	2	Q7T114	Q7t114 brachydanio
1328	103	5.4	538	2	Q9QY07	Q9qyg7 mus musculu	1401	101.5	5.3	310	2	Q6MG95	Q6mg95 rattus norv
1329	103	5.4	547	2	Q6MG93	P40200 homo sapien	1402	101.5	5.3	332	2	Q90Z82	Q90z82 brachydanio
1330	103	5.4	569	1	TACT_HUMAN	Q99m67 mus musculu	1403	101.5	5.3	402	2	Q9GMZ7	Q9gmz7 felis silve
1331	103	5.4	601	2	Q99M67	Q99m67 mus musculu	1404	101.5	5.3	423	2	Q15227	Q15227 homo sapien
1332	103	5.4	624	2	Q9ES86	Q9es86 rattus norv	1405	101.5	5.3	457	2	Q6CTJ9	Q6ctj9 kluyveromyc
1333	103	5.4	645	2	Q8MJZ5	Q8mjz5 pan troglod	1406	101.5	5.3	461	2	Q61396	Q61396 mus musculu
1334	103	5.4	678	2	Q6PGN8	Q6pgn8 homo sapien	1407	101.5	5.3	597	1	SILL_PANTR	S35947 mesocricetu
1335	103	5.4	680	2	O55001	O55001 mus musculu	1408	101.5	5.3	602	2	Q8C9U6	Q8c9u6 mus musculu
1336	103	5.4	739	1	VCAL_RAT	P29534 rattus norv	1409	101.5	5.3	873	2	Q8C9U6	Q8c9u6 mus musculu
1337	103	5.4	898	1	UN5A_MOUSE	Q8k1s4 mus musculu	1410	101.5	5.3	939	2	Q9VH85	Q9vh85 gallus gall
1338	103	5.4	904	2	Q6POG2	Q6pog2 homo sapien	1411	101.5	5.3	948	2	Q9VME2	Q9vme2 drosophila
1339	103	5.4	960	2	Q7PV74	Q7pv74 anopheles g	1412	101.5	5.3	1166	2	Q9QVNA	Q9qvn4 rattus sp.
1340	103	5.4	1019	2	Q8UVR8	Q8uvr8 fugu rubrip	1413	101.5	5.3	1249	2	Q7TM29	Q7tm29 rattus norv
1341	103	5.4	1189	2	Q9P2J2	Q9p2j2 homo sapien	1414	101.5	5.3	1259	2	Q6RGJ3	Q6rgj3 mus musculu
1342	103	5.4	1240	1	NFAS_HUMAN	Q94856 homo sapien	1415	101.5	5.3	6048	2	Q7JN85	Q7jn85 caenorhabdi
1343	103	5.4	1259	1	CAML_RAT	Q05695 rattus norv	1416	101.5	5.3				
1344	103	5.4	1280	2	Q9EPX2	Q9epx2 mus musculu	1417	101.5	5.3				
1345	103	5.4	1365	2	Q9UFS4	Q9upe4 homo sapien	1418	101.5	5.3				

1419	101	5.3	215	1	EVAL MOUSE	070255	mus musculus	1492	100.5	5.3	1363	2	Q7Z3G9	Q7Z3G9	homo sapien
1420	101	5.3	215	2	Q91W14	Q91w14	mus musculus	1493	100.5	5.3	1391	2	Q8GQP2	Q8gqp2	haemophilus
1421	101	5.3	265	2	Q7PUU3	Q7puu3	anopheles g	1494	100.5	5.3	1401	2	Q6AWCO	Q6awc0	homo sapien
1422	101	5.3	305	2	Q75308	Q75308	homo sapien	1495	100.5	5.3	1401	2	Q6AWC1	Q6awc1	homo sapien
1423	101	5.3	316	2	Q8WP58	Q8wp58	dtrosophila	1496	100.5	5.3	1461	2	Q8T9F6	Q8t9f6	dtrosophila
1424	101	5.3	316	2	Q8WP94	Q8wp94	dtrosophila	1497	100.5	5.3	1461	2	Q8T9F6	Q8t9f6	dtrosophila
1425	101	5.3	333	1	ANAL DROME	P15364	dtrosophila	1498	100.5	5.3	1474	2	Q8T4M0	Q8t4m0	dtrosophila
1426	101	5.3	341	2	Q7KX52	Q7kx52	dtrosophila	1499	100.5	5.3	1503	2	Q8T4L8	Q8t4l8	dtrosophila
1427	101	5.3	342	2	Q642G9	Q642g9	brachydanio	1500	100.5	5.3	1503	2	Q7KTI8	Q7kti8	dtrosophila
1428	101	5.3	344	2	P91017	P91017	caenorhabdi						Q8IPGI	Q8ipgi	dtrosophila
1429	101	5.3	353	2	Q8MHQ3	Q8mhq3	gallus gall								
1430	101	5.3	391	2	Q7QJG1	Q7qjg1	anopheles g								
1431	101	5.3	532	2	Q6NNU3	Q6nnu3	dtrosophila								
1432	101	5.3	532	2	Q9VLF0	Q9vlf0	dtrosophila								
1433	101	5.3	606	2	Q6IRH8	Q6irh8	rattus norv								
1434	101	5.3	606	2	Q9ESS7	Q9ess7	mus musculus								
1435	101	5.3	633	2	Q9VD13	Q9vd13	dtrosophila								
1436	101	5.3	648	2	Q9EPF1	Q9epf1	mus musculus								
1437	101	5.3	648	2	Q8R2Y2	Q8r2y2	mus musculus								
1438	101	5.3	771	1	P1GR MOUSE	Q70570	mus musculus								
1439	101	5.3	915	2	Q8R4B3	Q8r4b3	mus musculus								
1440	101	5.3	974	2	Q90777	Q90777	gallus gall								
1441	101	5.3	976	2	Q9W755	Q9w755	brachydanio								
1442	101	5.3	1176	1	XMLS BOVIN	Q28824	bos taurus								
1443	101	5.3	1210	1	AF4 HUMAN	P51825	homo sapien								
1444	101	5.3	1211	2	Q6LA76	Q6la76	homo sapien								
1445	101	5.3	1237	2	Q75147	Q75147	homo sapien								
1446	101	5.3	1255	2	Q7Z3Z9	Q7z3z9	homo sapien								
1447	101	5.3	1255	2	Q7YQL7	Q7yql7	pongo pygma								
1448	101	5.3	1255	2	Q7YQL8	Q7yql8	pan troglod								
1449	101	5.3	1257	1	CAML HUMAN	P32004	homo sapien								
1450	101	5.3	1258	2	Q76LL6	Q76ll6	mus musculus								
1451	101	5.3	1723	2	Q8CHB2	Q8chb2	mus musculus								
1452	101	5.3	2053	2	Q8WXU7	Q8wxu7	homo sapien								
1453	101	5.3	2092	2	Q76MU9	Q76mu9	homo sapien								
1454	101	5.3	2113	2	Q8TD84	Q8td84	homo sapien								
1455	101	5.3	4369	2	Q8MXD7	Q8mxd7	caenorhabdi								
1456	101	5.3	4650	2	Q15598	Q15598	homo sapien								
1457	100.5	5.3	174	2	Q3GMZ9	Q9gmz9	felis silve								
1458	100.5	5.3	201	2	Q9NBA9	Q9nba9	dtrosophila								
1459	100.5	5.3	212	2	Q9NBB0	Q9nbb0	dtrosophila								
1460	100.5	5.3	235	2	Q6UWV2	Q6uwv2	homo sapien								
1461	100.5	5.3	245	1	MOC RAT	Q6j345	rattus norv								
1462	100.5	5.3	245	2	Q6MF9X	Q6mf9x	rattus norv								
1463	100.5	5.3	249	1	BASI CRIGR	Q99pab3	cricetulus								
1464	100.5	5.3	305	2	Q8VBW0	Q8vbw0	mus musculus								
1465	100.5	5.3	314	2	Q6X1Z6	Q6x1z6	bovine herp								
1466	100.5	5.3	326	2	Q8UV70	Q8uv70	brachydanio								
1467	100.5	5.3	332	2	Q95L16	Q95l16	felis silve								
1468	100.5	5.3	335	1	PSG2 HUMAN	P11465	homo sapien								
1469	100.5	5.3	345	2	Q811H7	Q811h7	mus musculus								
1470	100.5	5.3	359	1	HPL3 MOUSE	Q80wm5	mus musculus								
1471	100.5	5.3	366	1	CD44 BOVIN	Q29423	bos taurus								
1472	100.5	5.3	371	2	Q7Q1Z7	Q7qlz7	anopheles g								
1473	100.5	5.3	413	2	Q9VAR6	Q9var6	dtrosophila								
1474	100.5	5.3	440	2	Q8MK37	Q8mk37	macaca mula								
1475	100.5	5.3	440	2	Q8MK38	Q8mk38	macaca mula								
1476	100.5	5.3	449	2	Q9UE16	Q9ue16	homo sapien								
1477	100.5	5.3	457	1	CD4 MOUSE	P06332	mus musculus								
1478	100.5	5.3	472	2	Q6PIZ7	Q6piz7	homo sapien								
1479	100.5	5.3	527	2	Q675X8	Q675x8	olkopleura								
1480	100.5	5.3	620	2	Q6UD74	Q6ud74	medicago tr								
1481	100.5	5.3	708	1	KIR2 HUMAN	Q6uwl6	homo sapien								
1482	100.5	5.3	719	1	GROU DROME	P16371	dtrosophila								
1483	100.5	5.3	719	1	LRF5 HUMAN	Q98ni6	homo sapien								
1484	100.5	5.3	730	2	Q7KRZ4	Q7krz4	dtrosophila								
1485	100.5	5.3	829	2	Q95KJ9	Q95kj9	macaca fasc								
1486	100.5	5.3	872	1	CADI XENLA	P30944	xenopus lae								
1487	100.5	5.3	913	1	E4LB HUMAN	Q9b329	homo sapien								
1488	100.5	5.3	1026	2	Q7R0D0	Q7r0d0	giardia lam								
1489	100.5	5.3	1172	2	Q6ZRG7	Q6zrg7	homo sapien								
1490	100.5	5.3	1215	2	Q7KTI7	Q7kti7	dtrosophila								
1491	100.5	5.3	1256	2	Q35158	Q35158	rattus norv								

ALIGNMENTS

RESULT 1

Q9H6B4	PRELIMINARY;	PRT;	373 AA.
AC	Q9H6B4;		
DT	01-MAR-2001 (TRENBLrel. 16, Created)		
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)		
DT	25-OCT-2004 (TRENBLrel. 28, Last annotation update)		
DE	Hypothetical protein FLJ22415 (Adipocyte adhesion molecule)		
DE	(Adipocyte-specific adhesion molecule) (CAR-like membrane protein CLMP) (SLLL318).		
DE	Name=ASAM; Synonyms=CLMP; ORFNames=UNQ318;		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_taxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kawabata A., Hikiuji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		
RA	Okitani R., Ota T., Suzuki Y., Ohtsuka M., Nishi T., Shibahara T.,		
RA	Tanaka T., Nakamura Y., Isegai T., Sugano S.;		
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBAJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Eguchi J., Wada J., Hida K., Zhang H.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBAJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RX	MEDLINE=22378257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RA	Strausberg R.;		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBAJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A.		
EX	PubMed=1457322; DOI=10.1074/jbc.M308249200;		
RA	Raschperger E., Engstrom U., Petersson R.F., Fuxe J.;		
RT	"CLMP, a novel member of the CTX family and a new component of		


```
RT epithelial tight junctions.";  
RL J. Biol. Chem. 279:796-804(2004).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Weand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; AK026068; BAB15347.1; -  
DR EMBL; AY326422; AAP88386.1; -  
DR EMBL; BC09371; AA09371.1; -  
DR EMBL; AY358340; AAQ88706.1; -  
DR EMBL; BK001245; DAA01139.1; -  
DR HSSP; P78310; IKAC.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
SQ SEQUENCE 373 AA; 41280 MW; FDA215EB3B3C4335 CRC64;  
  
Query Match 100.0%; Score 1908; DB 2; Length 373;  
Best Local Similarity 100.0%; Pred. No. 1.2e-123;  
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MSLLLLLLSVYVGTLTGTHTEIKRVAEEKVTLPCHHQGLPEKOTLDIEWLLTDNEGNQ 60  
Db 1 MSLLLLLLSVYVGTLTGTHTEIKRVAEEKVTLPCHHQGLPEKOTLDIEWLLTDNEGNQ 60  
  
QY 61 KVVITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYV 120  
Db 61 KVVITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYV 120  
  
QY 121 WSHVILKVLVRSPKPCKELEGBLTGSDLTQCESSSGTEPIVYVQRIREKEGEDRLP 180  
Db 121 WSHVILKVLVRSPKPCKELEGBLTGSDLTQCESSSGTEPIVYVQRIREKEGEDRLP 180  
  
QY 181 PKSRIDYHNPGRVLLQNLTMVSYGLYQCTAGNEAGKESCVVRVTQVYQSIGWAGAVTG 240  
Db 181 PKSRIDYHNPGRVLLQNLTMVSYGLYQCTAGNEAGKESCVVRVTQVYQSIGWAGAVTG 240  
  
QY 241 IVAGALLIFLLVLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSGSRSSRG 300  
Db 241 IVAGALLIFLLVLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSGSRSSRG 300  
  
QY 301 SSSTSTANSASRSORTLSTDAAPQGLATQAYSLVGPVEVRSPPKVVHANLTKAETTP 360  
Db 301 SSSTSTANSASRSORTLSTDAAPQGLATQAYSLVGPVEVRSPPKVVHANLTKAETTP 360  
  
QY 361 SMIPSQSRAFTV 373  
Db 361 SMIPSQSRAFTV 373  
  
RESULT 2  
Q8K1G0 PRELIMINARY; PRT; 372 AA.  
AC Q8K1G0  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE Adipocyte adhesion molecule.  
GN Name=Acam;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
  
QY 1 MSLLLLLLSVYVGTLTGTHTEIKRVAEEKVTLPCHHQGLPEKOTLDIEWLLTDNEGNQ 60  
Db 1 MSLLLLLLSVYVGTLTGTHTEIKRVAEEKVTLPCHHQGLPEKOTLDIEWLLTDNEGNQ 60  
  
QY 61 KVVITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYV 120  
Db 61 KVVITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYV 120  
  
QY 121 WSHVILKVLVRSPKPCKELEGBLTGSDLTQCESSSGTEPIVYVQRIREKEGEDRLP 180  
Db 121 WSHVILKVLVRSPKPCKELEGBLTGSDLTQCESSSGTEPIVYVQRIREKEGEDRLP 180  
  
QY 181 PKSRIDYHNPGRVLLQNLTMVSYGLYQCTAGNEAGKESCVVRVTQVYQSIGWAGAVTG 240  
Db 181 PKSRIDYHNPGRVLLQNLTMVSYGLYQCTAGNEAGKESCVVRVTQVYQSIGWAGAVTG 240  
  
QY 241 IVAGALLIFLLVLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSGSRSSRG 300  
Db 241 IVAGALLIFLLVLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSGSRSSRG 300  
  
QY 301 SSSTSTANSASRSORTLSTDAAPQGLATQAYSLVGPVEVRSPPKVVHANLTKAETTP 360  
Db 301 SSSTSTANSASRSORTLSTDAAPQGLATQAYSLVGPVEVRSPPKVVHANLTKAETTP 360  
  
QY 361 SMIPSQSRAFTV 373  
Db 361 SMIPSQSRAFTV 373  
  
RESULT 3  
Q8R373 PRELIMINARY; PRT; 373 AA.  
AC Q8R373  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE CAR-like membrane protein (Adipocyte adhesion molecule) (Mus musculus  
DE adult male cecum cDNA, RIKEN full-length enriched library,  
DE clone:9130232017 product:ADIPOCYTE-SPECIFIC PROTEIN 5, full insert  
DE sequence).  
GN Name=9030425E11rik; Synonyms=CLMP;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=FVB/N; TISSUE=Mammary tumor;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI_TaxID=101116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=OLETF; TISSUE=Visceral adipose;  
RA Hida K., Wada J., Zhang H., Makino H.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF302047; AAM76974.1; -  
DR HSSP; P78310; IKAC.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig_c2.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
SQ SEQUENCE 372 AA; 41148 MW; 439AB3C4D3E56346 CRC64;  
  
Query Match 93.3%; Score 1781; DB 2; Length 372;  
Best Local Similarity 93.2%; Pred. No. 6.9e-115;  
Matches 345; Conservative 12; Mismatches 13; Indels 0; Gaps 0;  
  
QY 4 LLLLLLVSYVYVGTLTGTHTEIKRVAEEKVTLPCHHQGLPEKOTLDIEWLLTDNEGNQKV 63  
Db 3 LFFLLVLTYYVYVGTLTGTHTEIKRVAEEKVTLPCHHQGLPEKOTLDIEWLLTDNEGNQKV 62  
  
QY 64 ITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 123  
Db 63 ITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 122  
  
QY 124 VILKVLVRSPKPCKELEGBLTGSDLTQCESSSGTEPIVYVQRIREKEGEDRLP 183  
Db 123 VILKVLVRSPKPCKELEGBLTGSDLTQCESSSGTEPIVYVQRIREKEGEDRLP 182  
  
QY 184 RIDYHNPGRVLLQNLTMVSYGLYQCTAGNEAGKESCVVRVTQVYQSIGWAGAVTGIVA 243  
Db 183 RIDYHNPGRVLLQNLTMVSYGLYQCTAGNEAGKESCVVRVTQVYQSIGWAGAVTGIVA 242  
  
QY 244 GALLIFLLVLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSGSRSSRGSSSS 303  
Db 243 GALLIFLLVLLIRKDKERYEEERPNREDAEAPKARLVKPSSSSGSRSSRGSSSS 302  
  
QY 304 TSTANSASRSORTLSTDAAPQGLATQAYSLVGPVEVRSPPKVVHANLTKAETTPSMI 363  
Db 303 TSTANSASRSORTLSTDAAPQGLATQAYSLVGPVEVRSPPKVVHANLTKAETTPSMI 362  
  
QY 364 PQSQRAFQTV 373  
Db 363 PQSQRAFQTV 372  
  
RESULT 3  
Q8R373 PRELIMINARY; PRT; 373 AA.  
AC Q8R373  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE CAR-like membrane protein (Adipocyte adhesion molecule) (Mus musculus  
DE adult male cecum cDNA, RIKEN full-length enriched library,  
DE clone:9130232017 product:ADIPOCYTE-SPECIFIC PROTEIN 5, full insert  
DE sequence).  
GN Name=9030425E11rik; Synonyms=CLMP;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=FVB/N; TISSUE=Mammary tumor;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
```


RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavert T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster;
 RA Eguchi J., Wada J., Hida K., Zhang H.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 [9]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numataki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster/NIH;
 RX PubMed=14573622; DOI=10.1074/jbc.M308249200;
 RA Raschperger E., Engstrom U., Pettersson R.P., Fuxe J.;
 RT "CLMP, a novel member of the CTX family and a new component of
 RT epithelial tight junctions.";
 RL J. Biol. Chem. 279:796-804 (2004).
 DR EMBL; BC026447; AAH26447.1; -;
 DR EMBL; AY326421; AAP88385.1; -;
 DR EMBL; AK033723; BAC28446.1; -;
 DR EMBL; AY259213; AAP15240.1; -;
 DR HSSP; P78310; IKAC.
 DR MGD; MGI:1918816; 9030425E11rik.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 SQ SEQUENCE 373 AA; 41214 MW; 9C6288484AF95512 CRC64;
 Query Match 92.4%; Score 1763.5; DB 2; Length 373;
 Best Local Similarity 92.7%; Pred. No. 1.1e-113;
 Matches 344; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 4 LLLLLVSYVYVGTGTHTEIKRVAEKKVTLPCHHQLGLPEKDTLDIEWLLTDNEGKQKV 63
 DB 3 LFFLWLVSYVYVGTGTHTEIKRVAEKKVTLPCHHQLGLPEKDTLDIEWLLTDNEGKQKV 62
 QY 64 ITYSRRHYNNLTBEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 123
 DB 63 ITYSRRHYNNLTBEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 122
 QY 124 VILKVLVRPSKPKCELGELTEGSDTLTQCSSSGTBPVIVYVQIRIRKEGEDEHLPPKS 183
 DB 123 VILKVLVRPSKPKCELGELTEGSDTLTQCSSSGTBPVIVYVQIRIRKEGEDEHLPPKS 182
 QY 184 RIDYNNHGRVLLQNLTWSSGLYOCYTAGNEAGKSCVVRVTYVQVQSIGMVAGAVTGIVA 243
 DB 183 RIDYNNHGRVLLQNLTWSSGLYOCYTAGNEAGKSCVVRVTYVQVQSIGMVAGAVTGIVA 242
 QY 244 GALLIFLLVLLIRRKDKERYEEERPNIEDEAEAPKARLVKPPSSSSSGSSSSSGSS 303
 DB 243 GALLIFLLVLLIRRKDKERYEEERPNIEDEAEAPKARLVKPPSSSSSGSSSSSGSS 302
 QY 304 TRSTANSASRSQRTLSLTDAP-QGLATQAYSLVGVPEVRGSEPKVHHANLTAKATTFSM 362
 DB 303 TRSTGNSASRSQRTLSLSEAPQGLAPQAYSLVGVPEVRGSEPKVHHANLTAKATTFSM 362
 QY 363 IPSQSRAFQTV 373
 DB 363 TPSQSKAFQTV 373
 RESULT 4
 Q920S5 PRELIMINARY; PRT; 373 AA.
 ID Q920S5
 AC Q920S5;

wed May 11 07:24:24 2005

```

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adipocyte-specific protein 5.
GN Name=9030425E11rik; Synonyms=asp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL Tsuruga H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040490; BAB68503.1; -.
DR HSP; P78310; 1KAC.
DR MGD; MGI:1918916; 9030425E11rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0036021; C:integral to membrane; TAS.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; Igc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;

Query Match 92.2%; Score 1759.5; DB 2; Length 373;
Best Local Similarity 92.5%; Pred. No. 2.1e-113;
Matches 343; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 4 LLLLLVSYVVGTLGTHTEIKRVAEKKVLPCHQGLGPEKDTLDIEWLLTDNEGNQKV 63
DB 3 LPFLVLSVYVVGTLGTHTEIKRVAEKKVLPCHQGLGPEKDTLDIEWLLTDNEGNQKV 62
QY 64 ITYSSRHVYNNLTTEQKGRVAFASNLGADSLQIEPLKPSDEGRYTKVNSGRYVWSH 123
DB 63 ITYSSRHVYNNLTTEQKGRVAFASNLGADSLQIEPLKPSDEGRYTKVNSGRYVWSH 122
QY 124 VILKVLVRPSKPCKELEGTEGSDLTQCESSGTEPIVYVQIRKEGEDERLPPKS 183
DB 123 VILKVLVRPSKPCKELEGTEGSDLTQCESSGTEPIVYVQIRKEGEDERLPPKS 182
QY 184 RIDYNNHGRVLLQNLNLTWSGLYQCTAGNEAGKESCVVRVTYVQVSGIMVAGVTGIVA 243
DB 183 RIDYNNHGRVLLQNLNLTWSGLYQCTAGNEAGKESCVVRVTYVQVSGIMVAGVTGIVA 242
QY 244 GALLIFLLVWLLIRRKDKERYEEERPNREDAEAPKARLVKPSSSSGSSSSSGSS 303
DB 243 GALLIFLLVWLLIRRKDKERYEEERPNREDAEAPKARLVKPSSSSGSSSSSGSS 302
QY 304 TRSTANSASRSQRTLSTDAAP-QPGLATQAYSLVGPVGRSEPKVHHANLTKAETTPSN 362
DB 303 TRSTANSASRSQRTLSTDAAP-QPGLATQAYSLVGPVGRSEPKVHHANLTKAETTPSN 362
QY 363 IPSQSRAFQTV 373
DB 363 TPSQSRAFQTV 373

RESULT 5
Q640U3 PRELIMINARY; PRT; 332 AA.
AC Q640U3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RL TISSUE=Whole body;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RX

RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fabey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Skalska U., Smailus D.E., Schnrer A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnrer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RL TISSUE=Whole body; D.S.; to the EMBL/GenBank/DBJ databases.
RA Klein S., Gerhard D.S.;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC082496; AAH82496.1; -.
KW Hypothetical protein.
SQ SEQUENCE 332 AA; 36851 MW; 0DF9DEB7D4BB426C CRC64;

Query Match 41.3%; Score 787.5; DB 2; Length 332;
Best Local Similarity 51.1%; Pred. No. 2.4e-46;
Matches 165; Conservative 51; Mismatches 102; Indels 5; Gaps 3;

QY 2 SLILLLLVSYVVGTLGTHTEIKRVAEKKVLPCHQGLGPEKDTLDIEWLLTDNEGNQK 61
DB 3 TLIRSLGLVYVVGTLGTHTEIKRVAEKKVLPCHQGLGPEKDTLDIEWLLTDNEGNQK 61
QY 62 VWTYSRRHYNNLTTEQKGRVAFASNLGADSLQIEPLKPSDEGRYTKVNSGRYVW 121
DB 62 VLTYSRRHYNNLTTEQKGRVAFASNLGADSLQIEPLKPSDEGRYTKVNSGRYVW 119
QY 122 SHVILKVLVRPSKPCKELEGTEGSDLTQCESSGTEPIVYVQIRKEGEDERLPP 181
DB 120 SFITVIVLVRPSKPCKELEGTEGSDLTQCESSGTEPIVYVQIRKEGEDERLPP 179
QY 182 KSRIDYNNHGRVLLQNLNLTWSGLYQCTAGNEAGKESCVVRVTYVQVSGIMVAGVTGI 241
DB 180 TARTI--OPENQLLHNLKTDNGSYRCVNSVGVKTCDDVTVQVSVNTGILAGVACGV 237
QY 242 VAGALLIFLLVWLLIRRKDKERYEEERPNREDAEAPKARLVKPSSSSGSSSSSGSS 301
DB 238 VGVFLIFFTVWLLFHKKEFKKEEERPNREDAEAPKARLVKPSSSSGSSSSSGSS 297
QY 302 SSTRSTANSASRSQRTLSTDAAP 324
DB 298 SSTRSTANSASRSQRTLSTDAAP 320

RESULT 6
Q8CIH8 PRELIMINARY; PRT; 160 AA.
ID Q8CIH8
AC Q8CIH8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male colon cDNA, RIKEN full-length enriched
DE library, clone:9030425E11 product:ADIPOCYTE-SPECIFIC PROTEIN 5, full
DE insert sequence. (Fragment).
GN Name=9030425E11rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```


RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -I- FUNCTION: Serves as a receptor for group B coxsackieviruses and
 CC subgroup C of adenoviruses (AD2 and AD5).
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Y07593; CAA68868.1; -;
 DR EMBL; AF0716; AAC51234.1; -;
 DR EMBL; AF169366; AAF05908.1; JOINED.
 DR EMBL; AF169360; AAF05908.1; JOINED.
 DR EMBL; AF169361; AAF05908.1; JOINED.
 DR EMBL; AF169362; AAF05908.1; JOINED.
 DR EMBL; AF169363; AAF05908.1; JOINED.
 DR EMBL; AF169364; AAF05908.1; JOINED.
 DR EMBL; AF169365; AAF05908.1; JOINED.
 DR EMBL; AF200465; AAF24344.1; -;
 DR EMBL; AF242865; AAG01088.1; -;
 DR EMBL; AF242862; AAG01088.1; JOINED.
 DR EMBL; AF242864; AAG01088.1; JOINED.
 DR EMBL; BC003684; AAH03684.1; -;
 DR EMBL; BC010536; AAH10536.1; -;
 DR PDB; 1E4J; X-ray; A/B=15-140.
 DR PDB; 1F5W; X-ray; A/B=15-140.
 DR PDB; 1KAC; X-ray; B=21-144.
 DR Genew; HGNC:2559; CXADR.
 DR H-InvDB; HIX0016031; -;
 DR MM; 602621; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0004872; F: receptor activity; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR 3D-structure; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 365 Coxsackievirus and adenovirus receptor.
 FT DOMAIN 20 237 Extracellular (Potential).
 FT TRANSMEM 238 258 Potential.
 FT DOMAIN 259 365 Cytoplasmic (Potential).
 FT DOMAIN 259 365 Ig-like C2-type 1.
 FT DOMAIN 141 228 Ig-like C2-type 2.
 FT DOMAIN 41 120 By similarity.
 FT DISULFID 162 212 By similarity.
 FT

FT CARBOHYD 106 106 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).
 FT STRAND 21 22
 FT STRAND 27 32
 FT TURN 33 34
 FT STRAND 37 39
 FT STRAND 42 44
 FT TURN 47 48
 FT STRAND 53 61
 FT TURN 62 63
 FT STRAND 69 75
 FT TURN 76 77
 FT STRAND 78 80
 FT TURN 82 83
 FT TURN 86 90
 FT STRAND 91 93
 FT HELIX 98 100
 FT TURN 101 101
 FT STRAND 102 102
 FT STRAND 105 107
 FT HELIX 112 114
 FT STRAND 116 124
 FT TURN 125 126
 FT STRAND 127 138
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;
 Query Match 24.4%; Score 465; DB 1; Length 365;
 Best Local Similarity 31.6%; Pred. No. 5e-24;
 Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;
 QY 1 MSLLLLLLVSYVG-----TLGTHTR-IRKVAEKEVTLPCHQHGLPEKDTLDIEWLLT 54
 DB 1 MALLLCFVLLCGVVDFAFARSLSITTPPEMIEKAKGETAYLPCKFTLSPEQDQGLDIEWLIS 60
 QY 55 --DNEGKQKVITYSSRHVYNNLTTEEOKGRVAFASNEL-AGDASIOIEPLKPSDEGRVTC 111
 DB 61 PADNQKVDQVILLYSGDKYDDYDPLDKRVHFTSNDLKSGDASINVNLQSLDITGYQC 120
 QY 112 KVKNSGRYVWWSHVLKVLVRPSKPCLEGLTSGSLTLQCESSSGTTEPIVYVWQRIRE 171
 DB 121 KVKAPGVANKIHLVVLKPSGARCVDGSEELGSDKICEKESGLPQYEWQKL-- 178
 QY 172 KEGEDERLPKSRIDYVNHGKRVLLQNTMSVSGLYQCTAGNEAKGKSCVVRV-TVQYVQS 230
 DB 179 ---SDSQKPTSLAEMTSSVISVKNASSEYSGTYSCTVRNRVSGDQCLLRNVVPPSNK 235
 QY 231 IGVAVAGTVGIVAGALLIFLLVLLIRRKOKERYEEERPNIEBEDAEAPKARL----- 284
 DB 236 AGLIAGAIIGTLALALIGLIIFCCRKKRREKYEKVH-HDIREDVPPPKSRSTARSY 294
 QY 285 --VKPSSSGSRSSRSSTRANSASRSQRTSLTDAAPQPLATQAYSLVGPVVRG 342
 DB 295 IGSNHSSLSGMSPSNMEGYSKYQNVPSDFETPTQSPITLP----- 336
 QY 343 SEPKKVHANLTKAETTPSPMQSR 368
 DB 337 --PAKVAAPNLSRMGAIPVMIPAQSK 360
 RESULT 10
 Q9R066 PRELIMINARY; PRT; 358 AA.
 ID Q9R066 AC Q9R066;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Coxsackie-adenovirus-receptor homolog (fragment).
 GN Name=CAR1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=101116;
 RN [1]


```

SEQUENCE FROM N.A.
RT STRAIN=Wistar; TISSUE=Liver;
RL MEDLINE=99422053; PubMed=10490761;
RN Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RP Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RX Lamers J.W.J., Poller W.;
RA "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109644; AAF01255.1; -.
DR HSP; P78310; 1KAC.
DR GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003598; IG_C2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 358 AA; 39261 MW; 731B7384A786BB04 CRC64;

Query Match 24.3%; Score 463; DB 2; Length 358;
Best Local Similarity 32.2%; Pred. No. 6.7e-24; Indels 34; Gaps 11;
Matches 122; Conservative 71; Mismatches 152;

QY 1 MSLLLLLL--VSYYVGLTGTHTTEIKRVAE---EKVTLPCCHQGLPEKDTLDIEWLL- 53
DB 1 MALLLCFVLLCGVAOFTSSLSITTPQRIEAKAGETAYLPCKFTLEPEDQGLDIEWLLS 60

QY 54 -TDNEGNQKVITYSSRHVYNNLTTEQGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
DB 61 PSDNQKVDQVILYSGDKTYDNYYPDLKGRVHFTSNDVKSGDASINVTNLQSLDIGTYQC 120

QY 112 KVKNSGRYVWSHVLKVLVPRSPKPCLEGELEGTSGDLTLCQESSSGTEPIVYVQRIRE 171
DB 121 KVKAPCVANRKFLLVLPKPSGTRCFVDSGEIGNDFKLCPEKSGSLPQYEWQKL-- 178

QY 172 KEGEDERLPKSIDYVNHGPRVLLQNLTMSYGLVQCTAGNEAGKESCVRVY-TQYVQS 230
DB 179 --SDSQMPTFLAEMTSP-VISVKNASSEYSGTSCVTQNVGSDQCLRLDVPVPSNR 235

QY 231 IGWVAGAVTGIVAGALLIFLLWLLIRKDKERYEEERPNFIREDAEAPKARLVKPPSS 290
DB 236 AGTIAGAVIGTLALVILGAILFCCHKGRKEEYKEVH-HDIREDPVPPKSTARSYS 294

QY 291 SSGSRSSRSSSTRSTANSASRSQRTLTSD--AAQ-QPLATQAVSLVGPVGRSGEPK 347
DB 295 IGSNHSILGMSPSNMGYSKTYQNVQPSDFERAPQSPTLA-----PAK 339

QY 348 VHHANLTKAETTPSMIPSQ 366
DB 340 VAAPNLSRMGAVPMIPFAQ 358

RESULT 11
CXAR_MOUSE STANDARD; PRT; 365 AA.
ID CXAR_MOUSE
AC P97792; O09052;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
GN Name=Cxadr; Synonyms=Cxr;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=90356860; DOI=10.1126/science.275.5304.1320;
RN Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RA "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5."
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096397; DOI=10.1073/pnas.94.7.3352;
RN Tomko R.P., Xu R., Philipson L.;
RA "HCAR and WCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=98080429; PubMed=9420240;
RN Bergelson J.M., Krithivas A., Celi L., Droguett G., Horwitz M.S.,
RA Wickham T., Crowell R.L., Finberg R.W.;
RT "The murine CAR homolog is a receptor for coxsackie B viruses and
RT adenoviruses."
RL J. Virol. 72:415-419(1998).
RN [4]
RP SUBCELLULAR LOCATION: Type 1 membrane protein.
CC - SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; Y10320; CAA71368.1; -.
CC EMBL; U90715; AAC53148.1; -.
CC EMBL; Y11929; CAA72679.1; -.
CC HSP; P78310; 1KAC.
CC MGD; MGI:1201679; Cxadr.
CC InterPro; IPR007110; IG-Like.
CC Pfam; PF00047; ig; 2.
CC PROSITE; PS50835; IG_LIKE; 2.
CC Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT DOMAIN 259 365
FT DOMAIN 20 136
FT DOMAIN 141 228
FT DISULFID 41 120
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
FT CONFLICT 340 365
FT SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 24.0%; Score 457.5; DB 1; Length 365;
Best Local Similarity 32.0%; Pred. No. 1.6e-23;
Matches 121; Conservative 70; Mismatches 154; Indels 33; Gaps 11;

QY 3 LLLLLL--VSYYVGLTGTHTTEIKRVAE---EKVTLPCCHQGLPEKDTLDIEWLL--TD 55
DB 4 LLLCFVLLCGIADFTSGLSITTPQRIEAKAGETAYLPCKFTLSPEQGLDIEWLLISPSD 63

QY 56 NEGNQKVITYSSRHVYNNLTTEQGRVAFASNFL-AGDASLQIEPLKPSDEGRYTCVK 114
DB 64 NOIVDQVILYSGDKTYDNYYPDLKGRVHFTSNDVKSGDASINVTNLQSLDIGTYQC 123

QY 115 NSGRYVWSHVLKVLVPRSPKPCLEGELEGTSGDLTLCQESSSGTEPIVYVQRIREK 174
DB 124 KAPGVANKKFLVLPKPSGTRCFVDSGEIGNDFKLCPEKSGSLPQYEWQKL----S 179

```



```
Qy 175 EDERLPKSRIDYNHPRVLLQNLTMSTYGLYOCTAGNEAGKESCVVRV-TVQYVQSIGM 233
Db 180 DSQTMPTPLAEMTSP-VISVKNASSESGYSCVTQVRVSGDQCMLDLVDVPPSNRAGT 238
Qy 234 VAGAVTGIVAGALLIFLAVLLIRKDKERYEERPNIEEDAEAPKARLVKPSSSSG 293
Db 239 IAGAVIGTLLALVLIGAILFCCHRRKREKEVH-HDIREDVPPKSRSTARSYIGS 297
Qy 294 SRSSRGSSSTRSTANSASRQTLSTD--AAPQ-PGLATQAYSILVGEVRGSEPKVKVHH 350
Db 298 NHSSILGMSPSNMEGYSKTYNQVPSDFERAPQSPTLA-----PAKVAA 342
Qy 351 ANLTKAETTPSMIPQSR 368
Db 343 PNLGRMGAVPVMIPQSK 360

RESULT 12
Q9DBJ8 PRELIMINARY; PRT; 365 AA.
AC Q9DBJ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE library, clone:130005A16 product:coxsaekievirus and adenovirus
DE receptor, full insert sequence.
GN Name=Cxadr;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
```

```
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Hanagaki T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004908; BAB23660.2; -
DR HSSP; P78310; 1KAC.
DR MGD; MGI:1201679; Cxadr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;
Query Match 24.0%; Score 457.5; DB 2; Length 365;
Best Local Similarity 32.0%; Pred. No. 1.6e-23;
Matches 121; Conservative 70; Mismatches 154; Indels 33; Gaps 11;
Qy 3 LLLLLL--VSYVYVGLTGTETKRVAB---EKTLPCHQLGLPEKDTLDIEMLL--TD 55
Db 4 LLCFVLLCGIADFTSGLSITTPQRIEAKAGETAYLPCKFTLSPEQDGLDIEMLISPD 63
Qy .56 NEGNQKVITYSSRHVYNNLTETEEQGRVAFASNFL-AGDASLQIEPLKPSDEGRYTCVK 114
Db 64 NQIVDQVILYSGDKIYDNYVPLKGRVHFTSNDVKSGDASINVTNLQLSDIGTYQCKVK 123
Qy 115 NSGRYVWVSHVLKVLVRPSKPCBLEGLTSGSLDTLQCESSSGTEPIVYVQRIREK 174
Db 124 KAPGVANKKFLTLVLRPSGTRCFVDGSEETGNDPKLCEPKESGLPQFQWKL----S 179
Qy 175 EDERLPKSRIDYNHPRVLLQNLTMSTYGLYOCTAGNEAGKESCVVRV-TVQYVQSIGM 233
Db 180 DSQTMPTPLAEMTSP-VISVKNASSESGYSCVTQVRVSGDQCMLDLVDVPPSNRAGT 238
Qy 234 VAGAVTGIVAGALLIFLAVLLIRKDKERYEERPNIEEDAEAPKARLVKPSSSSG 293
Db 239 IAGAVIGTLLALVLIGAILFCCHRRKREKEVH-HDIREDVPPKSRSTARSYIGS 297
Qy 294 SRSSRGSSSTRSTANSASRQTLSTD--AAPQ-PGLATQAYSILVGEVRGSEPKVKVHH 350
Db 298 NHSSILGMSPSNMEGYSKTYNQVPSDFERAPQSPTLA-----PAKVAA 342
Qy 351 ANLTKAETTPSMIPQSR 368
Db 343 PNLGRMGAVPVMIPQSK 360

RESULT 13
Q9TU79 PRELIMINARY; PRT; 319 AA.
AC Q9TU79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coxsackie-adenovirus-receptor homolog (Fragment).
GN Name=CAR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
FT NON TER 344 344
SQ SEQUENCE 344 AA; 38030 MW; D436498820D8B9B7 CRC64;

Query Match 22.7%; Score 433.5; DB 2; Length 344;
Best Local Similarity 32.7%; Pred. No. 6.9e-22;
Matches 112; Conservative 68; Mismatches 143; Indels 19; Gaps 10;

Qy 1 MSLLALLLL--VSYYVCTLGTHTTEIKRVAS--EKVTLPCHHQLGLPEKDTLDIEWLL- 53
Db 1 MALLLCFVLLCGVADFTSSLSITTPQRIEAKGETAYLPCKFTLEPEDQGPLDIWLLIS 60

Qy 54 -TDNEGKQKVITYSSRRVYNNLTETEOKGRVAFASNEL-AGDASLQIEPLKPSDEGRYTC 111
Db 61 PSDNQKVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVKSGDASINVTNLQLSDIGTYQC 120

Qy 112 KVKNSGRYVWSHVILKVLVRPSKPKCELEGLTEGSDLTLOCESSSGTEPIVYVWQRIRE 171
Db 121 KVKKAPGVANRKFLTLTVLVKPSGTRCFVDGSGEIGNDFKLKCEPKESLPLQYEWQKL-- 178

Qy 172 KEGEDERLPPKSRIDYNHHPGRVLLQNLTMYSGLYQCTAGNEAKGSCVVRV-TVQYVQS 230
Db 179 --SDSQKPTWLAEMTSP-VISVKNASSEYSGTYSCTVQNRVGSDDQCMRLDVPVPSNR 235

Qy 231 IGMVAGAVTGIVAGALLIFLVLVLLIRRKOKERYEEERPNIEDEAEAPKARLVKPSSS 290
Db 236 AGTIAGAVICTLLALVLIGALFCCHKKREKEKEVH-HDIREDVPPPKSRTSTARSY 294

Qy 291 SSGRSRSRSGSSSTRSTANSASRSQRTLSTD--AAPQ-PGLA 329
Db 295 IGSNHSSILGSMSPSNMEGYSKTYNQVPSEDFERAPQSPTLA 336

Search completed: May 6, 2005, 08:08:55
Job time : 196 secs

THIS PAGE BLANK (USPTO)


```
Run on: May 6, 2005, 02:09:53 ; Search time 1225 Seconds
        (without alignments)
        11878.142 Million cell updates/sec

Title: US-09-978-544A-58
Perfect score: 2458
Sequence: 1 gcgcggagagccatctgcc.....acagagcgggactccgtctc 2458
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
               Maximum Match 100%
Database : N_Geneseq_16Dec04.*
Listing first 1500 summaries
1: _geneseqn1980a.*
2: _geneseqn1990a.*
3: _geneseqn2000a.*
4: _geneseqn2001a.*
5: _geneseqn2001bs.*
6: _geneseqn2002a.*
7: _geneseqn2002bs.*
8: _geneseqn2003a.*
9: _geneseqn2003bs.*
10: _geneseqn2003cs.*
11: _geneseqn2003ds.*
12: _geneseqn2004a.*
13: _geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description
RESULT 1
ID AA333941 standard; cDNA; 2458 BP.
DE Human PRO363 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 2; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 2
ID AAC58595 standard; cDNA; 2458 BP.
DE Human PRO363 protein UNQ318 encoding cDNA SEQ ID NO:86.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 3; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID AAC78473 standard; cDNA; 2458 BP.
DE Human PRO363 (UNQ318) nucleotide sequence SEQ ID NO:58.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 3; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 4
ID AAG21437 standard; cDNA; 2458 BP.
DE Human cDNA sequence encoding for PRO363 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 4; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 5
ID AAF44262 standard; cDNA; 2458 BP.
DE Human PRO363 nucleotide sequence SEQ ID NO:502.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2458; DB 5; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 6
ID ABL88103 standard; cDNA; 2458 BP.
DE Human PRO363 cDNA sequence SEQ ID NO:63.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 6; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID ABL95592 standard; cDNA; 2458 BP.
DE Human angiogenesis related cDNA PRO363 SEQ ID NO: 63.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 6; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID AC63509 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 8; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID AC64513 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US20030303531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 8; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 10
ID ACA03796 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US200303036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 8; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ACA71673 standard; cDNA; 2458 BP.
DE Human secreted and transmembrane polypeptide PRO363 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 8; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ABX89334 standard; cDNA; 2458 BP.
DE DNA encoding novel secreted and transmembrane protein PRO363.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 8; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
```



```

RESULT 13
ID ABX92313 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 14
ID ABX80972 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane protein cDNA, #176.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 15
ID ACD44481 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 16
ID ACD41988 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #194.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 17
ID ACA66054 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 18
ID ACA8561 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 19
ID ABX79652 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane protein cDNA, #176.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 20
ID ACA93673 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 21
ID ABX81355 standard; DNA; 2458 BP.
DE Novel human secreted or transmembrane protein PRO5723 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 22
ID ACA04217 standard; cDNA; 2458 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 397.
PN US2003032155-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 23
ID ACA93171 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 24
ID ABX17255 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 8; Length 2458;
Pred. No. 0;
RESULT 25
ID ACA68110 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;
RESULT 26
ID ACA88559 standard; cDNA; 2458 BP.
DE Human secreted and transmembrane polypeptide PRO363 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;
RESULT 27
ID ACD82066 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;
RESULT 28
ID ADA45906 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;
RESULT 29
ID ADA76337 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;
RESULT 30
ID AET44290 standard; cDNA; 2458 BP.
DE Human PRO363 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;
RESULT 31
ID ADA18987 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 9; Length 2458;
Pred. No. 0;

```


Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADA61610 standard; cDNA; 2458 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADB19395 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ADB27936 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADA86415 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ADB15979 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADA38013 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADA47765 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADA21699 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO363.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADA10486 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADA67560 standard; cDNA; 2458 BP.

DE Human PRO polynucleotide #194.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADE30567 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADA85863 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ADA18030 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADA97075 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADA79379 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADA87518 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADB16720 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADA218138 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADA91812 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADA94718 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADA24597 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADB18836 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADA94051 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB19947 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADB13259 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ACD98617 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US200304945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID AC029655 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADA12258 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO363.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADA94718 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADA74513 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADB24746 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ADA82270 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADA75233 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADA85311 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADA84759 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADB30015 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADA80543 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADA12258 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO363.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 69
ID ADA75785 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADA38943 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADA47010 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADB25306 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADA93482 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADB26832 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADB31119 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ABT44573 standard; cDNA; 2458 BP.
DE Human PRO363 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADA93064 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADA61047 standard; cDNA; 2458 BP.
DE Homo sapiens.

PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADB24194 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADA96523 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADA81095 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADA95971 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADB26280 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADB21765 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ACD82240 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane polypeptide PRO 363 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ACD29070 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #16.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADA77544 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003068797-A1.
PD 10-APR-2003.


```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADB18284 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADA86967 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADA88070 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADA46458 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADB28488 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ADB29040 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ACH5627 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ADA76992 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADA22625 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO363.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADA88622 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADA97627 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADB27384 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADB22317 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ACD39617 standard; cDNA; 2458 BP.
DE Human cDNA encoding PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADA06791 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #140.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ABT43946 standard; cDNA; 2458 BP.
DE Human membrane bound receptor/protein PRO363 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADA39484 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADA67008 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADB2869 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
```


Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ADB23642 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADA92364 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADB15427 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADB83619 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADB80725 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US200308068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADB73266 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADB38679 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADB96510 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADB78348 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 116
ID ADB38127 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 9; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADB66599 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADB84996 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADB89679 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADB90411 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ADB93512 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ADB78102 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ADB73564 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide sequence #16.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ADB87168 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US200308067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADB87168 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US200308067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;

ID ADB84750 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ADB47135 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ADB83865 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ADB86742 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ADB73020 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ADB76280 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide sequence #16.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ADB77347 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ADB34504 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ADB35608 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADB33952 standard; cDNA; 2458 BP.

DE Human PRO polynucleotide SEQ ID NO 387.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ADB35056 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ADB36160 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide SEQ ID NO 387.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ADB46555 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ADC43706 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ADC57982 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ADC55346 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141
ID ADC12213 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ADC61466 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADC63430 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 144
ID ADC66530 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 145
ID ADC56635 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 146
ID ADC68654 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 147
ID ADC62714 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 148
ID ADC67779 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 149
ID ADC11680 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 150
ID ADC41099 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 151
ID ADC67154 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 152
ID ADC62090 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 153

ID ADC36858 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US200308065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 154
ID ADC41723 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 155
ID ADC21848 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 156
ID ADC50428 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 157
ID ADC71975 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 158
ID ADC59954 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 159
ID ADC49879 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 160
ID ADC49078 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 161
ID ADC49595 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 162
ID ADC47456 standard; cDNA; 2458 BP.

DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADC52961 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADC57315 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADC60506 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADC50981 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADC65508 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADC54606 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADC53567 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADC59090 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADC55968 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.

PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADC58538 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID387.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADC14802 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADC47201 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADD08334 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADD03212 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ADC90204 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ADC82159 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADC69623 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ADC48512 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ADD10041 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ADD07801 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ADC78076 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ADD04616 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ADC82692 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ADD06311 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ADC80572 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ADD11079 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADD10352 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #32.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190

ID ADC47960 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADD08872 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ADC77830 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ADC80020 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADD07121 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ADD11312 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #32.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADD09489 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ADC83368 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ADD50793 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ADD41202 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003203438-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 200
ID ADD50520 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 201
ID ADD51039 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 202
ID ADD53081 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 203
ID ADD53633 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 204
ID ADD5475 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 205
ID ADD37105 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #32.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 206
ID ADD56433 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 207
ID ADD51789 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 208
ID ADD02568 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ADD50520 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 210
ID ADD02022 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 211
ID ADD54204 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 212
ID ADD54871 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 213
ID ADD50274 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 214
ID ADD51285 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 215
ID ADE49092 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 216
ID ADD92521 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;
RESULT 217
ID ADD91417 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 10; Length 2458;

RESULT 218
ID ADE04031 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ADE31890 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ADE27025 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ADE32328 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ADE22260 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ADD79484 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ADE35146 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ADE16260 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ADD72875 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ADE42020 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199026-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADE17837 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ADD31969 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ADE33432 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ADE33984 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ADD80036 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID ADD93073 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID ADD72233 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ADE19493 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ADE18941 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199026-A1.

PD 23-OCT-2003.	Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;
PA (GETH) GENENTECH INC.	Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 237	ID ADE43137 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003199033-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 238	ID ADE43137 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003199033-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 239	ID ADE22812 standard; cDNA; 2458 BP.				
DE cDNA encoding human PRO polypeptide #194.	PN US2003199064-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 240	ID ADE26492 standard; cDNA; 2458 BP.				
DE Novel human secreted and transmembrane protein PRO363 cDNA.	PN US2003087305-Al.				
PD 08-MAY-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 241	ID ADE26492 standard; cDNA; 2458 BP.				
DE Novel human secreted and transmembrane protein PRO363 cDNA.	PN US2003194766-Al.				
PD 16-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 242	ID ADE32890 standard; cDNA; 2458 BP.				
DE Novel human secreted and transmembrane protein PRO363 cDNA.	PN US2003194766-Al.				
PD 16-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 243	ID ADE42572 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003199032-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 244	ID ADE16884 standard; cDNA; 2458 BP.				
DE Human cDNA encoding secreted/transmembrane protein, PRO363.	PN US2003203433-Al.				
PD 30-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 245	ID ADD80588 standard; cDNA; 2458 BP.				
DE cDNA encoding human PRO polypeptide #194.	PN US2003207418-Al.				
PD 06-NOV-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 246	ID ADD89616 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003199028-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 247	ID ADE40900 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003199031-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 248	ID ADE04699 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003199034-Al.				
PD 23-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 249	ID ADE92828 standard; cDNA; 2458 BP.				
DE Human PRO polynucleotide #194.	PN US2003194777-Al.				
PD 16-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 250	ID ADF48898 standard; cDNA; 2458 BP.				
DE Human cDNA encoding secreted/transmembrane protein, PRO363.	PN US2003195333-Al.				
PD 16-OCT-2003.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 251	ID ADF67429 standard; cDNA; 2458 BP.				
DE Human PRO363 nucleotide sequence SEQ ID NO:502.	PN US2002198148-Al.				
PD 26-DEC-2002.	PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 2458;	DB 10;	Length 2458;	
Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 252	ID ADG2153				

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 255
ID ADG80577 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207373-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 256
ID ADG52655 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003216561-Al.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 257
ID ADG59975 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003206915-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 258
ID ADG80025 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207372-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 259
ID ADH55317 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207381-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 260
ID ADH5569 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207379-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 261
ID ADI35683 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003050457-Al.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 262
ID ADI60735 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003077700-Al.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 263
ID ADI64088 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207385-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 264
ID ADI63536 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207387-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 265
ID ADH81950 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207388-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 266
ID ADI00176 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003049682-Al.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 267
ID ADH81398 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207377-Al.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ABX78056 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #140.
PN US2003027163-Al.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ABX80468 standard; cDNA; 2458 BP.
DE Novel human secreted or transmembrane protein PRO5723 DNA.
PN US2002132252-Al.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 270
ID ACA69374 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003032023-Al.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 271
ID ACD24046 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003032156-Al.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 272
ID ABX90445 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane protein cDNA, #176.
PN US2002160384-Al.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 273
ID ACA66905 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #65.
PN US2003036635-Al.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 274
ID ACD4474 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 275
ID ACD6857 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 276
ID ABX64291 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ACA67187 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 10; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 278
ID ADM82567 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 11; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 279
ID ADN15966 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 11; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 280
ID ADN16595 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 11; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 281
ID ADN15414 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 11; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 282
ID ADN14862 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2458; DB 11; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 283
ID ADI65037 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 11; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ADC48832 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ADC81124 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ADE21003 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ADE05847 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ADD76572 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ADD75076 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ADD75822 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ADD85054 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;

Best Local Similarity 100.0%; Pred. No. 0;
ID ADD8680 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ADE20757 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ADE39054 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003093632-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ADD87936 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ADD86340 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ADE05601 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ADD73586 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ADE75788 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ADE48392 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 301
ID ADD78426 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ADE41313 standard; cDNA; 2458 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #32.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADE23364 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ADE21249 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ADD77364 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ADE20511 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ADD75576 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ADD74092 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ADD74338 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ADD74338 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311

ID ADD76068 standard; cDNA; 2458 BP.
 DE Novel human secreted and transmembrane protein PRO363 cDNA.
 PN US2003100718-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 311
 ID ADD85560 standard; cDNA; 2458 BP.
 DE Novel human secreted and transmembrane protein PRO363 cDNA.
 PN US2003100721-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 312
 ID ADE23916 standard; cDNA; 2458 BP.
 DE cDNA encoding human PRO polypeptide #194.
 PN US2003092110-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 313
 ID ADE24559 standard; cDNA; 2458 BP.
 DE cDNA encoding human PRO polypeptide #194.
 PN US2003092111-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 314
 ID ADD87384 standard; cDNA; 2458 BP.
 DE Human PRO polynucleotide #194.
 PN US2003203439-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 315
 ID ADE05109 standard; cDNA; 2458 BP.
 DE Human PRO polynucleotide #65.
 PN US2003100726-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 316
 ID ADD75322 standard; cDNA; 2458 BP.
 DE Human PRO polynucleotide #65.
 PN US2003100714-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 317
 ID ADD76866 standard; cDNA; 2458 BP.
 DE Novel human secreted and transmembrane protein PRO363 cDNA.
 PN US2003100715-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 318
 ID ADD86634 standard; cDNA; 2458 BP.
 DE Novel human secreted and transmembrane protein PRO363 cDNA.
 PN US2003100719-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 319
 ID ADE89250 standard; cDNA; 2458 BP.

DE Human PRO polynucleotide #194.
 PN US2003199062-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 320
 ID ADD78102 standard; cDNA; 2458 BP.
 DE Novel human secreted and transmembrane protein PRO363 cDNA.
 PN US2003100731-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 321
 ID ADE18389 standard; cDNA; 2458 BP.
 DE Human PRO polynucleotide #194.
 PN US2003194794-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 322
 ID ADE88698 standard; cDNA; 2458 BP.
 DE Human PRO polynucleotide #194.
 PN US2003199054-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 323
 ID ADE89493 standard; cDNA; 2458 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO363.
 PN US2003130181-A1.
 PD 10-JUL-2003.
 PA (ASHK/) ASHKENAZI A J.
 PA (BAKE/) BAKER K P.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (PERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GIRM/) GIRMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (KUOS/) KUO S S.
 PA (NAPI/) NAPIER M A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (SHEL/) SHELTON D L.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 324
 ID ADD77610 standard; cDNA; 2458 BP.
 DE Novel human secreted and transmembrane protein PRO363 cDNA.
 PN US2003100729-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 2458; DB 12; Length 2458;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 325

ID ADD77856 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 326
ID ADD95314 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 327
ID ADD73846 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 328
ID ADD74584 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 329
ID ADD77112 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 330
ID ADD85806 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 331
ID ADE05355 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 332
ID ADD74830 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 333
ID ADF61133 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 334
ID ADF39825 standard; cDNA; 2458 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 335
ID ADF45621 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 336
ID ADE94718 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 337
ID ADE91129 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 338
ID ADF35628 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ADE95270 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ADE93380 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ADF24017 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ADF40449 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ADF23393 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003203402-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ADF33376 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ADF34961 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ADF26843 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ADF27479 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ADE92276 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ADE90577 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ADF41073 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ADF32752 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ADF25118 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003211092-A1.
PD 13-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ADF26219 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ADF34008 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ADF46245 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ADE91724 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID ADG11878 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO363 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ADG05642 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ADG27196 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ADG02303 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ADG22089 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 362
ID ADG20159 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 363
ID ADF98065 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 364
ID ADG24282 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 365
ID ADF98636 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 366
ID ADG03467 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 367
ID ADF99188 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 368
ID ADG16773 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 369
ID ADG05332 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 370
ID ADG19499 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ADG11259 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 372
ID ADG13336 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 373
ID ADG08393 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 374
ID ADG15563 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 375
ID ADG12038 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 376
ID ADF96961 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 377
ID ADG06146 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 378
ID ADG23730 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
RESULT 379
ID ADG04019 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;

RESULT 380
ID ADG24920 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
ID ADF94595 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 382
ID ADG07217 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 383
ID ADG07769 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID ADG06691 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ADG55264 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ADG60928 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ADG62032 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ADG82233 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ADG50231 standard; cDNA; 2458 BP.

ID ADG57472 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ADG56920 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ADG5816 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ADG58576 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ADG70942 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ADH39035 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ADG58024 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ADG53608 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID ADG71494 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID ADG50231 standard; cDNA; 2458 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 399
ID ADG81681 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 400
ID ADH19748 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 401
ID ADH30643 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 402
ID ADH12010 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 403
ID ADG49607 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 404
ID ADG51479 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 405
ID ADG52432 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 406
ID ADG54160 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 407
ID ADG48983 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003216305-A1.

PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 408
ID ADG81129 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 409
ID ADG56368 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 410
ID ADH12634 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 411
ID ADG48359 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 412
ID ADH21241 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 413
ID ADG61480 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 414
ID ADH20281 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO363.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 415
ID ADH28567 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2458; DB 12; Length 2458;
Pred. No. 0;
RESULT 416
ID ADG54712 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Wed May 11 07:24:22 2005

Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 417
ID ADG59752 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 418
ID ADG50855 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 419
ID ADH43496 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #32.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 420
ID ADG58799 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 421
ID ADG34125 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 422
ID ADG62255 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 423
ID ADI18176 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 424
ID ADI33595 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 425
ID ADH69689 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 426
ID ADH25280 standard; cDNA; 2458 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:58.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 427
ID ADG09919 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 428
ID ADI15390 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 429
ID ADG09267 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 430
ID ADI14722 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 431
ID ADI29850 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 432
ID ADI18317 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 433
ID ADM7247 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 434
ID ADJ63598 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 435
ID ADJ77493 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #194.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 436
ID ADK82841 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #32.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 437
ID ADK66605 standard; cDNA; 2458 BP.
DE Human PRO polynucleotide #65.
PN US2004041180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 438
ID ADJ65615 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 439
ID ADM27751 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 440
ID ADM17057 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ADL06891 standard; cDNA; 2458 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO363.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ADM42475 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID ADM28337 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 12; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ADI95819 standard; cDNA; 2458 BP.
DE cDNA encoding human PRO polypeptide #194.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 13; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ADI96371 standard; cDNA; 2458 BP.
DE Novel human secreted and transmembrane protein PRO363 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2458; DB 13; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ADQ24720 standard; DNA; 3120 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7540.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 99.7%; Score 2450; DB 12; Length 3120;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 447
ID ADO36719 standard; DNA; 5120 BP.
DE Human UKW DNA sequence, SEQ ID NO:1.
PN EP1416279-A1.
PD 06-MAY-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 99.6%; Score 2448.4; DB 12; Length 5120;
Best Local Similarity 99.8%; Pred. No. 0;
RESULT 448
ID ABK33600 standard; cDNA; 2457 BP.
DE cDNA encoding human PRO protein, Seq ID No 129.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 99.5%; Score 2446; DB 6; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ABS70504 standard; cDNA; 2184 BP.
DE Human bone remodelling gene #161.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 80.8%; Score 1986.4; DB 6; Length 2184;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 450
ID ADN05372 standard; cDNA; 2000 BP.
DE Antipsoriatic cDNA sequence #909.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 75.2%; Score 1848; DB 12; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID AAC84383 standard; cDNA; 1948 BP.
DE Human A236 polypeptide encoding cDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 73.4%; Score 1804.8; DB 4; Length 1948;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 452
ID AAD44196 standard; cDNA; 1948 BP.
DE Human A236 cDNA.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZWAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.

Wed May 11 07:24:22 2005

PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match
Best Local Similarity 73.4%; Score 1804.8; DB 6; Length 1948;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 453
ID AAC84415 standard; cDNA; 1948 BP.
DE Human A236 variant 3 CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 73.4%; Score 1803.2; DB 4; Length 1948;
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 454
ID AAC84413 standard; cDNA; 1948 BP.
DE Human A236 variant 1 CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 73.4%; Score 1803.2; DB 4; Length 1948;
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 455
ID AAC84414 standard; cDNA; 1948 BP.
DE Human A236 variant 2 CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 73.4%; Score 1803.2; DB 4; Length 1948;
Best Local Similarity 99.6%; Pred. No. 0;
RESULT 456
ID AAL36788 standard; DNA; 5183 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3153.
PN WO200153367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 58.6%; Score 1441; DB 4; Length 5183;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 457
ID ABX59776 standard; cDNA; 5183 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2120.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 58.6%; Score 1441; DB 8; Length 5183;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 458
ID ADJ30526 standard; DNA; 5183 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3153.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 58.6%; Score 1441; DB 12; Length 5183;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 459
ID ADQ23301 standard; DNA; 1942 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6121.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 57.9%; Score 1422.4; DB 12; Length 1942;
Best Local Similarity 99.5%; Pred. No. 0;
RESULT 460
ID AAC84384 standard; cDNA; 1122 BP.
DE Human A236 polypeptide coding sequence.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 45.6%; Score 1122; DB 4; Length 1122;
Best Local Similarity 100.0%; Pred. No. 8e-298;
Query Match

RESULT 461
ID AAC84391 standard; cDNA; 1949 BP.
DE Mouse A236 polypeptide encoding CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 42.5%; Score 1045; DB 4; Length 1949;
Best Local Similarity 79.3%; Pred. No. 1.7e-276;
RESULT 462
ID AAD44197 standard; cDNA; 1949 BP.
DE Mouse A236 CDNA.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match
Best Local Similarity 42.5%; Score 1045; DB 6; Length 1949;
Best Local Similarity 79.3%; Pred. No. 1.7e-276;
RESULT 463
ID AAC84418 standard; cDNA; 1949 BP.
DE Mouse A236 variant 3 CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 42.4%; Score 1043.4; DB 4; Length 1949;
Best Local Similarity 79.2%; Pred. No. 4.7e-276;
RESULT 464
ID AAC84417 standard; cDNA; 1949 BP.
DE Mouse A236 variant 2 CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 42.4%; Score 1043.4; DB 4; Length 1949;
Best Local Similarity 79.2%; Pred. No. 4.7e-276;
RESULT 465
ID AAC84416 standard; cDNA; 1949 BP.
DE Mouse A236 variant 1 CDNA.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 42.4%; Score 1043.4; DB 4; Length 1949;
Best Local Similarity 79.2%; Pred. No. 4.7e-276;
RESULT 466
ID AAH76376 standard; DNA; 1927 BP.
DE Murine adipocytes-derived protein encoding DNA.
PN WO200166720-A1.
PD 13-SEP-2001.
PA (KITA/) KITAMURA T.
PA (TSUR/) TSURUGA H.
Query Match
Best Local Similarity 42.0%; Score 1031.2; DB 4; Length 1927;
Best Local Similarity 79.1%; Pred. No. 1.1e-272;
RESULT 467
ID AAC84392 standard; cDNA; 1122 BP.
DE Mouse A236 polypeptide coding sequence.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 35.9%; Score 881.8; DB 4; Length 1122;
Best Local Similarity 87.5%; Pred. No. 1.1e-231;
RESULT 468
ID ADL62334 standard; DNA; 1233 BP.
DE Human ovarian cancer DNA marker #20546.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 23.4%; Score 575.2; DB 5; Length 1233;
Query Match

Best Local Similarity 98.4%; Pred. No. 2.8e-147;
RESULT 469
ID AC005560 standard; cDNA; 426 BP.
DE CDNA encoding novel human polypeptide #70.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 17.3%; Score 426; DB 8; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-106;
RESULT 470
ID AC005879 standard; cDNA; 425 BP.
DE Novel human contig #53.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 16.7%; Score 411.4; DB 8; Length 425;
Best Local Similarity 99.5%; Pred. No. 1.9e-102;
RESULT 471
ID ADQ20749 standard; DNA; 392 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3569.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 15.5%; Score 380; DB 12; Length 392;
Best Local Similarity 98.7%; Pred. No. 8e-94;
RESULT 472
ID ACN90389 standard; DNA; 1496 BP.
DE Breast cancer related marker, seq id 11539.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 14.3%; Score 352.6; DB 11; Length 1496;
Best Local Similarity 98.9%; Pred. No. 5.9e-86;
RESULT 473
ID ADL41533 standard; DNA; 405 BP.
DE Human ovarian cancer DNA marker #15423.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 13.8%; Score 339.4; DB 5; Length 405;
Best Local Similarity 95.6%; Pred. No. 1.2e-82;
RESULT 474
ID ADQ18931 standard; DNA; 332 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1750.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.5%; Score 308; DB 12; Length 332;
Best Local Similarity 99.1%; Pred. No. 4.8e-74;
RESULT 475
ID ADI76297 standard; DNA; 295 BP.
DE Human ovarian cancer DNA marker #9039.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 9.0%; Score 221.6; DB 5; Length 295;
Best Local Similarity 91.4%; Pred. No. 2.7e-50;
RESULT 476
ID ADI69964 standard; DNA; 295 BP.
DE Human ovarian cancer DNA marker #2706.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 9.0%; Score 221.6; DB 5; Length 295;
Best Local Similarity 91.4%; Pred. No. 2.7e-50;
RESULT 477
ID AAS72919 standard; cDNA; 1602 BP.
DE DNA encoding novel human diagnostic protein #8723.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 203.2; DB 5; Length 1602;
Best Local Similarity 98.2%; Pred. No. 8.1e-45;

RESULT 478
ID ACN43906 standard; DNA; 43454 BP.
DE Human genomic sequence hCG15249.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 3.2%; Score 79.4; DB 11; Length 43454;
Best Local Similarity 72.4%; Pred. No. 6.1e-10;
RESULT 479
ID AAS36066 standard; DNA; 319 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1566.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 72.2; DB 4; Length 319;
Best Local Similarity 78.9%; Pred. No. 3.8e-09;
RESULT 480
ID ADE46760 standard; DNA; 319 BP.
DE Human cardiovascular system related genomic DNA #326.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 72.2; DB 10; Length 319;
Best Local Similarity 78.9%; Pred. No. 3.8e-09;
RESULT 481
ID ADJ08178 standard; DNA; 319 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1566.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 72.2; DB 13; Length 319;
Best Local Similarity 78.9%; Pred. No. 3.8e-09;
RESULT 482
ID ADP75185 standard; DNA; 22693 BP.
DE Human NR2 gene fragment #1.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.9%; Score 72; DB 11; Length 22693;
Best Local Similarity 93.8%; Pred. No. 4.6e-08;
RESULT 483
ID ABA17250 standard; DNA; 839 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9581.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 71.6; DB 5; Length 839;
Best Local Similarity 70.9%; Pred. No. 9.5e-09;
RESULT 484
ID ABZ35015 standard; cDNA; 136328 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 127.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 2.9%; Score 71.6; DB 6; Length 136328;
Best Local Similarity 70.9%; Pred. No. 1.6e-07;
RESULT 485
ID ABN15760 standard; DNA; 1000 BP.
DE Human GDMPLP-1 putative promoter sequence SEQ ID NO:15752.
PN WO200192524-A2.
PD 06-DEC-2001.
PA (AEOM-) AEOMICA INC.
Query Match 2.9%; Score 70.6; DB 6; Length 1000;
Best Local Similarity 74.5%; Pred. No. 2e-08;
RESULT 486
ID AAL46723 standard; DNA; 1000 BP.
DE Human myosin-like gene hGDMPLP-1 transcriptional control region.
PN EP1158049-A1.
PD 28-NOV-2001.
PA (AEOM-) AEOMICA INC.
Query Match 2.9%; Score 70.6; DB 6; Length 1000;
Best Local Similarity 74.5%; Pred. No. 2e-08;
RESULT 487

PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM. 2.9%; Score 70.4; DB 6; Length 149480;
Query Match
Best Local Similarity 92.5%; Pred. No. 3.6e-07;
RESULT 496
ID ABL6365 standard; DNA; 149480 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6702.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM. 2.9%; Score 70.4; DB 6; Length 149480;
Query Match
Best Local Similarity 92.5%; Pred. No. 3.6e-07;
RESULT 497
ID ABL61948 standard; DNA; 149480 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:285.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM. 2.9%; Score 70.4; DB 6; Length 149480;
Query Match
Best Local Similarity 92.5%; Pred. No. 3.6e-07;
RESULT 498
ID AA536067 standard; DNA; 299 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1567.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.9%; Score 70.2; DB 4; Length 299;
Query Match
Best Local Similarity 78.5%; Pred. No. 1.3e-08;
RESULT 499
ID AD846761 standard; DNA; 299 BP.
DE Human cardiovascular system related genomic DNA #327.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC. 2.9%; Score 70.2; DB 10; Length 299;
Query Match
Best Local Similarity 78.5%; Pred. No. 1.3e-08;
RESULT 500
ID ADJ08179 standard; DNA; 299 BP.
DE Human cardiovascular system associated polypeptide-related DNA
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC. 2.9%; Score 70.2; DB 13; Length 299;
Query Match
Best Local Similarity 78.5%; Pred. No. 1.3e-08;
RESULT 501
ID ADB82573 standard; cDNA; 659 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP. 2.8%; Score 70; DB 9; Length 659;
PA (HYSE-) HYSEQ INC. 84.0%; Pred. No. 2.3e-08;
Query Match
Best Local Similarity 84.0%; Pred. No. 2.4e-08;
RESULT 502
ID ABQ89631 standard; cDNA; 730 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 887.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP. 2.8%; Score 70; DB 6; Length 730;
PA (HYSE-) HYSEQ INC. 84.0%; Pred. No. 2.4e-08;
Query Match
Best Local Similarity 84.0%; Pred. No. 2.4e-08;
RESULT 503
ID ABL66477 standard; DNA; 34641 BP.
DE Lung cancer related gene sequence SEQ ID NO:4814.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM. 2.8%; Score 70; DB 6; Length 34641;
Query Match
Best Local Similarity 71.1%; Pred. No. 2.1e-07;
RESULT 504
ID ABL65800 standard; DNA; 34641 BP.
DE Lung cancer related gene sequence SEQ ID NO:4137.

PN' WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 2.8%; Score 70; DB 6; Length 34641;
 Best Local Similarity 71.1%; Pred. No. 2.1e-07;
 RESULT 505
 ID ACN44350 standard; DNA; 276276 BP.
 DE Human genomic sequence hCG17121.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 2.8%; Score 69.8; DB 11; Length 276276;
 Best Local Similarity 91.4%; Pred. No. 7.4e-07;
 RESULT 506
 ID ADOM1322 standard; cDNA; 933 BP.
 DE Human cDNA probe useful for disease diagnosis #473.
 PN WO2004046382-A2.
 PD 03-JUN-2004.
 PA (DIAG-) DIAGENIC AS.
 PA (JONE/) JONES E L.
 Query Match 2.8%; Score 69.4; DB 12; Length 933;
 Best Local Similarity 92.4%; Pred. No. 4.1e-08;
 RESULT 507
 ID ADJ12490 standard; DNA; 45698 BP.
 DE DNA fragment of a BAC clone that encodes a human secreted protein Seq344.
 PN US2004010132-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (DUAN/) DUAN R D.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (GREE/) GREENE J M.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (FLOR/) FLORENCE C.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match 2.8%; Score 69.4; DB 12; Length 45698;
 Best Local Similarity 92.4%; Pred. No. 3.5e-07;
 RESULT 508
 ID ACN44170 standard; DNA; 196686 BP.
 DE Human genomic sequence hCG39530.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 2.8%; Score 69.4; DB 11; Length 196686;
 Best Local Similarity 92.4%; Pred. No. 7.9e-07;
 RESULT 509
 ID ACN44002 standard; DNA; 228139 BP.
 DE Human genomic sequence hCG37533.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 2.8%; Score 69.4; DB 11; Length 228139;
 Best Local Similarity 83.2%; Pred. No. 8.6e-07;
 RESULT 510
 ID ADS99918 standard; cDNA; 4666 BP.
 DE Human integrin, alpha X (ITGAX), cDNA.
 PN US2003148327-A1.
 PD 07-AUG-2003.
 PA (OLEK/) OLEK A.
 PA (PIEP/) PIEPENBROCK C.
 PA (BERL/) BERLIN K.
 Query Match 2.8%; Score 69; DB 7; Length 4666;
 Best Local Similarity 83.9%; Pred. No. 1.3e-07;
 RESULT 511
 ID ADP44060 standard; cDNA; 4666 BP.
 DE Human CD11C encoding cDNA SEQ ID NO:13.
 PN WO2004053094-A2.
 PD 24-JUN-2004.
 PA (PPDP-) PPD DEV LP.

Query Match 2.8%; Score 69; DB 12; Length 4666;
 Best Local Similarity 83.9%; Pred. No. 1.3e-07;
 RESULT 512
 ID AAK65953 standard; DNA; 158 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20765.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 4; Length 158;
 Best Local Similarity 91.2%; Pred. No. 2.2e-08;
 RESULT 513
 ID AAK65950 standard; DNA; 158 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20762.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 4; Length 158;
 Best Local Similarity 91.2%; Pred. No. 2.2e-08;
 RESULT 514
 ID ABZ74262 standard; DNA; 232 BP.
 DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1409.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 8; Length 232;
 Best Local Similarity 91.2%; Pred. No. 2.8e-08;
 RESULT 515
 ID ADA98791 standard; DNA; 232 BP.
 DE Human secreted protein-related DNA sequence #384.
 PN WO2003004623-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 8; Length 232;
 Best Local Similarity 91.2%; Pred. No. 2.8e-08;
 RESULT 516
 ID ABZ67828 standard; DNA; 232 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1351.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 10; Length 232;
 Best Local Similarity 91.2%; Pred. No. 2.8e-08;
 RESULT 517
 ID ABK42318 standard; DNA; 251 BP.
 DE Genomic sequence #217 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 4; Length 251;
 Best Local Similarity 91.2%; Pred. No. 2.9e-08;
 RESULT 518
 ID ADB60474 standard; DNA; 251 BP.
 DE Connective tissue related genomic DNA #217.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.8%; Score 68.8; DB 9; Length 251;
 Best Local Similarity 91.2%; Pred. No. 2.9e-08;
 RESULT 519
 ID ABQ5630 standard; cDNA; 316 BP.
 DE Human colon cancer related nucleotide sequence SEQ ID NO:325.
 PN WO200229086-A2.
 PD 11-APR-2002.
 PA (FARB-) BAYER CORP.
 Query Match 2.8%; Score 68.8; DB 6; Length 316;
 Best Local Similarity 91.2%; Pred. No. 3.3e-08;
 RESULT 520
 ID ABV97474 standard; cDNA; 325 BP.
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 2882.
 PN WO200260317-A2.
 PD 08-AUG-2002.
 PA (CORI-) CORIAX CORP.
 Query Match 2.8%; Score 68.8; DB 6; Length 325;

Best Local Similarity 91.2%; Pred. No. 3.3e-08;
RESULT 521
ID ADO34635 standard; DNA; 1001 BP.
DE Human SLIT-3 gene microsatellite polymorphic region #200.
PN WO2004042358-A2.
PD 21-MAY-2004.
PA (DSCO-) DECODE GENETICS EHF.
Query Match 2.8%; Score 68.8; DB 12; Length 1001;
Best Local Similarity 91.2%; Pred. No. 6.2e-08;
RESULT 522
ID ADC78806 standard; DNA; 1406 BP.
DE Human PRO protein coding sequence #18.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GTH) GENENTECH INC.
Query Match 2.8%; Score 68.8; DB 10; Length 1406;
Best Local Similarity 91.2%; Pred. No. 7.5e-08;
RESULT 523
ID ADC78892 standard; DNA; 1406 BP.
DE Human PRO protein coding sequence #61.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GTH) GENENTECH INC.
Query Match 2.8%; Score 68.8; DB 10; Length 1406;
Best Local Similarity 91.2%; Pred. No. 7.5e-08;
RESULT 524
ID ADS63519 standard; cDNA; 2091 BP.
DE Human cDNA encoding clone TESTI20254090.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.8%; Score 68.8; DB 10; Length 2091;
Best Local Similarity 91.2%; Pred. No. 9.3e-08;
RESULT 525
ID ADS32753 standard; DNA; 2723 BP.
DE Human FR-alpha promoter-luciferase gene fragment SEQ ID NO:6.
PN WO2004082463-A2.
PD 30-SEP-2004.
PA (MEDI-) MEDICAL COLLEGE OHIO.
Query Match 2.8%; Score 68.8; DB 13; Length 2723;
Best Local Similarity 91.2%; Pred. No. 1.1e-07;
RESULT 526
ID ADS32763 standard; DNA; 2723 BP.
DE Human FR-alpha P1 and P4 promoter gene fragment SEQ ID NO:16.
PN WO2004082463-A2.
PD 30-SEP-2004.
PA (MEDI-) MEDICAL COLLEGE OHIO.
Query Match 2.8%; Score 68.8; DB 13; Length 2723;
Best Local Similarity 91.2%; Pred. No. 1.1e-07;
RESULT 527
ID ADP48653 standard; cDNA; 2820 BP.
DE Human PF7518 cDNA #SEQ ID 10.
PN CN1369505-A.
PD 18-SEP-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.8%; Score 68.8; DB 10; Length 2820;
Best Local Similarity 91.2%; Pred. No. 1.1e-07;
RESULT 528
ID AAK75099 standard; DNA; 3806 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29911.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 3806;
Best Local Similarity 91.2%; Pred. No. 1.3e-07;
RESULT 529
ID AAK76629 standard; DNA; 5331 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31441.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 5331;

Best Local Similarity 91.2%; Pred. No. 1.6e-07;
RESULT 530
ID ADP87499 standard; DNA; 5638 BP.
DE Human brain-derived gene SEQ ID NO:2.
PN JF2004173637-A.
PD 24-JUN-2004.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 2.8%; Score 68.8; DB 12; Length 5638;
Best Local Similarity 91.2%; Pred. No. 1.6e-07;
RESULT 531
ID ABK4132 standard; DNA; 6902 BP.
DE Genomic sequence #31 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 6902;
Best Local Similarity 91.2%; Pred. No. 1.8e-07;
RESULT 532
ID ADB60288 standard; DNA; 6902 BP.
DE Connective tissue related genomic DNA #31.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 9; Length 6902;
Best Local Similarity 91.2%; Pred. No. 1.8e-07;
RESULT 533
ID AAC91210 standard; DNA; 7720 BP.
DE Human folate receptor I gene SEQ ID NO: 5.
PN WO200071754-A1.
PD 30-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 2.8%; Score 68.8; DB 5; Length 7720;
Best Local Similarity 91.2%; Pred. No. 1.9e-07;
RESULT 534
ID ABL68258 standard; DNA; 7720 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6595.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.8%; Score 68.8; DB 6; Length 7720;
Best Local Similarity 91.2%; Pred. No. 1.9e-07;
RESULT 535
ID ABL66279 standard; DNA; 7720 BP.
DE Lung cancer related gene sequence SEQ ID NO:4616.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.8%; Score 68.8; DB 6; Length 7720;
Best Local Similarity 91.2%; Pred. No. 1.9e-07;
RESULT 536
ID ABL68540 standard; DNA; 7720 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6877.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.8%; Score 68.8; DB 6; Length 7720;
Best Local Similarity 91.2%; Pred. No. 1.9e-07;
RESULT 537
ID ABL68876 standard; DNA; 7720 BP.
DE Kidney cancer related gene sequence SEQ ID NO:7213.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.8%; Score 68.8; DB 6; Length 7720;
Best Local Similarity 91.2%; Pred. No. 1.9e-07;
RESULT 538
ID ABL65636 standard; DNA; 7720 BP.
DE Lung cancer related gene sequence SEQ ID NO:3973.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.8%; Score 68.8; DB 6; Length 7720;
Best Local Similarity 91.2%; Pred. No. 1.9e-07;

RESULT 539
ID AAS36827 standard; DNA; 7960 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2327.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 7960;
Best Local Similarity 97.2%; Pred. No. 2e-07;
RESULT 540
ID ADE47521 standard; DNA; 7960 BP.
DE Human cardiovascular system related genomic DNA #1087.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 10; Length 7960;
Best Local Similarity 97.2%; Pred. No. 2e-07;
RESULT 541
ID ABZ67712 standard; DNA; 7960 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1235.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 10; Length 7960;
Best Local Similarity 97.2%; Pred. No. 2e-07;
RESULT 542
ID ADJ08939 standard; DNA; 7960 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2327.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 13; Length 7960;
Best Local Similarity 97.2%; Pred. No. 2e-07;
RESULT 543
ID AAL02697 standard; DNA; 9339 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5385.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 9339;
Best Local Similarity 91.2%; Pred. No. 2.1e-07;
RESULT 544
ID ABL55889 standard; DNA; 10012 BP.
DE Human small inducible cytokine subfamily A (Cys-Cys), member 24 gene.
PN WO200220851-A1.
PD 14-MAR-2002.
PA (GENA-) GENA/SSANCE PHARM INC.
Query Match 2.8%; Score 68.8; DB 6; Length 10012;
Best Local Similarity 91.2%; Pred. No. 2.2e-07;
RESULT 545
ID AAK89955 standard; DNA; 12724 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2531.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 12724;
Best Local Similarity 91.2%; Pred. No. 2.5e-07;
RESULT 546
ID AAK81662 standard; DNA; 13578 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36474.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 13578;
Best Local Similarity 91.2%; Pred. No. 2.6e-07;
RESULT 547
ID AAK87099 standard; DNA; 16817 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41911.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 16817;
Best Local Similarity 91.2%; Pred. No. 3e-07;
RESULT 548

ID AAS36826 standard; DNA; 17239 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2326.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 17239;
Best Local Similarity 97.2%; Pred. No. 3e-07;
RESULT 549
ID ADE47520 standard; DNA; 17239 BP.
DE Human cardiovascular system related genomic DNA #1086.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 10; Length 17239;
Best Local Similarity 97.2%; Pred. No. 3e-07;
RESULT 550
ID ABZ67711 standard; DNA; 17239 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1234.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 10; Length 17239;
Best Local Similarity 97.2%; Pred. No. 3e-07;
RESULT 551
ID ADJ08938 standard; DNA; 17239 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2326.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 13; Length 17239;
Best Local Similarity 97.2%; Pred. No. 3e-07;
RESULT 552
ID AAL04753 standard; DNA; 18408 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7441.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 18408;
Best Local Similarity 74.6%; Pred. No. 3.1e-07;
RESULT 553
ID AAL04754 standard; DNA; 18408 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7442.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 18408;
Best Local Similarity 74.6%; Pred. No. 3.1e-07;
RESULT 554
ID ABL97656 standard; DNA; 18408 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2308.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 18408;
Best Local Similarity 74.6%; Pred. No. 3.1e-07;
RESULT 555
ID ABL97657 standard; DNA; 18408 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2309.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 18408;
Best Local Similarity 74.6%; Pred. No. 3.1e-07;
RESULT 556
ID AAK65368 standard; DNA; 18564 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20180.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 18564;
Best Local Similarity 73.9%; Pred. No. 3.1e-07;
RESULT 557
ID ABZ74461 standard; DNA; 18564 BP.

DE Secreted protein gene 300 genomic fragment HSQD085, SEQ ID NO:1608.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 8; Length 18564;
Best Local Similarity 73.9%; Pred. No. 3.1e-07;
RESULT 558
ID ADA98881 standard; DNA; 18564 BP.
DE Human secreted protein-related DNA sequence #474.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 8; Length 18564;
Best Local Similarity 73.9%; Pred. No. 3.1e-07;
RESULT 559
ID ABK42133 standard; DNA; 22161 BP.
DE Genomic sequence #32 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 22161;
Best Local Similarity 91.2%; Pred. No. 3.5e-07;
RESULT 560
ID ADB60289 standard; DNA; 22161 BP.
DE Connective tissue related genomic DNA #32.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 9; Length 22161;
Best Local Similarity 91.2%; Pred. No. 3.5e-07;
RESULT 561
ID AAK81665 standard; DNA; 24908 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36477.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 24908;
Best Local Similarity 91.2%; Pred. No. 3.7e-07;
RESULT 562
ID ACM44246 standard; DNA; 26047 BP.
DE Human genomic sequence HCG20994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 68.8; DB 11; Length 26047;
Best Local Similarity 91.2%; Pred. No. 3.8e-07;
RESULT 563
ID AAL06991 standard; DNA; 32082 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9679.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 32082;
Best Local Similarity 91.2%; Pred. No. 4.2e-07;
RESULT 564
ID ADR67012 standard; DNA; 32229 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:58.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 68.8; DB 13; Length 32229;
Best Local Similarity 91.2%; Pred. No. 4.3e-07;
RESULT 565
ID AAL51501 standard; DNA; 35057 BP.
DE Human pantothenate Kinase 2 (PANK2) genomic DNA sequence.
PN WO2003008626-A2.
PD 30-JAN-2003.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.8%; Score 68.8; DB 8; Length 35057;
Best Local Similarity 91.2%; Pred. No. 4.5e-07;
RESULT 566
ID AAK70780 standard; DNA; 37783 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25592.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 37783;
Best Local Similarity 91.2%; Pred. No. 4.7e-07;
RESULT 567
ID AAK76625 standard; DNA; 37783 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31437.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 37783;
Best Local Similarity 91.2%; Pred. No. 4.7e-07;
RESULT 568
ID AAK80913 standard; DNA; 37783 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35725.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 37783;
Best Local Similarity 91.2%; Pred. No. 4.7e-07;
RESULT 569
ID AAK82628 standard; DNA; 48203 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37440.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 48203;
Best Local Similarity 91.2%; Pred. No. 5.3e-07;
RESULT 570
ID AAK81663 standard; DNA; 48203 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36475.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 48203;
Best Local Similarity 91.2%; Pred. No. 5.3e-07;
RESULT 571
ID AAK70161 standard; DNA; 48203 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24973.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 48203;
Best Local Similarity 91.2%; Pred. No. 5.3e-07;
RESULT 572
ID AAK81666 standard; DNA; 48204 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36478.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 48204;
Best Local Similarity 91.2%; Pred. No. 5.3e-07;
RESULT 573
ID AAK82630 standard; DNA; 48204 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37442.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 48204;
Best Local Similarity 91.2%; Pred. No. 5.3e-07;
RESULT 574
ID AAK70164 standard; DNA; 48204 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24976.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68.8; DB 4; Length 48204;
Best Local Similarity 91.2%; Pred. No. 5.3e-07;
RESULT 575
ID ABN89533 standard; DNA; 48436 BP.
DE Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.

RESULT 585
ID ADB87941 standard; DNA; 68355 BP.
DE Human UTR1al gene sequence SEQ ID NO:665.
FN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 68355;
Best Local Similarity 91.2%; Pred. No. 6.5e-07;
RESULT 586
ID ADB96924 standard; DNA; 68355 BP.
DE Human MDRI related DNA sequence SEQ ID NO:665.
FN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 68355;
Best Local Similarity 91.2%; Pred. No. 6.5e-07;
RESULT 587
ID ADB92115 standard; DNA; 68355 BP.
DE Human MDRI related DNA sequence SEQ ID NO:665.
FN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 68355;
Best Local Similarity 91.2%; Pred. No. 6.5e-07;
RESULT 588
ID ADP68568 standard; cDNA; 86000 BP.
DE Human PPAR-alpha cDNA.
FN US2004115637-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.8%; Score 68.8; DB 12; Length 86000;
Best Local Similarity 91.2%; Pred. No. 7.3e-07;
RESULT 589
ID ADA03026 standard; DNA; 96588 BP.
DE Human MBL carcinoma associated gene, SEQ ID NO:1544.
FN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 68.8; DB 9; Length 96588;
Best Local Similarity 91.2%; Pred. No. 7.8e-07;
RESULT 590
ID ADB72764 standard; DNA; 96588 BP.
DE Human MBL gene.
FN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 68.8; DB 10; Length 96588;
Best Local Similarity 91.2%; Pred. No. 7.8e-07;
RESULT 591
ID ADC85506 standard; DNA; 96588 BP.
DE Human MBL genomic sequence.
FN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 68.8; DB 10; Length 96588;
Best Local Similarity 91.2%; Pred. No. 7.8e-07;
RESULT 592
ID ADM74621 standard; DNA; 96588 BP.
DE Human carcinoma associated (CA) nucleic acid #145.
FN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.8%; Score 68.8; DB 12; Length 96588;
Best Local Similarity 91.2%; Pred. No. 7.8e-07;
RESULT 593
ID ABD33432 standard; DNA; 106938 BP.
DE Human cancer-associated (CA) gene HD07-081.
FN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 68.8; DB 13; Length 106938;
Best Local Similarity 91.2%; Pred. No. 8.3e-07;

RESULT 594
ID ADR67034 standard; DNA; 106938 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:80.
FN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 68.8; DB 13; Length 106938;
Best Local Similarity 91.2%; Pred. No. 8.3e-07;
RESULT 595
ID ADG70184 standard; DNA; 379652 BP.
DE DNA of BAC BAZ36mi5-00303.
FN WO2003000727-A2.
PD 03-JAN-2003.
PA (IGIS-) ISIS INNOVATIONS LTD.
Query Match 2.8%; Score 68.8; DB 10; Length 110000;
Best Local Similarity 91.2%; Pred. No. 8.4e-07;
RESULT 596
ID ACF2745 standard; DNA; 354391 BP.
DE Human ALMS1 genomic DNA sequence.
FN WO2003034072-A2.
PD 24-APR-2003.
PA (UYSO-) UNIV SOUTHAMPTON.
Query Match 2.8%; Score 68.8; DB 10; Length 110000;
Best Local Similarity 91.2%; Pred. No. 8.4e-07;
RESULT 597
ID ADA42607 standard; DNA; 113604 BP.
DE Human IQTS genomic DNA #2.
FN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 2.8%; Score 68.8; DB 9; Length 113604;
Best Local Similarity 91.2%; Pred. No. 8.6e-07;
RESULT 599
ID ADA42606 standard; DNA; 113604 BP.
DE Human IQTS genomic DNA #1.
FN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 2.8%; Score 68.8; DB 9; Length 113604;
Best Local Similarity 91.2%; Pred. No. 8.6e-07;
RESULT 600
ID ADS19853 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:1.
FN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 2.8%; Score 68.8; DB 13; Length 113604;
Best Local Similarity 91.2%; Pred. No. 8.6e-07;
RESULT 601
ID ADS19854 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:2.
FN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 2.8%; Score 68.8; DB 13; Length 113604;
Best Local Similarity 91.2%; Pred. No. 8.6e-07;
RESULT 602
ID ABT17385 standard; DNA; 118951 BP.
DE Human IG gene related nucleic acid SEQ ID No 11.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 2.8%; Score 68.8; DB 8; Length 118951;
Best Local Similarity 91.2%; Pred. No. 8.8e-07;
RESULT 603
ID ADQ59167 standard; DNA; 120670 BP.

DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:4.
FN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 2.8%; Score 68.8; DB 12; Length 120670;
Best Local Similarity 91.2%; Pred. No. 8.9e-07;
RESULT 604
ID AQO80254 standard; cDNA; 127145 BP.
DE Hermansky-Pudlak syndrome associated cDNA.
FN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 2.8%; Score 68.8; DB 13; Length 127145;
Best Local Similarity 73.9%; Pred. No. 9.1e-07;
RESULT 605
ID ABD33104 standard; DNA; 130877 BP.
DE Human cancer-associated (CA) gene HD07-009.
FN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 68.8; DB 13; Length 130877;
Best Local Similarity 91.2%; Pred. No. 9.3e-07;
RESULT 606
ID ABK84795 standard; cDNA; 139389 BP.
DE Human cDNA differentially expressed in granulocytic cells #1366.
FN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.8%; Score 68.8; DB 6; Length 139389;
Best Local Similarity 91.2%; Pred. No. 9.6e-07;
RESULT 607
ID ADB70369 standard; cDNA; 139389 BP.
DE PAC 6802 cDNA SEQ ID NO:61.
FN WO2003021229-A2.
PD 13-MAR-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 2.8%; Score 68.8; DB 9; Length 139389;
Best Local Similarity 91.2%; Pred. No. 9.6e-07;
RESULT 608
ID ADJ37148 standard; cDNA; 139389 BP.
DE Human malignant pleural mesothelioma (MPM) cDNA #27.
FN US2003219760-A1.
PD 27-NOV-2003.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 2.8%; Score 68.8; DB 12; Length 139389;
Best Local Similarity 91.2%; Pred. No. 9.6e-07;
RESULT 609
ID AAD02697 standard; DNA; 160552 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
FN WO200106015-A1.
PD 25-JAN-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.8%; Score 68.8; DB 4; Length 160552;
Best Local Similarity 91.2%; Pred. No. 1e-06;
RESULT 610
ID ADP13586 standard; DNA; 170245 BP.
DE Renal cell carcinoma differentially expressed gene #322.
FN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 2.8%; Score 68.8; DB 12; Length 170245;
Best Local Similarity 91.2%; Pred. No. 1.1e-06;
RESULT 611
ID ACF62750 standard; DNA; 186591 BP.

DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:682.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 8; Length 186591;
Best Local Similarity 91.2%; Pred. No. 1.1e-06;
RESULT 612
ID ADB20869 standard; DNA; 186591 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:682.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 8; Length 186591;
Best Local Similarity 91.2%; Pred. No. 1.1e-06;
RESULT 613
ID ADB87958 standard; DNA; 186591 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:682.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 186591;
Best Local Similarity 91.2%; Pred. No. 1.1e-06;
RESULT 614
ID ADB96941 standard; DNA; 186591 BP.
DE Human MDRI related DNA sequence SEQ ID NO:682.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 186591;
Best Local Similarity 91.2%; Pred. No. 1.1e-06;
RESULT 615
ID ADB92132 standard; DNA; 186591 BP.
DE Human MDRI related DNA sequence SEQ ID NO:682.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 186591;
Best Local Similarity 91.2%; Pred. No. 1.1e-06;
RESULT 616
ID ACF62735 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:663.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 8; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 617
ID ACF62740 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:668.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 8; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 618
ID ADB20850 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:663.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 8; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 619
ID ADB20855 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:668.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 8; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 620
ID ADB87944 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:668.

PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 621
ID ADB87939 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:663.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 622
ID ADB96922 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:663.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 623
ID ADB96927 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:668.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 624
ID ADB92113 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:663.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 625
ID ADB92118 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:668.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.
Query Match 2.8%; Score 68.8; DB 10; Length 208648;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 626
ID ACN44418 standard; DNA; 213040 BP.
DE Human genomic sequence hCG41574.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.8%; Score 68.8; DB 11; Length 213040;
Best Local Similarity 91.2%; Pred. No. 1.2e-06;
RESULT 627
ID ABR83497 standard; cDNA; 227968 BP.
DE Human cDNA differentially expressed in granulocytic cells #68.
PN WO2002028999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.8%; Score 68.8; DB 6; Length 227968;
Best Local Similarity 91.2%; Pred. No. 1.3e-06;
RESULT 628
ID ADQ18538 standard; DNA; 227968 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.8%; Score 68.8; DB 12; Length 227968;
Best Local Similarity 91.2%; Pred. No. 1.3e-06;
RESULT 629
ID ADB33366 standard; DNA; 243390 BP.
DE Human cancer-associated (CA) gene HD07-067.
PN WO2004058146-A2.

Wed May 11 07:24:22 2005

```

PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC. 2.8%; Score 68.8; DB 13; Length 243390;
Query Match
Best Local Similarity 91.2%; Pred. No. 1.3e-06;
RESULT 630
ID AAS43104 standard; DNA; 325791 BP.
DE Human Oestrogen receptor beta gene.
PN WO200162793-A2.
PD 30-AUG-2001.
PA (PSKE-) PE CORP NY. 2.8%; Score 68.8; DB 4; Length 325791;
Query Match
Best Local Similarity 91.2%; Pred. No. 1.5e-06;
RESULT 631
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity 91.2%; Pred. No. 1.6e-06;
RESULT 632
ID ADQ97183 standard; DNA; 138627 BP.
DE Human cancer associated sequence HD08-011, SEQ ID 159.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC. 2.8%; Score 68.6; DB 12; Length 138627;
Query Match
Best Local Similarity 77.6%; Pred. No. 1.1e-06;
RESULT 633
ID ACH27522 standard; cDNA; 461 BP.
DE Human adult ovary cDNA #5902.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 92.3%; Pred. No. 5.2e-08;
RESULT 634
ID AAL61326 standard; DNA; 91000 BP.
DE Human farnesoid x receptor (FXR) DNA #2.
PN WO2003044167-A2.
PD 30-MAY-2003.
PA (ISIS-) ISIS PHARM INC. 2.8%; Score 68.4; DB 9; Length 461;
Query Match
Best Local Similarity 92.3%; Pred. No. 9.8e-07;
RESULT 635
ID AAS38779 standard; cDNA; 345 BP.
DE Novel human diagnostic and therapeutic gene #1837.
PN WO200166753-A2.
PD 13-SEP-2001.
PA (CHIR-) CHIRON CORP. 2.8%; Score 68.2; DB 4; Length 345;
PA (HYSE-) HYSEQ INC. 2.8%; Score 68.4; DB 9; Length 91000;
Query Match
Best Local Similarity 90.1%; Pred. No. 5e-08;
RESULT 636
ID ABV49051 standard; cDNA; 405 BP.
DE Human prostate expression marker cDNA 49042.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 90.1%; Pred. No. 5.5e-08;
RESULT 637
ID ABV19277 standard; cDNA; 415 BP.
DE Human prostate expression marker cDNA 19268.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 90.1%; Pred. No. 5.5e-08;
RESULT 638
ID AAI12635 standard; cDNA; 543 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:9470.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 2.8%; Score 68.2; DB 4; Length 543;
Query Match
Best Local Similarity 71.4%; Pred. No. 6.5e-08;
RESULT 639
ID AAK85658 standard; DNA; 963 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40470.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.8%; Score 68.2; DB 4; Length 963;
Query Match
Best Local Similarity 90.1%; Pred. No. 8.9e-08;
RESULT 640
ID ADM01714 standard; cDNA; 1938 BP.
DE Human cDNA of the invention SEQ ID NO:399.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 90.1%; Pred. No. 1.3e-07;
RESULT 641
ID ADL45944 standard; DNA; 5370 BP.
DE Human ovarian cancer DNA marker #19834.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 90.1%; Pred. No. 2.3e-07;
RESULT 642
ID ADC86456 standard; DNA; 34118 BP.
DE Human GPCR gene SEQ ID NO:909.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity 90.1%; Pred. No. 6.4e-07;
RESULT 643
ID ADI14677 standard; cDNA; 34875 BP.
DE Human src biomarker polynucleotide SEQ ID NO:71.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO. 2.8%; Score 68.2; DB 10; Length 34118;
Query Match
Best Local Similarity 90.1%; Pred. No. 6.5e-07;
RESULT 644
ID ADR52965 standard; DNA; 34875 BP.
DE Drug therapy altered expressed gene #316.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP-) WYETH.
PA (BURC-) BURCZYNSKI M.
PA (TWIN-) TWINE N.
PA (DORN-) DORNER A J.
PA (TREP-) TREPICCHIO W L.
Query Match
Best Local Similarity 90.1%; Pred. No. 6.5e-07;
RESULT 645
ID ACN44154 standard; DNA; 101209 BP.
DE Human genomic sequence hCG28567.
PN WO2003071826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 90.1%; Pred. No. 1.2e-06;
RESULT 646
ID ADH76849 standard; DNA; 122557 BP.
DE Melanin-concentrating hormone receptor 1 locus clone.

```


PN WO2003104489-A2.
PD. 18-DEC-2003.
PA (UYPH-) UNIV PHILIPPS MARBURG.
Query Match 2.8%; Score 68.2; DB 12; Length 122557;
Best Local Similarity 90.1%; Pred. No. 1.3e-06;
RESULT 647
ID ADJ08109 standard; DNA; 247682 BP.
DE Human gene associated with low HDL-C AT3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 2.8%; Score 68.2; DB 12; Length 247682;
Best Local Similarity 90.1%; Pred. No. 1.9e-06;
RESULT 648
ID AHI18046 standard; cDNA; 1812 BP.
DE Human cDNA sequence SEQ ID NO:17874.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.8%; Score 68; DB 4; Length 1812;
Best Local Similarity 74.6%; Pred. No. 1.4e-07;
RESULT 649
ID AAS36911 standard; DNA; 3560 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2411.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68; DB 4; Length 3560;
Best Local Similarity 80.0%; Pred. No. 2.1e-07;
RESULT 650
ID ADE47605 standard; DNA; 3560 BP.
DE Human cardiovascular system related genomic DNA #1171.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68; DB 10; Length 3560;
Best Local Similarity 80.0%; Pred. No. 2.1e-07;
RESULT 651
ID ADJ09023 standard; DNA; 3560 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2411.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68; DB 13; Length 3560;
Best Local Similarity 80.0%; Pred. No. 2.1e-07;
RESULT 652
ID AAS36910 standard; DNA; 3561 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2410.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68; DB 4; Length 3561;
Best Local Similarity 80.0%; Pred. No. 2.1e-07;
RESULT 653
ID ADE47604 standard; DNA; 3561 BP.
DE Human cardiovascular system related genomic DNA #1170.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68; DB 10; Length 3561;
Best Local Similarity 80.0%; Pred. No. 2.1e-07;
RESULT 654
ID ADJ09022 standard; DNA; 3561 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2410.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 68; DB 13; Length 3561;
Best Local Similarity 80.0%; Pred. No. 2.1e-07;
RESULT 655
ID ADN06010 standard; cDNA; 5785 BP.
DE Antiporotatic cDNA sequence #1240.
PN WO2004028479-A2.

PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 2.8%; Score 68; DB 12; Length 5785;
Best Local Similarity 80.0%; Pred. No. 2.7e-07;
RESULT 656
ID ABN83970 standard; DNA; 6799 BP.
DE Human gene sequence #17.
PN WO200252005-A1.
PD 04-JUL-2002.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (CELE-) CELESTAR LEXICO-SCI LTD.
Query Match 2.8%; Score 68; DB 6; Length 6799;
Best Local Similarity 75.0%; Pred. No. 3e-07;
RESULT 657
ID ABQ88139 standard; cDNA; 103747 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 46.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 2.8%; Score 68; DB 6; Length 103747;
Best Local Similarity 71.8%; Pred. No. 1.4e-06;
RESULT 658
ID ABL84391 standard; cDNA; 318 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:7369.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.8%; Score 67.8; DB 6; Length 318;
Best Local Similarity 82.1%; Pred. No. 6.2e-08;
RESULT 659
ID AAI63976 standard; DNA; 4096 BP.
DE Human polynucleotide SEQ ID NO 348.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 67.8; DB 4; Length 4096;
Best Local Similarity 91.1%; Pred. No. 2.6e-07;
RESULT 660
ID ADM24691 standard; cDNA; 4096 BP.
DE Human PRO polynucleotide #174.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 67.8; DB 12; Length 4096;
Best Local Similarity 91.1%; Pred. No. 2.6e-07;
RESULT 661
ID AAS27823 standard; DNA; 16489 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1483.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 67.8; DB 4; Length 16489;
Best Local Similarity 82.1%; Pred. No. 5.5e-07;
RESULT 662
ID ADB94626 standard; DNA; 16489 BP.
DE Novel human protein DNA #235.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.8%; Score 67.8; DB 10; Length 16489;
Best Local Similarity 82.1%; Pred. No. 5.5e-07;
RESULT 663
ID ABL68348 standard; DNA; 25000 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6685.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.8%; Score 67.8; DB 6; Length 25000;
Best Local Similarity 75.7%; Pred. No. 7e-07;
RESULT 664

ID AAK77103 standard; DNA; 26372 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31915.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 67.8; DB 4; Length 26372;
Best Local Similarity 82.1%; Pred. No. 7.2e-07;
RESULT 665
ID ABAL19222 standard; DNA; 27571 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11553.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 67.8; DB 5; Length 27571;
Best Local Similarity 91.1%; Pred. No. 7.4e-07;
RESULT 666
ID ABAL19221 standard; DNA; 27572 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11552.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.8%; Score 67.8; DB 5; Length 27572;
Best Local Similarity 91.1%; Pred. No. 7.4e-07;
RESULT 667
ID ADQ97301 standard; DNA; 127722 BP.
DE Human cancer associated sequence HD08-028, SEQ ID 278.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 67.8; DB 12; Length 127722;
Best Local Similarity 82.1%; Pred. No. 1.7e-06;
RESULT 669
ID AA196289 standard; cDNA; 826 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2364.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM-) HISAMITSU PHARM CO LTD.
Query Match 2.8%; Score 67.6; DB 4; Length 826;
Best Local Similarity 70.0%; Pred. No. 1.2e-07;
RESULT 670
ID AAS03388 standard; DNA; 36741 BP.
DE Human adenosine deaminase (ADA) genomic DNA.
PN US6207876-B1.
PD 27-MAR-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 2.8%; Score 67.6; DB 4; Length 36741;
Best Local Similarity 89.0%; Pred. No. 9.8e-07;
RESULT 671
ID ABQ88153 standard; cDNA; 36741 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 60.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 2.8%; Score 67.6; DB 6; Length 36741;
Best Local Similarity 89.0%; Pred. No. 9.8e-07;
RESULT 672
ID ABS69890 standard; DNA; 36741 BP.
DE Human adenosine deaminase (ADA) gene.
PN US2002102731-A1.
PD 01-AUG-2002.
PA (UNYV) UNIV NEW YORK STATE RES FOUND.
Query Match 2.8%; Score 67.6; DB 6; Length 36741;
Best Local Similarity 89.0%; Pred. No. 9.8e-07;
RESULT 673
ID ABS52806 standard; DNA; 36741 BP.
DE DNA encoding human adenosine deaminase (ADA).
PN US2002088017-A1.
PD 04-JUL-2002.

PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 2.8%; Score 67.6; DB 6; Length 36741;
Best Local Similarity 89.0%; Pred. No. 9.8e-07;
RESULT 674
Query Match 2.8%; Score 67.6; DB 10; Length 110000;
Best Local Similarity 73.5%; Pred. No. 1.8e-06;
RESULT 675
ID ADL13941 standard; DNA; 125515 BP.
DE Osteoarthritis-associated polymorphic nucleotide #473.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.8%; Score 67.6; DB 10; Length 125515;
Best Local Similarity 72.9%; Pred. No. 1.9e-06;
RESULT 676
ID AAK89419 standard; DNA; 185 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2995.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 4; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 677
ID AAK89420 standard; DNA; 185 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2996.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 4; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 678
ID AAS31925 standard; DNA; 185 BP.
DE Human liver associated genomic DNA #99.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 5; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 679
ID AAS31924 standard; DNA; 185 BP.
DE Human liver associated genomic DNA #98.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 5; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 680
ID ASN90279 standard; DNA; 185 BP.
DE Human liver antigen HLDRI94 genomic sequence, SEQ ID NO:400.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.4; DB 6; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 681
ID ASN90280 standard; DNA; 185 BP.
DE Human liver antigen HLDRI94 genomic sequence, SEQ ID NO:401.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.4; DB 6; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 682
ID ADJ15193 standard; DNA; 185 BP.
DE Human liver-related genomic DNA - SEQ ID 401.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 11; Length 185;

Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 683
ID ADJ15192 standard; DNA; 185 BP.
DE Human liver-related genomic DNA - SEQ ID 400.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 11; Length 185;
Best Local Similarity 87.1%; Pred. No. 5.9e-08;
RESULT 684
ID ACD96444 standard; cDNA; 583 BP.
DE Human colon cancer cell expressed cDNA #4856.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 2.7%; Score 67.4; DB 10; Length 583;
Best Local Similarity 87.1%; Pred. No. 1.1e-07;
RESULT 685
ID AAK68070 standard; DNA; 2480 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22882.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.4; DB 4; Length 2480;
Best Local Similarity 87.1%; Pred. No. 2.5e-07;
RESULT 686
ID ADM03547 standard; cDNA; 2884 BP.
DE Human cDNA of the invention SEQ ID NO:2232.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.4; DB 11; Length 2884;
Best Local Similarity 87.1%; Pred. No. 2.7e-07;
RESULT 687
ID AAA34884 standard; DNA; 4654 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2573.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 2.7%; Score 67.4; DB 3; Length 4654;
Best Local Similarity 82.8%; Pred. No. 3.5e-07;
RESULT 688
ID AAF21006 standard; DNA; 4654 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2573.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 2.7%; Score 67.4; DB 3; Length 4654;
Best Local Similarity 82.8%; Pred. No. 3.5e-07;
RESULT 689
ID AB296700 standard; DNA; 4654 BP.
DE Human nuclear acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 10; Length 4654;
Best Local Similarity 82.8%; Pred. No. 3.5e-07;
RESULT 690
ID ABD20549 standard; DNA; 4654 BP.
DE Human pulmonary and inflammatory target DNA #160.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 11; Length 4654;
Best Local Similarity 82.8%; Pred. No. 3.5e-07;
RESULT 691
ID ADQ17509 standard; DNA; 4654 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 326.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 67.4; DB 12; Length 4654;
Best Local Similarity 82.8%; Pred. No. 3.5e-07;
RESULT 692
ID ADM01990 standard; DNA; 4698 BP.
DE Human inflammatory bowel disease marker gene - CD11c.
PN JP2004065120-A.
PD 04-MAR-2004.
PA (SUNU) SUMITOMO SEIYAKU KK.
Query Match 2.7%; Score 67.4; DB 12; Length 4698;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 693
ID AAA34883 standard; DNA; 4704 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2572.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 2.7%; Score 67.4; DB 3; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 694
ID AAF21005 standard; DNA; 4704 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2572.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 2.7%; Score 67.4; DB 3; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 695
ID ABR84729 standard; cDNA; 4704 BP.
DE Human cDNA differentially expressed in granulocytic cells #1300.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 67.4; DB 6; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 696
ID AB296699 standard; DNA; 4704 BP.
DE Human nuclear acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 10; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 697
ID ADI32032 standard; cDNA; 4704 BP.
DE Human cDNA #1358.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.7%; Score 67.4; DB 11; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 698
ID ABD20548 standard; DNA; 4704 BP.
DE Human pulmonary and inflammatory target DNA #159.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 11; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 699
ID ADR44042 standard; DNA; 4704 BP.
DE Human kidney tumour associated gene clone-53 SEQ ID NO:52.
PN WO2004074506-A2.
PD 02-SEP-2004.
PA (MERG-) MERGEN LTD.
Query Match 2.7%; Score 67.4; DB 13; Length 4704;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 700
ID ADQ22218 standard; DNA; 4800 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5038.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 67.4; DB 12; Length 4800;
Best Local Similarity 82.8%; Pred. No. 3.6e-07;
RESULT 701
ID 'AAA34886 standard; DNA; 11648 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2575.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 2.7%; Score 67.4; DB 3; Length 11648;
Best Local Similarity 82.8%; Pred. No. 5.9e-07;
RESULT 702
ID AAF21008 standard; DNA; 11649 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2575.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 2.7%; Score 67.4; DB 3; Length 11649;
Best Local Similarity 82.8%; Pred. No. 5.9e-07;
RESULT 703
ID ABZ96702 standard; DNA; 11649 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 10; Length 11649;
Best Local Similarity 82.8%; Pred. No. 5.9e-07;
RESULT 704
ID ABD20551 standard; DNA; 11649 BP.
DE Human pulmonary and inflammatory target DNA #162.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 11; Length 11649;
Best Local Similarity 82.8%; Pred. No. 5.9e-07;
RESULT 705
ID ADK16022 standard; DNA; 25373 BP.
DE Human mamaglobin gene promoter.
PN WO2004016652-A2.
PD 26-FEB-2004.
PA (UYMC-) UNIV MCMASTER.
Query Match 2.7%; Score 67.4; DB 12; Length 25373;
Best Local Similarity 76.1%; Pred. No. 9.1e-07;
RESULT 706
ID ADP49338 standard; DNA; 80000 BP.
DE Human B-cell chronic lymphocytic leukaemia associated genomic DNA #2.
PN WO2004046376-A2.
PD 03-JUN-2004.
PA (HSRI-) HS RIGSHOSPITALET.
PA (UYAR-) UNIV ARHUS.
Query Match 2.7%; Score 67.4; DB 12; Length 80000;
Best Local Similarity 71.2%; Pred. No. 1.7e-06;
RESULT 707
ID ADH77123 standard; DNA; 126001 BP.
DE Human PAZ/PIWI domain-containing protein polynucleotide #3.
PN US2003232442-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 67.4; DB 12; Length 126001;
Best Local Similarity 92.2%; Pred. No. 2.2e-06;
RESULT 708
ID AAK72075 standard; DNA; 101 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26887.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 101;
Best Local Similarity 90.0%; Pred. No. 4.8e-08;
RESULT 709
ID AAS27782 standard; DNA; 110 BP.
DE DNA encoding novel signal transduction pathway protein, Seq ID 1442.
PN WO200154733-A1.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 110;
Best Local Similarity 90.0%; Pred. No. 5e-08;
RESULT 710
ID ADB94585 standard; DNA; 110 BP.
DE Novel human protein DNA #194.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 10; Length 110;
Best Local Similarity 90.0%; Pred. No. 5e-08;
RESULT 711
ID AAK67157 standard; DNA; 128 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21969.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 128;
Best Local Similarity 90.0%; Pred. No. 5.5e-08;
RESULT 712
ID AAS34757 standard; DNA; 142 BP.
DE Human DNA for a novel foetal antigen, SEQ ID NO 2181.
PN WO200155312-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 142;
Best Local Similarity 90.0%; Pred. No. 5.8e-08;
RESULT 713
ID AAS34756 standard; DNA; 142 BP.
DE Human DNA for a novel foetal antigen, SEQ ID NO 2180.
PN WO200155312-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 142;
Best Local Similarity 90.0%; Pred. No. 5.8e-08;
RESULT 714
ID AAK89597 standard; DNA; 144 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3173.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 144;
Best Local Similarity 90.0%; Pred. No. 5.8e-08;
RESULT 715
ID AAK89595 standard; DNA; 154 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3171.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 154;
Best Local Similarity 90.0%; Pred. No. 6.1e-08;
RESULT 716
ID AAK89594 standard; DNA; 157 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3170.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 157;
Best Local Similarity 90.0%; Pred. No. 6.1e-08;
RESULT 717
ID AAS28164 standard; DNA; 160 BP.
DE Genomic sequence #4 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 160;
Best Local Similarity 90.0%; Pred. No. 6.2e-08;
RESULT 718
ID ADG41360 standard; DNA; 160 BP.
DE Human respiratory system associated genomic DNA seq id 598.

PN US2003215933-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 160;
Best Local Similarity 90.0%; Pred. No. 6.2e-08;
RESULT 719
ID ADI97134 standard; DNA; 160 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID598.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 11; Length 160;
Best Local Similarity 90.0%; Pred. No. 6.2e-08;
RESULT 720
ID ABA16882 standard; DNA; 172 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9213.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 172;
Best Local Similarity 90.0%; Pred. No. 6.4e-08;
RESULT 721
ID AAK89421 standard; DNA; 186 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2997.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 186;
Best Local Similarity 90.0%; Pred. No. 6.7e-08;
RESULT 722
ID AAK90804 standard; DNA; 186 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4380.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 186;
Best Local Similarity 90.0%; Pred. No. 6.7e-08;
RESULT 723
ID AAS31926 standard; DNA; 186 BP.
DE Human liver associated genomic DNA #100.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 186;
Best Local Similarity 90.0%; Pred. No. 6.7e-08;
RESULT 724
ID ABN90281 standard; DNA; 186 BP.
DE Human liver antigen HLDRI94 genomic sequence, SEQ ID NO:402.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 6; Length 186;
Best Local Similarity 90.0%; Pred. No. 6.7e-08;
RESULT 725
ID ADJ15194 standard; DNA; 186 BP.
DE Human liver-related genomic DNA - SEQ ID 402.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 11; Length 186;
Best Local Similarity 90.0%; Pred. No. 6.7e-08;
RESULT 726
ID ABA16332 standard; DNA; 250 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8663.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 250;
Best Local Similarity 90.0%; Pred. No. 7.9e-08;
RESULT 727
ID AA199014 standard; DNA; 275 BP.

DE Human excretory related polynucleotide SEQ ID NO 778.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 275;
Best Local Similarity 90.0%; Pred. No. 8.4e-08;
RESULT 728
ID AAI63364 standard; DNA; 275 BP.
DE Human kidney related polynucleotide SEQ ID NO 679.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 275;
Best Local Similarity 90.0%; Pred. No. 8.4e-08;
RESULT 729
ID AAZ13311 standard; cDNA; 294 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:780.
PN WO9938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 2; Length 294;
Best Local Similarity 90.0%; Pred. No. 8.7e-08;
RESULT 730
ID AAK67132 standard; DNA; 310 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21944.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 310;
Best Local Similarity 90.0%; Pred. No. 8.9e-08;
RESULT 731
ID ABZ74226 standard; DNA; 312 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1373.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 8; Length 312;
Best Local Similarity 90.0%; Pred. No. 9e-08;
RESULT 732
ID ADA98755 standard; DNA; 312 BP.
DE Human secreted protein-related DNA sequence #348.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 8; Length 312;
Best Local Similarity 90.0%; Pred. No. 9e-08;
RESULT 733
ID ABZ67792 standard; DNA; 312 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1315.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 312;
Best Local Similarity 90.0%; Pred. No. 9e-08;
RESULT 734
ID AAK72194 standard; DNA; 336 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27006.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 336;
Best Local Similarity 90.0%; Pred. No. 9.3e-08;
RESULT 735
ID AAL05103 standard; DNA; 336 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7791.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 336;
Best Local Similarity 90.0%; Pred. No. 9.3e-08;
RESULT 736
ID AAL05102 standard; DNA; 336 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 7790.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 336;
Best Local Similarity 90.0%; Pred. No. 9.3e-08;
RESULT 737
ID ABL97995 standard; DNA; 336 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2647.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 336;
Best Local Similarity 90.0%; Pred. No. 9.3e-08;
RESULT 738
ID ABL97996 standard; DNA; 336 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2648.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 336;
Best Local Similarity 90.0%; Pred. No. 9.3e-08;
RESULT 739
ID ACD22142 standard; cDNA; 355 BP.
DE Human colon cancer cell expressed cDNA #554.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
Query Match 2.7%; Score 67.2; DB 10; Length 355;
Best Local Similarity 90.0%; Pred. No. 9.6e-08;
RESULT 740
ID ADD71335 standard; DNA; 360 BP.
DE Glutamine:fructose-6-phosphate amide transferase 1 gene intron 16.
PN WO2003023063-A1.
PD 20-MAR-2003.
PA (SANY) SANKYO CO LTD.
Query Match 2.7%; Score 67.2; DB 10; Length 360;
Best Local Similarity 90.0%; Pred. No. 9.7e-08;
RESULT 741
ID AA186639 standard; cDNA; 394 BP.
DE Human polynucleotide SEQ ID NO 6699.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 4; Length 394;
Best Local Similarity 90.0%; Pred. No. 1e-07;
RESULT 742
ID AAS30632 standard; DNA; 424 BP.
DE DNA encoding novel lung cancer antigen, Seq ID No 84.
PN WO200155300-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 743
ID AAS28178 standard; DNA; 424 BP.
DE Genomic sequence #18 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 744
ID AA192285 standard; cDNA; 424 BP.
DE Human polynucleotide SEQ ID NO 12345.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 4; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 745

ID ACA03395 standard; DNA; 424 BP.
DE DNA encoding human lung cancer antigen HCLSC85.
PN US2002173454-A1.
PD 21-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 8; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 746
ID ADB96743 standard; DNA; 424 BP.
DE Novel lung cancer antigen genomic DNA #14.
PN US2003049703-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 9; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 747
ID ADG41374 standard; DNA; 424 BP.
DE Human respiratory system associated genomic DNA seq id 612.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 748
ID ADI97148 standard; DNA; 424 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID612.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 11; Length 424;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 749
ID ABV19326 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 19317.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 67.2; DB 5; Length 429;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 750
ID ABL87490 standard; cDNA; 451 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10468.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 67.2; DB 6; Length 451;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 751
ID ABV50841 standard; cDNA; 463 BP.
DE Human prostate expression marker cDNA 50832.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 67.2; DB 5; Length 463;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 752
ID ABV61721 standard; cDNA; 470 BP.
DE Human prostate expression marker cDNA 61712.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 67.2; DB 5; Length 470;
Best Local Similarity 90.0%; Pred. No. 1.1e-07;
RESULT 753
ID ADL41307 standard; DNA; 491 BP.
DE Human ovarian cancer DNA marker #15197.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 67.2; DB 5; Length 491;
Best Local Similarity 90.0%; Pred. No. 1.2e-07;

RESULT 754
ID AAZ15513 standard; cDNA; 745 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:2982.
PN WO9318972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 2; Length 745;
Best Local Similarity 90.0%; Pred. No. 1.5e-07;
RESULT 755
ID ADB82858 standard; cDNA; 763 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 1071).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 9; Length 763;
Best Local Similarity 90.0%; Pred. No. 1.5e-07;
RESULT 756
ID ABQ99819 standard; cDNA; 834 BP.
DE Human prostate expressed polynucleotide SEQ ID NO 1075.
PN WO200255700-A2.
PD 18-JUL-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 6; Length 834;
Best Local Similarity 90.0%; Pred. No. 1.5e-07;
RESULT 757
ID AAK55574 standard; DNA; 845 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20386.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 845;
Best Local Similarity 90.0%; Pred. No. 1.6e-07;
RESULT 758
ID AAL37008 standard; DNA; 1130 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3373.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 1130;
Best Local Similarity 90.0%; Pred. No. 1.8e-07;
RESULT 759
ID ABA20629 standard; DNA; 1130 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12960.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 1130;
Best Local Similarity 90.0%; Pred. No. 1.8e-07;
RESULT 760
ID ABX59986 standard; cDNA; 1130 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2340.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 8; Length 1130;
Best Local Similarity 90.0%; Pred. No. 1.8e-07;
RESULT 761
ID ADJ30746 standard; DNA; 1130 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3373.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 12; Length 1130;
Best Local Similarity 90.0%; Pred. No. 1.8e-07;
RESULT 762
ID AAF64199 standard; cDNA; 1167 BP.
DE Human secreted protein gene 24 SEQ ID NO:34.
PN WO200077026-A1.

PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.7%; Score 67.2; DB 4; Length 1167;
Best Local Similarity 90.0%; Pred. No. 1.9e-07;
RESULT 763
ID AAX24734 standard; DNA; 1297 BP.
DE Human APP genomic clone containing polyadenylation signals.
PN WO9909150-A1.
PD 25-FEB-1999.
PA (FARB) BAYER CORP.
Query Match 2.7%; Score 67.2; DB 2; Length 1297;
Best Local Similarity 90.0%; Pred. No. 2e-07;
RESULT 764
ID AAK70343 standard; DNA; 1389 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25155.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 1389;
Best Local Similarity 90.0%; Pred. No. 2.1e-07;
RESULT 765
ID ABS56842 standard; cDNA; 1389 BP.
DE Human HUMSIAH protein 14.74 cDNA.
PN CN1345799-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 2.7%; Score 67.2; DB 6; Length 1389;
Best Local Similarity 90.0%; Pred. No. 2.1e-07;
RESULT 766
ID ABQ77752 standard; cDNA; 1440 BP.
DE Serine protease 9.02-encoding cDNA.
PN CN1352297-A.
PD 05-JUN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 67.2; DB 6; Length 1440;
Best Local Similarity 90.0%; Pred. No. 2.1e-07;
RESULT 767
ID AAI89482 standard; cDNA; 1674 BP.
DE Human polynucleotide SEQ ID NO 9542.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 4; Length 1674;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 768
ID AAK90386 standard; DNA; 1713 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3962.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 1713;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 769
ID AAK90385 standard; DNA; 1713 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3961.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 1713;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 770
ID AAG39943 standard; DNA; 1713 BP.
DE Genomic sequence #362 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 1713;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 771
ID AAG39940 standard; DNA; 1713 BP.
DE Genomic sequence #359 encoding human colon associated polypeptide.
PN WO200155302-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 1713;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 772
ID ADB32900 standard; DNA; 1713 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 837.
FN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 9; Length 1713;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 773
ID ADB32903 standard; DNA; 1713 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 840.
FN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 9; Length 1713;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
RESULT 774
ID ADH22627 standard; cDNA; 1774 BP.
DE cDNA encoding a human transporter & ion channel (TRICH) protein SeqID125.
FN WO2003093444-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.7%; Score 67.2; DB 12; Length 1774;
Best Local Similarity 65.1%; Pred. No. 2.4e-07;
RESULT 775
ID AAD08354 standard; cDNA; 1786 BP.
DE Human secreted protein-encoding gene 10 cDNA clone HCBGK81, SEQ ID NO:20.
FN WO200077022-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 1786;
Best Local Similarity 90.0%; Pred. No. 2.4e-07;
RESULT 776
ID ADB83246 standard; cDNA; 1817 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 1459).
FN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 67.2; DB 9; Length 1817;
Best Local Similarity 90.0%; Pred. No. 2.4e-07;
RESULT 777
ID AAS19209 standard; cDNA; 1873 BP.
DE DNA encoding human transformer 2-beta protein 29.15.
FN WO200192517-A1.
PD 06-DEC-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 2.7%; Score 67.2; DB 6; Length 1873;
Best Local Similarity 90.0%; Pred. No. 2.4e-07;
RESULT 778
ID ADR07789 standard; cDNA; 2085 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1295.
FN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.2; DB 13; Length 2085;
Best Local Similarity 90.0%; Pred. No. 2.6e-07;
RESULT 779
ID ABK54129 standard; cDNA; 2246 BP.
DE cDNA encoding human secreted protein sequence #11.
FN WO200218412-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 6; Length 2246;
Best Local Similarity 90.0%; Pred. No. 2.7e-07;

RESULT 780
ID AAH14338 standard; cDNA; 2263 BP.
DE Human cDNA sequence SEQ ID NO:11903.
FN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 67.2; DB 4; Length 2263;
Best Local Similarity 90.0%; Pred. No. 2.7e-07;
RESULT 781
ID ACM41092 standard; cDNA; 2407 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA327102, SEQ ID NO:6302.
FN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 67.2; DB 13; Length 2407;
Best Local Similarity 90.0%; Pred. No. 2.8e-07;
RESULT 782
ID ADB62665 standard; cDNA; 2547 BP.
DE Human cDNA encoding clone LIVER20010510.
FN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.2; DB 10; Length 2547;
Best Local Similarity 90.0%; Pred. No. 2.9e-07;
RESULT 783
ID ADM01722 standard; cDNA; 2647 BP.
DE Human cDNA of the invention SEQ ID NO:407.
FN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.2; DB 11; Length 2647;
Best Local Similarity 90.0%; Pred. No. 2.9e-07;
RESULT 784
ID AAH17104 standard; cDNA; 2675 BP.
DE Human cDNA sequence SEQ ID NO:16707.
FN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 67.2; DB 4; Length 2675;
Best Local Similarity 90.0%; Pred. No. 3e-07;
RESULT 785
ID AAX27233 standard; DNA; 2713 BP.
DE Human Rab protein, RABP-3, coding sequence.
FN WO909182-A2.
PD 25-FEB-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.7%; Score 67.2; DB 2; Length 2713;
Best Local Similarity 90.0%; Pred. No. 3e-07;
RESULT 786
ID ADN05948 standard; cDNA; 2894 BP.
DE Antipsoriatic cDNA sequence #1208.
FN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 67.2; DB 12; Length 2894;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;
RESULT 787
ID ADP56222 standard; cDNA; 2894 BP.
DE Human PRO cDNA sequence SEQ ID NO:2198.
FN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 67.2; DB 13; Length 2894;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;
RESULT 788
ID AAH44832 standard; cDNA; 2947 BP.
DE Rat cDNA encoding tricarboxylate carrier 39.
FN WO200138369-A1.
PD 31-MAY-2001.
PA (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
Query Match 2.7%; Score 67.2; DB 5; Length 2947;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;

RESULT 789
ID AAK79326 standard; DNA; 2997 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34138.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 2997;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;
RESULT 790
ID AAS29192 standard; DNA; 2997 BP.
DE Genomic sequence #35 encoding novel human DNA-binding protein.
PN WO200155162-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 2997;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;
RESULT 791
ID ABS68332 standard; DNA; 2997 BP.
DE Human DNA-binding protein genomic DNA sequence #35.
PN US2002102638-A1.
PD 01-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 6; Length 2997;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;
RESULT 792
ID ADC25454 standard; cDNA; 2997 BP.
DE Human cDNA from extracellular matrix gene 60 #2.
PN US2003049650-A1.
PD 13-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 2997;
Best Local Similarity 90.0%; Pred. No. 3.1e-07;
RESULT 793
ID ABV72847 standard; cDNA; 3078 BP.
DE Signal peptidase 11.88 cDNA.
PN CN1352292-A.
PD 05-JUN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 67.2; DB 6; Length 3078;
Best Local Similarity 90.0%; Pred. No. 3.2e-07;
RESULT 794
ID ADK60442 standard; DNA; 3139 BP.
DE Angiogenesis differentially expressed gene GS-N16.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.7%; Score 67.2; DB 12; Length 3139;
Best Local Similarity 90.0%; Pred. No. 3.2e-07;
RESULT 795
ID ADK60743 standard; DNA; 3139 BP.
DE Angiogenesis differentially expressed gene GS-N16.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.7%; Score 67.2; DB 12; Length 3139;
Best Local Similarity 90.0%; Pred. No. 3.2e-07;
RESULT 796
ID ADP73065 standard; DNA; 3139 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N16.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 2.7%; Score 67.2; DB 12; Length 3139;
Best Local Similarity 90.0%; Pred. No. 3.2e-07;
RESULT 797
ID ADQ63046 standard; cDNA; 3151 BP.
DE Novel human cDNA sequence #207.
PN EP1440981-A2.

PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.2; DB 12; Length 3151;
Best Local Similarity 90.0%; Pred. No. 3.2e-07;
RESULT 798
ID ADRO8110 standard; cDNA; 3268 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1616.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.2; DB 13; Length 3268;
Best Local Similarity 90.0%; Pred. No. 3.3e-07;
RESULT 799
ID ABZ80230 standard; cDNA; 3434 BP.
DE Human transordin 1 encoding cDNA SEQ ID NO:3.
PN WO2003016502-A2.
PD 27-FEB-2003.
PA (MCLA-) MCLAUGHLIN RES INST.
Query Match 2.7%; Score 67.2; DB 8; Length 3434;
Best Local Similarity 90.0%; Pred. No. 3.4e-07;
RESULT 800
ID AAK75977 standard; DNA; 3452 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30789.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 3452;
Best Local Similarity 90.0%; Pred. No. 3.4e-07;
RESULT 801
ID ADRO7160 standard; cDNA; 3494 BP.
DE Full length human cDNA useful for treating neurological disease Seq 666.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 67.2; DB 13; Length 3494;
Best Local Similarity 90.0%; Pred. No. 3.4e-07;
RESULT 802
ID ABZ42800 standard; DNA; 3758 BP.
DE Human C-C chemokine receptor 6 nucleotide SEQ ID NO:389.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 2.7%; Score 67.2; DB 8; Length 3758;
Best Local Similarity 90.0%; Pred. No. 3.6e-07;
RESULT 803
ID AAL07337 standard; DNA; 4059 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10025.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 4059;
Best Local Similarity 90.0%; Pred. No. 3.7e-07;
RESULT 804
ID AAK65573 standard; DNA; 4998 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20385.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 4998;
Best Local Similarity 90.0%; Pred. No. 4.2e-07;
RESULT 805
ID ABV77901 standard; DNA; 5779 BP.
DE Hypoxia-repressed protein coding sequence #12.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 2.7%; Score 67.2; DB 6; Length 5779;
Best Local Similarity 90.0%; Pred. No. 4.5e-07;
RESULT 806
ID ADN03639 standard; cDNA; 5779 BP.
DE Antipsoriatic cDNA sequence #17.
PN WO2004028479-A2.
PD 08-APR-2004.

Wed May 11 07:24:22 2005

PA (GETH) GENENTECH INC.
 Query Match 2.7%; Score 67.2; DB 12; Length 5779;
 Best Local Similarity 90.0%; Pred. No. 4.5e-07;
 RESULT 807
 ID ADF22971 standard; cDNA; 5779 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:65.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 2.7%; Score 67.2; DB 13; Length 5779;
 Best Local Similarity 90.0%; Pred. No. 4.5e-07;
 RESULT 808
 ID ABZ09932 standard; DNA; 6621 BP.
 DE Human 5' and/or regulatory region of CDC25A DNA SEQ ID NO:72.
 PN WO200277272-A2.
 PD 03-OCT-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 2.7%; Score 67.2; DB 8; Length 6621;
 Best Local Similarity 90.0%; Pred. No. 4.9e-07;
 RESULT 809
 ID ABZ09875 standard; DNA; 6621 BP.
 DE Human 5' and/or regulatory region of CDC25A DNA SEQ ID NO:15.
 PN WO200277272-A2.
 PD 03-OCT-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 2.7%; Score 67.2; DB 8; Length 6621;
 Best Local Similarity 90.0%; Pred. No. 4.9e-07;
 RESULT 810
 ID ADE84011 standard; DNA; 6621 BP.
 DE 5' regulatory region of human gene CDC25A.
 PN WO2003044226-A2.
 PD 30-MAY-2003.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 2.7%; Score 67.2; DB 10; Length 6621;
 Best Local Similarity 90.0%; Pred. No. 4.9e-07;
 RESULT 811
 ID AAS36827 standard; DNA; 7960 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2327.
 PN WO200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 4; Length 7960;
 Best Local Similarity 90.0%; Pred. No. 5.4e-07;
 RESULT 812
 ID ADE47521 standard; DNA; 7960 BP.
 DE Human cardiovascular system related genomic DNA #1087.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 10; Length 7960;
 Best Local Similarity 90.0%; Pred. No. 5.4e-07;
 RESULT 813
 ID ABZ67712 standard; DNA; 7960 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1235.
 PN WO200277186-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 10; Length 7960;
 Best Local Similarity 90.0%; Pred. No. 5.4e-07;
 RESULT 814
 ID ADJ08939 standard; DNA; 7960 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2327.
 PN US2004005575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 13; Length 7960;
 Best Local Similarity 90.0%; Pred. No. 5.4e-07;
 RESULT 815
 ID AAL04087 standard; DNA; 8253 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6775.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.7%; Score 67.2; DB 4; Length 8253;
 Best Local Similarity 90.0%; Pred. No. 5.5e-07;
 RESULT 816
 ID AAS40470 standard; DNA; 8253 BP.
 DE DNA encoding human prostate cancer antigen, Seq ID No 622.
 PN WO200155316-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 5; Length 8253;
 Best Local Similarity 90.0%; Pred. No. 5.5e-07;
 RESULT 817
 ID ADJ09676 standard; DNA; 8253 BP.
 DE Human prostate cancer associated gene-related DNA SeqID622.
 PN US2003054373-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 11; Length 8253;
 Best Local Similarity 90.0%; Pred. No. 5.5e-07;
 RESULT 818
 ID ABA16439 standard; DNA; 8994 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 8770.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 5; Length 8994;
 Best Local Similarity 90.0%; Pred. No. 5.8e-07;
 RESULT 819
 ID AAS29226 standard; DNA; 10139 BP.
 DE Genomic sequence #69 encoding novel human DNA-binding protein.
 PN WO200155162-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 5; Length 10139;
 Best Local Similarity 90.0%; Pred. No. 6.2e-07;
 RESULT 820
 ID ABS68366 standard; DNA; 10139 BP.
 DE Human DNA-binding protein genomic DNA sequence #69.
 PN US2002102638-A1.
 PD 01-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 2.7%; Score 67.2; DB 6; Length 10139;
 Best Local Similarity 90.0%; Pred. No. 6.2e-07;
 RESULT 821
 ID ADC25488 standard; cDNA; 10139 BP.
 DE Human cDNA from extracellular matrix gene 78 #5.
 PN US2003049650-A1.
 PD 13-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 10; Length 10139;
 Best Local Similarity 90.0%; Pred. No. 6.2e-07;
 RESULT 822
 ID AAL05277 standard; DNA; 10855 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7965.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 4; Length 10855;
 Best Local Similarity 90.0%; Pred. No. 6.4e-07;
 RESULT 823
 ID ABL98161 standard; DNA; 10855 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2813.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67.2; DB 4; Length 10855;
 Best Local Similarity 90.0%; Pred. No. 6.4e-07;
 RESULT 824
 ID AAK83108 standard; DNA; 10914 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37920.
 PN WO200157182-A2.
 PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 10914;
Best Local Similarity 90.0%; Pred. No. 6.4e-07;
RESULT 825
ID ABZ70982 standard; DNA; 11173 BP.
DE Human HKR1 related DNA sequence SEQ ID NO:10.
PN WO2003004513-A1.
PD 16-JAN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 67.2; DB 9; Length 11173;
Best Local Similarity 90.0%; Pred. No. 6.5e-07;
RESULT 826
ID AAK81675 standard; DNA; 11819 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36487.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 11819;
Best Local Similarity 90.0%; Pred. No. 6.7e-07;
RESULT 827
ID AAK81910 standard; DNA; 12466 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36722.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 12466;
Best Local Similarity 90.0%; Pred. No. 6.9e-07;
RESULT 828
ID AAV62392 standard; DNA; 12565 BP.
DE Human interleukin-1 receptor antagonist gene.
PN WO9844150-A1.
PD 08-OCT-1998.
PA (GEMI-) GEMINI RES LTD.
Query Match 2.7%; Score 67.2; DB 2; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 829
ID AAX75925 standard; DNA; 12565 BP.
DE Human interleukin lrn gene.
PN WO9924615-A2.
PD 20-MAY-1999.
PA (MED-) MEDICAL SCI SYSTEMS INC.
Query Match 2.7%; Score 67.2; DB 2; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 830
ID ABX15530 standard; DNA; 12565 BP.
DE Human interleukin-1 receptor antagonist, IL-1RN, gene.
PN US2002146700-A1.
PD 10-OCT-2002.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 2; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 831
ID AAC63769 standard; DNA; 12565 BP.
DE Human IL-1RN gene.
PN WO2000060117-A2.
PD 12-OCT-2000.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 3; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 832
ID AAF27667 standard; DNA; 12565 BP.
DE IL-1RN DNA.
PN WO200100880-A2.
PD 04-JAN-2001.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 4; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 833
ID AAC91435 standard; DNA; 12565 BP.
DE Human IL-1RN nucleotide sequence.
PN WO200071753-A2.
PD 30-NOV-2000.
PA (INTE-) INTERLEUKIN GENETICS INC.

Query Match 2.7%; Score 67.2; DB 5; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 834
ID ACC44353 standard; DNA; 12565 BP.
DE Human interleukin 1 receptor antagonist genomic sequence.
PN WO2003026488-A2.
PD 03-APR-2003.
PA (VITI-) VITIVITY INC.
Query Match 2.7%; Score 67.2; DB 8; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 835
ID AAL54517 standard; DNA; 12565 BP.
DE Secreted interleukin-1RN nucleotide sequence.
PN WO2002103031-A2.
PD 27-DEC-2002.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 8; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 836
ID AAD51465 standard; DNA; 12565 BP.
DE Human interleukin-1RN (IL-1RN) gene.
PN WO2002101015-A2.
PD 19-DEC-2002.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 10; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 837
ID ADL83339 standard; DNA; 12565 BP.
DE Human secreted interleukin-1 receptor antagonist (IL-1RN) gene.
PN US6720141-B1.
PD 13-APR-2004.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 838
ID ADN04587 standard; cDNA; 12565 BP.
DE Antipsoriatic cDNA sequence #499.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 67.2; DB 12; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 839
ID ADN48840 standard; DNA; 12565 BP.
DE Human secreted interleukin-1RN (IL-1RN) DNA.
PN US6730476-B1.
PD 04-MAY-2004.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 840
ID ADO24452 standard; cDNA; 12565 BP.
DE Human DNA327777 cDNA clone SEQ ID NO:91.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 2.7%; Score 67.2; DB 12; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 841
ID ADO35266 standard; DNA; 12565 BP.
DE Human interleukin-1RN (IL-1RN) gene.
PN US6746839-B1.
PD 08-JUN-2004.
PA (INTE-) INTERLEUKIN GENETICS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 12565;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 842
ID ADP24574 standard; cDNA; 12565 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1752.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.

Wed May 11 07:24:22 2005

Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 843
ID AAX24730 standard; DNA; 12814 BP.
DE Swedish-FAD APP targeting vector pMTI-2398.
PN WO9909150-A1.
PD 25-FEB-1999.
PA (FARB) BAYER CORP.
Query Match 2.7%; Score 67.2; DB 2; Length 12814;
Best Local Similarity 90.0%; Pred. No. 7e-07;
RESULT 844
ID AAX32189 standard; DNA; 13204 BP.
DE Human platelet glycoprotein IIB exons 2-29 nucleotide sequence.
PN WO99050454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 2.7%; Score 67.2; DB 2; Length 13204;
Best Local Similarity 90.0%; Pred. No. 7.2e-07;
RESULT 845
ID AAL04086 standard; DNA; 13392 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6774.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 13392;
Best Local Similarity 90.0%; Pred. No. 7.2e-07;
RESULT 846
ID AAS40469 standard; DNA; 13392 BP.
DE DNA encoding human prostate cancer antigen, Seq ID No 621.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 13392;
Best Local Similarity 90.0%; Pred. No. 7.2e-07;
RESULT 847
ID ADJ09675 standard; DNA; 13392 BP.
DE Human prostate cancer associated gene-related DNA SeqID621.
PN US2003054373-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 11; Length 13392;
Best Local Similarity 90.0%; Pred. No. 7.2e-07;
RESULT 848
ID AAK73722 standard; DNA; 14085 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28534.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 14085;
Best Local Similarity 90.0%; Pred. No. 7.4e-07;
RESULT 849
ID ABA19751 standard; DNA; 14231 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12082.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 14231;
Best Local Similarity 90.0%; Pred. No. 7.5e-07;
RESULT 850
ID ABA15617 standard; DNA; 15186 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7948.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 15186;
Best Local Similarity 90.0%; Pred. No. 7.7e-07;
RESULT 851
ID ABA15616 standard; DNA; 15187 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7947.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 5; Length 15187;
Best Local Similarity 90.0%; Pred. No. 7.7e-07;
RESULT 852
ID AAK70808 standard; DNA; 15484 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25620.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 15484;
Best Local Similarity 90.0%; Pred. No. 7.8e-07;
RESULT 853
ID AAX24731 standard; DNA; 15692 BP.
DE London-FAD APP targeting vector pMTI-2453.
PN WO9909150-A1.
PD 25-FEB-1999.
PA (FARB) BAYER CORP.
Query Match 2.7%; Score 67.2; DB 2; Length 15692;
Best Local Similarity 90.0%; Pred. No. 7.9e-07;
RESULT 854
ID AAX24732 standard; DNA; 15692 BP.
DE Swedish/london-FAD APP targeting vector pMTI-2454.
PN WO9909150-A1.
PD 25-FEB-1999.
PA (FARB) BAYER CORP.
Query Match 2.7%; Score 67.2; DB 2; Length 15692;
Best Local Similarity 90.0%; Pred. No. 7.9e-07;
RESULT 855
ID AAX24733 standard; DNA; 15701 BP.
DE Swedish-FAD APP713 targeting vector pMTI-2454.
PN WO9909150-A1.
PD 25-FEB-1999.
PA (FARB) BAYER CORP.
Query Match 2.7%; Score 67.2; DB 2; Length 15701;
Best Local Similarity 90.0%; Pred. No. 7.9e-07;
RESULT 856
ID AAK79798 standard; DNA; 16682 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34610.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 16682;
Best Local Similarity 90.0%; Pred. No. 8.1e-07;
RESULT 857
ID AAK70010 standard; DNA; 16682 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24822.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 16682;
Best Local Similarity 90.0%; Pred. No. 8.1e-07;
RESULT 858
ID AAS36826 standard; DNA; 17239 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2326.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 17239;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 859
ID ADE47520 standard; DNA; 17239 BP.
DE Human cardiovascular system related genomic DNA #1086.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 17239;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 860
ID ABZ67711 standard; DNA; 17239 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1234.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 17239;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 861

ID ADJ08938 standard; DNA; 17239 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2326.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 13; Length 17239;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 862
ID AAL36869 standard; DNA; 17286 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3234.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 17286;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 863
ID ABX59857 standard; cDNA; 17286 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2201.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (ROBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 8; Length 17286;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 864
ID ADJ30607 standard; DNA; 17286 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3234.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 12; Length 17286;
Best Local Similarity 90.0%; Pred. No. 8.3e-07;
RESULT 865
ID AAK70445 standard; DNA; 18949 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25257.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 18949;
Best Local Similarity 90.0%; Pred. No. 8.7e-07;
RESULT 866
ID ADQ59165 standard; DNA; 19913 BP.
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:2.
PN KR2004008012-A.
PD 28-JAN-2004.
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
Query Match 2.7%; Score 67.2; DB 12; Length 19913;
Best Local Similarity 90.0%; Pred. No. 9e-07;
RESULT 867
ID AAK87416 standard; DNA; 19942 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42228.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 19942;
Best Local Similarity 90.0%; Pred. No. 9e-07;
RESULT 868
ID AAK66735 standard; DNA; 20067 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21547.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 20067;
Best Local Similarity 90.0%; Pred. No. 9e-07;
RESULT 869
ID AAK66733 standard; DNA; 20068 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21545.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 20068;
Best Local Similarity 90.0%; Pred. No. 9e-07;
RESULT 870
ID AAK72318 standard; DNA; 20245 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27130.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 871
ID ABK69845 standard; DNA; 20245 BP.
DE Human secreted protein gene 22 genomic DNA fragment #6.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 6; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 872
ID ACC50860 standard; cDNA; 20245 BP.
DE Human secreted protein BAC clone SEQ ID NO 1040.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 8; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 873
ID ABZ71482 standard; DNA; 20245 BP.
DE Secreted protein gene 12 genomic fragment HAUAI83, SEQ ID NO:592.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 8; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 874
ID ADB91838 standard; DNA; 20245 BP.
DE Human secreted protein related DNA #SEQ ID 784.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 9; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 875
ID ADC74613 standard; DNA; 20245 BP.
DE Human secreted protein-related DNA - SEQ ID 1246.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 876
ID ADD38133 standard; cDNA; 20245 BP.
DE cDNA clone in ATCC deposit #27.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 877
ID ADA57727 standard; DNA; 20245 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 20245;
Best Local Similarity 90.0%; Pred. No. 9.1e-07;
RESULT 878
ID AAK66731 standard; DNA; 20323 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21543.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 20323;
RESULT 879
ID AAK79760 standard; DNA; 20601 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34572.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 20601;
RESULT 880
ID AAS36234 standard; DNA; 21129 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1734.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 21129;
RESULT 881
ID ADE46928 standard; DNA; 21129 BP.
DE Human cardiovascular system related genomic DNA #494.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 10; Length 21129;
RESULT 882
ID ADJ08346 standard; DNA; 21129 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1734.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 13; Length 21129;
RESULT 883
ID AAD32039 standard; DNA; 21234 BP.
DE Human kinase protein gene.
PN WO200216567-A2.
PD 28-FEB-2002.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 6; Length 21234;
RESULT 884
ID AAK79799 standard; DNA; 21436 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34611.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 21436;
RESULT 885
ID AAK70011 standard; DNA; 21436 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24823.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 21436;
RESULT 886
ID ADC87234 standard; DNA; 21581 BP.
DE Human GPCR gene SEQ ID NO:1687.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 10; Length 21581;
RESULT 887
ID AAD62371 standard; DNA; 21784 BP.
DE Human protease gene.
PN US2003129726-A1.
PD 10-JUL-2003.
PA (APPL-) APPLERA CORP.

Query Match
Best Local Similarity 2.7%; Score 67.2; DB 10; Length 21784;
RESULT 888
ID ABX16008 standard; DNA; 21784 BP.
DE Human novel protease gene.
PN US2002142440-A1.
PD 03-OCT-2002.
PA (GANW/) GAN W.
PA (YEJ/) YE J.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 10; Length 21784;
RESULT 889
ID AAK67644 standard; DNA; 21982 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22456.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 21982;
RESULT 890
ID ABZ74479 standard; DNA; 21982 BP.
DE Secreted protein gene 310 genomic fragment HSYBI06, SEQ ID NO:1626.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 8; Length 21982;
RESULT 891
ID ADC20924 standard; DNA; 21982 BP.
DE Human secreted protein-related DNA sequence #342.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 10; Length 21982;
RESULT 892
ID ABZ68026 standard; DNA; 21982 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1549.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 10; Length 21982;
RESULT 893
ID AAL05829 standard; DNA; 23544 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8517.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 23544;
RESULT 894
ID ABL98393 standard; DNA; 23544 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3045.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 4; Length 23544;
RESULT 895
ID ABD32638 standard; DNA; 24810 BP.
DE Human cancer-associated genomic DNA HD13-026.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.7%; Score 67.2; DB 13; Length 24810;
RESULT 896
ID ADQ97272 standard; DNA; 24861 BP.
DE Human cancer associated sequence HD08-024, SEQ ID 248.
PN WO2004060304-A2.

PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 24861;
Best Local Similarity 90.0%; Pred. No. 1e-06;
RESULT 897
ID ACN44714 standard; DNA; 30030 BP.
DE Human genomic sequence HCG14997.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 30030;
Best Local Similarity 90.0%; Pred. No. 1.1e-06;
RESULT 898
ID AAK67239 standard; DNA; 30393 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22051.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 30393;
Best Local Similarity 90.0%; Pred. No. 1.1e-06;
RESULT 899
ID AAL06868 standard; DNA; 31304 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9556.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 31304;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 900
ID ABA08089 standard; DNA; 31304 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 884.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 31304;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 901
ID ACN44118 standard; DNA; 31652 BP.
DE Human genomic sequence HCG23908.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 31652;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 902
ID AAL37445 standard; DNA; 31730 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3810.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 31730;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 903
ID ABX60433 standard; cDNA; 31730 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2777.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 67.2; DB 8; Length 31730;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 904
ID ADJ31183 standard; DNA; 31730 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3810.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 12; Length 31730;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 905
ID ABA07160 standard; DNA; 31931 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 479.

PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 31931;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 906
ID AAL06975 standard; DNA; 32250 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9663.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 32250;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 907
ID AAK81578 standard; DNA; 32313 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36390.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 32313;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 908
ID AD018255 standard; DNA; 33414 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1073.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 33414;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 909
ID AAK73093 standard; DNA; 33747 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27905.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 33747;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 910
ID AAK69279 standard; DNA; 33747 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24091.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 33747;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 911
ID AAK67071 standard; DNA; 33923 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21883.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 33923;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 912
ID AAD44328 standard; DNA; 34667 BP.
DE Human transporter gene.
PN WO200248367-A2.
PD 20-JUN-2002.
Query Match 2.7%; Score 67.2; DB 6; Length 34667;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 913
ID ACN37240 standard; DNA; 34796 BP.
DE Human periodontal disease related gene PLOD SEQ ID NO:150.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (RUBI-) RUBIT GENOMIX INC.
PA (KAMO/) KAMO I K.
Query Match 2.7%; Score 67.2; DB 13; Length 34796;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 914
ID ADC87616 standard; DNA; 35425 BP.
DE Human GPCR gene SEQ ID NO:2069.
PN EP1270724-A2.

Wed May 11 07:24:22 2005

PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.7%; Score 67.2; DB 10; Length 35425;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 915
ID . ADC87616 standard; DNA; 35425 BP.
DE Human GPCR gene SEQ ID NO:2069.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.7%; Score 67.2; DB 10; Length 35425;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 916
ID AAF54723 standard; DNA; 35465 BP.
DE Nucleotide sequence of a human polynucleotide sequence.
PN WO200105422-A2.
PD 25-JAN-2001.
PA (INMR) BIOMERIEUX STELHVS.
Query Match 2.7%; Score 67.2; DB 4; Length 35465;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 917
ID ABT17380 standard; DNA; 35465 BP.
DE Human IG gene related nucleic acid SEQ ID No 6.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 2.7%; Score 67.2; DB 8; Length 35465;
Best Local Similarity 90.0%; Pred. No. 1.2e-06;
RESULT 918
ID ABD33508 standard; DNA; 36871 BP.
DE Human cancer-associated (CA) gene HD07-099.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 13; Length 36871;
Best Local Similarity 90.0%; Pred. No. 1.3e-06;
RESULT 919
ID ABT17382 standard; DNA; 36991 BP.
DE Human IG gene related nucleic acid SEQ ID No 8.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 2.7%; Score 67.2; DB 8; Length 36991;
Best Local Similarity 90.0%; Pred. No. 1.3e-06;
RESULT 920
ID ABL91800 standard; DNA; 39328 BP.
DE Human lipase endothelial (LIPG) isogene genomic DNA sequence.
PN WO200216397-A2.
PD 28-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 2.7%; Score 67.2; DB 6; Length 39328;
Best Local Similarity 90.0%; Pred. No. 1.3e-06;
RESULT 921
ID ABZ74459 standard; DNA; 39339 BP.
DE Secreted protein gene 299 genomic fragment HSOAH16, SEQ ID NO:1606.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 8; Length 39339;
Best Local Similarity 90.0%; Pred. No. 1.3e-06;
RESULT 922
ID ABZ68012 standard; DNA; 39339 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1535.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 39339;
Best Local Similarity 90.0%; Pred. No. 1.3e-06;
RESULT 923
ID ACN44798 standard; DNA; 40491 BP.
DE Human genomic sequence hCG41911.
PN WO20003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 40491;
Best Local Similarity 90.0%; Pred. No. 1.3e-06;
RESULT 924
ID ACN44166 standard; DNA; 41624 BP.
DE Human genomic sequence hCG1643838.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 41624;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 925
ID ACN45050 standard; DNA; 41966 BP.
DE Human genomic sequence hCG39344.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 41966;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 926
ID ABK84242 standard; cDNA; 43599 BP.
DE Human cDNA differentially expressed in granulocytic cells #813.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 67.2; DB 6; Length 43599;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 927
ID ADL95498 standard; DNA; 43936 BP.
DE Human MCM3AP genomic DNA.
PN US2003165878-A1.
PD 04-SEP-2003.
PA (MORR-) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.7%; Score 67.2; DB 11; Length 43936;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 928
ID ADC85386 standard; DNA; 44029 BP.
DE Human Mcm3ap genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 44029;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 929
ID ADA02906 standard; DNA; 44030 BP.
DE Human MCM3AP carcinoma associated gene, SEQ ID NO:1424.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 9; Length 44030;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 930
ID ADB72644 standard; DNA; 44030 BP.
DE Human MCM3AP gene.
PN WO2003008563-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 44030;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 931
ID ADM74501 standard; DNA; 44030 BP.
DE Human carcinoma associated (CA) nucleic acid #85.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR-) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.7%; Score 67.2; DB 12; Length 44030;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 932
ID ABE97975 standard; DNA; 44100 BP.

DE Human retroviral sequence RAM75.
PN WO9967395-A1.
PD 29-DEC-1999.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 2.7%; Score 67.2; DB 3; Length 44100;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 933
ID ABD32642 standard; DNA; 47096 BP.
DE Human cancer-associated genomic DNA HD13-028.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 13; Length 47096;
Best Local Similarity 90.0%; Pred. No. 1.4e-06;
RESULT 934
ID ADA02840 standard; DNA; 47573 BP.
DE Human MAP3K8 carcinoma associated gene, SEQ ID NO:1358.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 9; Length 47573;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 935
ID ADB72578 standard; DNA; 47573 BP.
DE Human MAP3K8 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 47573;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 936
ID ADC85319 standard; DNA; 47573 BP.
DE Mouse Map3k8 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 47573;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 937
ID ADM74435 standard; DNA; 47573 BP.
DE Human carcinoma associated (CA) nucleic acid #52.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.7%; Score 67.2; DB 12; Length 47573;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 938
ID ADO61194 standard; DNA; 48001 BP.
DE Human PPAR binding protein DNA.
PN US2004101855-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 67.2; DB 12; Length 48001;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 939
ID ACN44802 standard; DNA; 48469 BP.
DE Human genomic sequence hCG1640192.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 48469;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 940
ID ACN43950 standard; DNA; 49536 BP.
DE Human genomic sequence hCG1775160.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 49536;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 941
ID ADC20666 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence #84.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 51961;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 942
ID ABT16905 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 259.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 51961;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 943
ID ABZ67488 standard; DNA; 51961 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1011.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 10; Length 51961;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 944
ID ADA02666 standard; DNA; 52242 BP.
DE Human MDM2 carcinoma associated gene, SEQ ID NO:1184.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 9; Length 52242;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 945
ID ADB72404 standard; DNA; 52242 BP.
DE Human MDM2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 52242;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 946
ID ADE95914 standard; DNA; 52242 BP.
DE Human MDM2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 52242;
Best Local Similarity 90.0%; Pred. No. 1.5e-06;
RESULT 947
ID ACM44778 standard; DNA; 56577 BP.
DE Human genomic sequence hCG27352.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 56577;
Best Local Similarity 90.0%; Pred. No. 1.6e-06;
RESULT 948
ID ADQ97617 standard; DNA; 57008 BP.
DE Human cancer associated sequence HD10-015, SEQ ID 594.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 57008;
Best Local Similarity 90.0%; Pred. No. 1.6e-06;
RESULT 949
ID ACN43874 standard; DNA; 58945 BP.
DE Human genomic sequence hCG25637.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 58945;
Best Local Similarity 90.0%; Pred. No. 1.6e-06;
RESULT 950
ID ADA02696 standard; DNA; 59554 BP.
DE Human TK2 carcinoma associated gene, SEQ ID NO:1214.

PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 9; Length 59554;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
RESULT 951
ID ADB72434 standard; DNA; 59554 BP.
DE Human TK2 gene.
FN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 59554;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
RESULT 952
ID ADS95944 standard; DNA; 59554 BP.
DE Human TK2 gene genomic DNA sequence.
FN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 59554;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
RESULT 953
ID ACN44494 standard; DNA; 60381 BP.
DE Human genomic sequence hCG27935.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 10; Length 60381;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
RESULT 954
ID ACN43886 standard; DNA; 61103 BP.
DE Human genomic sequence hCG1784975.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 61103;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
RESULT 955
ID AAK86282 standard; DNA; 65854 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41094.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 67.2; DB 4; Length 65854;
Best Local Similarity 90.0%; Pred. No. 1.7e-06;
RESULT 956
ID ABK87050 standard; cDNA; 66804 BP.
DE Human transporter protein genomic DNA.
Query Match 2.7%; Score 67.2; DB 6; Length 66804;
Best Local Similarity 90.0%; Pred. No. 1.8e-06;
RESULT 957
ID ADG88330 standard; DNA; 66804 BP.
DE Human transporter protein genomic DNA.
Query Match 2.7%; Score 67.2; DB 10; Length 66804;
Best Local Similarity 90.0%; Pred. No. 1.8e-06;
RESULT 958
ID ABS56296 standard; cDNA; 73544 BP.
DE Human transporter protein gene.
FN WO200279252-A1.
PD 10-OCT-2002.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 67.2; DB 8; Length 73544;
Best Local Similarity 90.0%; Pred. No. 1.9e-06;
RESULT 959
ID ADP66763 standard; DNA; 75033 BP.
DE Human endochelial lipase polynucleotide seqid 18.
FN US2004115653-A1.
PD 17-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 67.2; DB 12; Length 75033;
Best Local Similarity 90.0%; Pred. No. 1.9e-06;
RESULT 960
ID ACN44342 standard; DNA; 78268 BP.

DE Human genomic sequence hCG17932.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 78268;
Best Local Similarity 90.0%; Pred. No. 1.9e-06;
RESULT 961
ID ACA64942 standard; DNA; 78539 BP.
DE Human FRAP1 DNA corresponding to AL049659.
FN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 2.7%; Score 67.2; DB 8; Length 78539;
Best Local Similarity 90.0%; Pred. No. 1.9e-06;
RESULT 962
ID ADL13866 standard; DNA; 79597 BP.
DE Osteoarthritis-associated polymorphic nucleotide #398.
FN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 67.2; DB 10; Length 79597;
Best Local Similarity 90.0%; Pred. No. 1.9e-06;
RESULT 963
ID ADO25290 standard; DNA; 80928 BP.
DE Human protein kinase C iota/lambda genomic sequence.
FN WO2004041212-A2.
PD 21-MAY-2004.
PA (SACK/) SACKTOR T C.
PA (CRAR/) CRARY J F.
PA (HERN/) HERNANDEZ A I.
PA (MIRR/) MIRRA S.
PA (SHAO/) SHAO C.
Query Match 2.7%; Score 67.2; DB 12; Length 80928;
Best Local Similarity 90.0%; Pred. No. 2e-06;
RESULT 965
ID AAL51405 standard; DNA; 80959 BP.
DE Human secreted protein gene sequence, SEQ ID NO 3.
Query Match 2.7%; Score 67.2; DB 8; Length 80959;
Best Local Similarity 90.0%; Pred. No. 2e-06;
RESULT 966
ID ADQ97623 standard; DNA; 86764 BP.
DE Human cancer associated sequence HD10-016, SEQ ID 600.
FN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 86764;
Best Local Similarity 90.0%; Pred. No. 2e-06;
RESULT 967
Query Match 2.7%; Score 67.2; DB 13; Length 88939;
Best Local Similarity 90.0%; Pred. No. 2.1e-06;
RESULT 968
Query Match 2.7%; Score 67.2; DB 11; Length 89182;
Best Local Similarity 90.0%; Pred. No. 2.1e-06;
RESULT 969
ID ADD71350 standard; DNA; 93390 BP.
DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.
FN WO2003023063-A1.
PD 20-MAR-2003.
PA (SANY) SANKYO CO LTD.
Query Match 2.7%; Score 67.2; DB 10; Length 93390;
Best Local Similarity 90.0%; Pred. No. 2.1e-06;
RESULT 970
ID AB078054 standard; cDNA; 98865 BP.
DE Human Ras-like protein encoding genomic DNA SEQ ID NO 3.
FN WO200261088-A2.
PD 08-AUG-2002.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 67.2; DB 6; Length 98865;
Best Local Similarity 90.0%; Pred. No. 2.2e-06;
RESULT 971

Wed May 11 07:24:22 2005

PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 2.7%; Score 67.2; DB 13; Length 110608;
Best Local Similarity 90.0%; Pred. No. 2.3e-06;
RESULT 996
ID ADA42607 standard; DNA; 113604 BP.
DE Human LQTS genomic DNA #2.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 2.7%; Score 67.2; DB 9; Length 113604;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 997
ID ADA42606 standard; DNA; 113604 BP.
DE Human LQTS genomic DNA #1.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 2.7%; Score 67.2; DB 9; Length 113604;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 998
ID ADS19853 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:1.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 2.7%; Score 67.2; DB 13; Length 113604;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 999
ID ADS19854 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:2.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 2.7%; Score 67.2; DB 13; Length 113604;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1000
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbm168.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI) MERCK & CO INC.
Query Match 2.7%; Score 67.2; DB 4; Length 114793;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1001
ID ACD13448 standard; DNA; 115756 BP.
DE Human DNA encoding a p53 modifier, SEQ ID 68.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 2.7%; Score 67.2; DB 8; Length 115756;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1002
ID ADR52890 standard; DNA; 115935 BP.
DE Drug therapy altered expressed gene #241.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 2.7%; Score 67.2; DB 13; Length 115935;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1003
ID ADJ74882 standard; DNA; 117143 BP.
DE Marker gene SEQ ID NO:134.
PN EPI394274-A2.
PD 03-MAR-2004.

PA (GENO-) GENOX RES INC.
Query Match 2.7%; Score 67.2; DB 12; Length 117143;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1004
ID ADQ97319 standard; DNA; 117829 BP.
DE Human cancer associated sequence HD08-031, SEQ ID 296.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 117829;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1005
ID ADQ97391 standard; DNA; 120447 BP.
DE Human cancer associated sequence HD08-042, SEQ ID 368.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 120447;
Best Local Similarity 90.0%; Pred. No. 2.4e-06;
RESULT 1006
ID ACN44026 standard; DNA; 122923 BP.
DE Human genomic sequence hCG24510.
PN WO2003073836-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 11; Length 122923;
Best Local Similarity 90.0%; Pred. No. 2.5e-06;
RESULT 1007
ID ADR52731 standard; DNA; 127917 BP.
DE Drug therapy altered expressed gene #82.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 2.7%; Score 67.2; DB 13; Length 127917;
Best Local Similarity 90.0%; Pred. No. 2.5e-06;
RESULT 1008
ID ADJ96282 standard; DNA; 130001 BP.
DE Human breast cancer-1 DNA #14.
PN US2004014051-A1.
PD 22-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 67.2; DB 12; Length 130001;
Best Local Similarity 90.0%; Pred. No. 2.5e-06;
RESULT 1009
ID ABK83573 standard; cDNA; 130263 BP.
DE Human cDNA differentially expressed in granulocytic cells #144.
PN WO20028959-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 67.2; DB 6; Length 130263;
Best Local Similarity 90.0%; Pred. No. 2.5e-06;
RESULT 1010
ID ACN45054 standard; DNA; 133632 BP.
DE Human genomic sequence hCG28560.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 11; Length 133632;
Best Local Similarity 90.0%; Pred. No. 2.6e-06;
RESULT 1011
ID ADH58564 standard; DNA; 139573 BP.
DE Human Na+-independent transporter-related transporter protein gene.
PN WO200250301-A2.
PD 27-JUN-2002.

PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 2.7%; Score 67.2; DB 6; Length 147708;
Best Local Similarity 90.0%; Pred. No. 2.7e-06;
RESULT 1013
ID ABD33075 standard; DNA; 152759 BP.
DE Human cancer-associated (CA) gene HD07-002.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 13; Length 152759;
Best Local Similarity 90.0%; Pred. No. 2.8e-06;
RESULT 1014
ID ADQ97531 standard; DNA; 153752 BP.
DE Human cancer associated sequence HD09-009, SEQ ID 508.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 153752;
Best Local Similarity 90.0%; Pred. No. 2.8e-06;
RESULT 1015
ID AAD28763 standard; DNA; 154465 BP.
DE Human AKAP allelic variant (AKAP10-1) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 6; Length 154465;
Best Local Similarity 90.0%; Pred. No. 2.8e-06;
RESULT 1016
ID ADL13861 standard; DNA; 154681 BP.
DE Osteoarthritis-associated polymorphic nucleotide #393.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 67.2; DB 10; Length 154681;
Best Local Similarity 90.0%; Pred. No. 2.8e-06;
RESULT 1017
ID ADQ19389 standard; DNA; 155937 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 155937;
Best Local Similarity 90.0%; Pred. No. 2.8e-06;
RESULT 1018
ID ABD32817 standard; DNA; 156416 BP.
DE Human cancer-associated genomic DNA HD17-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 13; Length 156416;
Best Local Similarity 90.0%; Pred. No. 2.8e-06;
RESULT 1019
ID ADL08116 standard; DNA; 160361 BP.
DE Human gene associated with low HDL-C FAPB-3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 160361;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1020
ID ABQ88179 standard; cDNA; 160771 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 86.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 2.7%; Score 67.2; DB 6; Length 160771;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1021
ID AAH02340 standard; DNA; 161425 BP.
DE Human AKAP10 gene SEQ ID NO: 36.
PN WO200127857-A2.

PD 19-APR-2001.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 4; Length 161425;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1022
ID AAH02339 standard; DNA; 162025 BP.
DE Human AKAP10 gene SEQ ID NO: 35.
PN WO200127857-A2.
PD 19-APR-2001.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 4; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1023
ID AAD28758 standard; DNA; 162025 BP.
DE Human AKAP allelic variant (AKAP10-6) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 6; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1024
ID AAD28759 standard; DNA; 162025 BP.
DE Human AKAP allelic variant (AKAP10-7) gene.
PN WO200204489-A2.
PD 17-JAN-2002.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 6; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1025
ID ADS75958 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-6 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 13; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1026
ID ADS75959 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-7 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 13; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1027
ID ADS75963 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 allele AKAP10-1 genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 13; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1028
ID ADS75962 standard; DNA; 162025 BP.
DE Human A-kinase anchoring protein 10 wild type genomic sequence.
PN WO2004081576-A2.
PD 23-SEP-2004.
PA (SEQU-) SEQUENOM INC.
Query Match 2.7%; Score 67.2; DB 13; Length 162025;
Best Local Similarity 90.0%; Pred. No. 2.9e-06;
RESULT 1029
ID AAD62833 standard; DNA; 170834 BP.
DE Human BAC #2 containing formin (Fmn)-2 genomic DNA.
PN US2003170683-A1.
PD 11-SEP-2003.
PA (LEDE/) LEADER P.
PA (LEAD/) LEADER B.
Query Match 2.7%; Score 67.2; DB 10; Length 170834;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1030
ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.

Wed May 11 07:24:22 2005

PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM. 2.7%; Score 67.2; DB 6; Length 174424;
Query Match 90.0%; Pred. No. 3e-06;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1031
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 174448;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1032
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 175077;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1033
ID ABK83571 standard; cDNA; 175737 BP.
DE Human cDNA differentially expressed in granulocytic cells #142.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 67.2; DB 6; Length 175737;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1034
ID ADL13596 standard; DNA; 175737 BP.
DE Osteoarthritis-associated polymorphic nucleotide #128.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 67.2; DB 10; Length 175737;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1035
ID ADQ18934 standard; DNA; 175737 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1753.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 175737;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1036
ID ADQ97687 standard; DNA; 179487 BP.
DE Human cancer associated sequence HD10-028, SEQ ID 664.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 179487;
Best Local Similarity 90.0%; Pred. No. 3e-06;
RESULT 1037
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 67.2; DB 12; Length 181343;
Best Local Similarity 90.0%; Pred. No. 3.1e-06;
RESULT 1038
ID ADQ97481 standard; DNA; 194534 BP.
DE Human cancer associated sequence HD09-002, SEQ ID 458.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 194534;
Best Local Similarity 90.0%; Pred. No. 3.2e-06;
RESULT 1039
ID ACN44010 standard; DNA; 198522 BP.
DE Human genomic sequence hCG1643869.
PN WO2003073826-A2.
PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 198522;
Best Local Similarity 90.0%; Pred. No. 3.2e-06;
RESULT 1040
ID ACN44702 standard; DNA; 220224 BP.
DE Human genomic sequence hCG1788599.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 220224;
Best Local Similarity 90.0%; Pred. No. 3.4e-06;
RESULT 1041
ID AAV57926 standard; DNA; 235033 BP.
DE Hereditary haemochromatosis subregion from an unaffected individual.
PN WO9814466-A1.
PD 09-APR-1998.
PA (PROG-) PROGENITOR INC.
Query Match 2.7%; Score 67.2; DB 2; Length 235033;
Best Local Similarity 90.0%; Pred. No. 3.5e-06;
RESULT 1042
ID AAV57903 standard; DNA; 237326 BP.
DE Hereditary haemochromatosis subregion from an HH affected individual.
PN WO9814466-A1.
PD 09-APR-1998.
PA (PROG-) PROGENITOR INC.
Query Match 2.7%; Score 67.2; DB 2; Length 237326;
Best Local Similarity 90.0%; Pred. No. 3.6e-06;
RESULT 1043
ID ADQ59422 standard; DNA; 246940 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 246940;
Best Local Similarity 90.0%; Pred. No. 3.6e-06;
RESULT 1044
ID ADL08109 standard; DNA; 247682 BP.
DE Human gene associated with low HDL-C AT3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VTI-) VITIVITY INC.
Query Match 2.7%; Score 67.2; DB 12; Length 247682;
Best Local Similarity 90.0%; Pred. No. 3.6e-06;
RESULT 1045
ID ABZ80229 standard; DNA; 249999 BP.
DE Human transmembrane gene region genomic DNA SEQ ID NO:26.
PN WO2003016502-A2.
PD 27-FEB-2003.
PA (MCLA-) MCLAUGHLIN RES INST.
Query Match 2.7%; Score 67.2; DB 8; Length 249999;
Best Local Similarity 90.0%; Pred. No. 3.7e-06;
RESULT 1046
ID ACN44650 standard; DNA; 256157 BP.
DE Human genomic sequence hCG38672.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 67.2; DB 11; Length 256157;
Best Local Similarity 90.0%; Pred. No. 3.7e-06;
RESULT 1047
ID ABD33570 standard; DNA; 256157 BP.
DE Human cancer-associated (CA) gene HD07-114.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 67.2; DB 13; Length 256157;
Best Local Similarity 90.0%; Pred. No. 3.7e-06;
RESULT 1048
ID ABD32602 standard; DNA; 277616 BP.
DE Human cancer-associated genomic DNA HD7-221.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 2.7%; Score 67.2; DB 13; Length 277616;
 Best Local Similarity 90.0%; Pred. No. 3.9e-06;
 RESULT 1049
 ID ADQ59380 standard; DNA; 299598 BP.
 DE Human Cancer-associated (CA) gene sequence SEQ ID NO:16.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.7%; Score 67.2; DB 12; Length 299598;
 Best Local Similarity 90.0%; Pred. No. 4e-06;
 RESULT 1050
 ID ADP69744 standard; DNA; 312477 BP.
 DE Human ROCK 1 DNA #2.
 PN US2004115641-A1.
 PD 17-JUN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 2.7%; Score 67.2; DB 12; Length 312477;
 Best Local Similarity 90.0%; Pred. No. 4.1e-06;
 RESULT 1051
 ID AAS43104 standard; DNA; 325791 BP.
 DE Human Oestrogen receptor beta gene.
 PN WO200162793-A2.
 PD 30-AUG-2001.
 PA (PEKE-) PE CORP NY.
 Query Match 2.7%; Score 67.2; DB 4; Length 325791;
 Best Local Similarity 90.0%; Pred. No. 4.2e-06;
 RESULT 1052
 ID ADC86916 standard; DNA; 349989 BP.
 DE Human GPCR gene SEQ ID NO:1369.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 2.7%; Score 67.2; DB 10; Length 349989;
 Best Local Similarity 90.0%; Pred. No. 4.4e-06;
 RESULT 1053
 ID ADF13332 standard; DNA; 1004 BP.
 DE Human Coproporphyrinogen oxidase DNA, SEQ ID 26.
 PN WO2003072813-A2.
 PD 04-SEP-2003.
 PA (FARB-) BAYER AG.
 Query Match 2.7%; Score 67; DB 10; Length 1004;
 Best Local Similarity 73.9%; Pred. No. 1.9e-07;
 RESULT 1054
 ID AAK82354 standard; DNA; 4164 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37156.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67; DB 4; Length 4164;
 Best Local Similarity 88.0%; Pred. No. 4.3e-07;
 RESULT 1055
 ID AAG32247 standard; DNA; 7219 BP.
 DE Human DNA repair and processing genomic DNA #33.
 PN WO200155204-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67; DB 5; Length 7219;
 Best Local Similarity 88.0%; Pred. No. 5.8e-07;
 RESULT 1056
 ID ABS67550 standard; DNA; 7219 BP.
 DE Novel human DNA repair protein, genomic sequence #33.
 PN US2002086353-A1.
 PD 04-JUL-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 2.7%; Score 67; DB 6; Length 7219;
 Best Local Similarity 88.0%; Pred. No. 5.8e-07;
 RESULT 1057
 ID AAX98620 standard; DNA; 14646 BP.
 DE Human HHV4 DNA replication inhibitor TB7 coding sequence #1.
 PN WO200198489-A1.

PD 27-DEC-2001.
 PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
 Query Match 2.7%; Score 67; DB 6; Length 14646;
 Best Local Similarity 88.0%; Pred. No. 8.6e-07;
 RESULT 1058
 ID AAL04676 standard; DNA; 32249 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7364.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67; DB 4; Length 32249;
 Best Local Similarity 88.0%; Pred. No. 1.3e-06;
 RESULT 1059
 ID ABL97583 standard; DNA; 32249 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2235.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 67; DB 4; Length 32249;
 Best Local Similarity 88.0%; Pred. No. 1.3e-06;
 RESULT 1060
 ID ADP65343 standard; DNA; 57038 BP.
 DE Human sequence from clone RP5-1009E24 on chromosome 20 Contains DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 2.7%; Score 67; DB 11; Length 57038;
 Best Local Similarity 73.9%; Pred. No. 1.8e-06;
 RESULT 1061
 ID ADP65471 standard; DNA; 92794 BP.
 DE Human sequence from clone RP5-1009E24 on chromosome 20 DNA.
 PN WO2003072827-A1.
 PD 04-SEP-2003.
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 Query Match 2.7%; Score 67; DB 11; Length 92794;
 Best Local Similarity 73.9%; Pred. No. 2.4e-06;
 RESULT 1062
 ID ADS19665 standard; cDNA; 161484 BP.
 DE Human PTPN13 CDNA.
 PN US2004115635-A1.
 PD 17-JUN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 2.7%; Score 67; DB 13; Length 161484;
 Best Local Similarity 93.3%; Pred. No. 3.3e-06;
 RESULT 1063
 ID ABZ72040 standard; DNA; 207433 BP.
 DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.
 PN WO200178894-A2.
 PD 25-OCT-2001.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 2.7%; Score 67; DB 5; Length 207433;
 Best Local Similarity 73.9%; Pred. No. 3.7e-06;
 RESULT 1064
 ID ABX74891 standard; DNA; 207433 BP.
 DE BAC1098L22 DNA sequence.
 PN WO200283077-A2.
 PD 24-OCT-2002.
 PA (SCHE-) SCHERING CORP.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 2.7%; Score 67; DB 8; Length 207433;
 Best Local Similarity 73.9%; Pred. No. 3.7e-06;
 RESULT 1065
 ID ADJ36614 standard; DNA; 207433 BP.
 DE Bacterial artificial chromosome RPCI-11.
 PN US2004002470-A1.
 PD 01-JAN-2004.
 PA (KEIT/) KEITH T.
 PA (LITT/) LITTLE R D.
 PA (VEER/) VAN EERDEWEGH P.
 PA (DUPU/) DUPUIS J.
 PA (DNAS/) DEL MASTRO R G.
 PA (SIMO/) SIMON J.
 PA (ALLE/) ALLEN K.

Wed May 11 07:24:22 2005

PA (PAND/) PANDIT S. 2.7%; Score 67; DB 12; Length 207433;
 Query Match
 Best Local Similarity 73.9%; Pred. No. 3.7e-06;
 RESULT 1066
 ID ADL81193 standard; DNA; 207433 BP.
 DE BAC1098L22 DNA sequence.
 PN US2004023215-A1.
 PD 05-FEB-2004.
 PA (KEIT/) KEITH T.
 PA (LITT/) LITTLE R. D.
 PA (EERD/) EERDEWEH P. V.
 PA (DUPU/) DUPUIS J.
 PA (DMAS/) DEL MASTRO R. G.
 PA (SIMO/) SIMON J.
 PA (ALLE/) ALLEN K.
 PA (PAND/) PANDIT S.
 Query Match
 Best Local Similarity 73.9%; Pred. No. 3.7e-06;
 RESULT 1067
 ID ADQ22654 standard; DNA; 3820 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5474.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match
 Best Local Similarity 86.0%; Pred. No. 4.6e-07;
 RESULT 1068
 ID ABD33520 standard; DNA; 34722 BP.
 DE Human cancer-associated (CA) gene HD07-102.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match
 Best Local Similarity 91.0%; Pred. No. 1.6e-06;
 RESULT 1069
 ID ABQ82235 standard; DNA; 43543 BP.
 DE Human phospholipase protein encoding DNA SEQ ID NO:3.
 DE Human phospholipase protein encoding DNA SEQ ID NO:3.
 Query Match
 Best Local Similarity 78.3%; Pred. No. 1.8e-06;
 RESULT 1070
 ID AAK78813 standard; DNA; 51469 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 86.0%; Pred. No. 2e-06;
 RESULT 1071
 ID AAK70270 standard; DNA; 51469 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 86.0%; Pred. No. 2e-06;
 RESULT 1072
 ID AAK69322 standard; DNA; 51469 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 86.0%; Pred. No. 2e-06;
 RESULT 1073
 ID AAD55116 standard; DNA; 9829 BP.
 DE Human ACE reference DNA (GI 13027555).
 PN WO2003020118-A2.
 PD 13-MAR-2003.
 PA (VITI-) VITIIVITY INC.
 Query Match
 Best Local Similarity 86.0%; Pred. No. 2.8e-06;
 RESULT 1074
 ID ADL08124 standard; DNA; 176080 BP.

DE Human gene associated with low HDL-C LRPAP1.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIIVITY INC. 2.7%; Score 66.8; DB 12; Length 176080;
 Query Match
 Best Local Similarity 86.0%; Pred. No. 3.9e-06;
 RESULT 1075
 ID AAC72115 standard; DNA; 792 BP.
 DE Single nucleotide polymorphism containing sequence #648.
 PN WO200058519-A2.
 PD 05-OCT-2000.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 2.2e-07;
 RESULT 1076
 ID AAC72109 standard; DNA; 792 BP.
 DE Single nucleotide polymorphism containing sequence #646.
 PN WO200058519-A2.
 PD 05-OCT-2000.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 2.2e-07;
 RESULT 1077
 ID AAC72079 standard; DNA; 792 BP.
 DE Single nucleotide polymorphism containing sequence #636.
 PN WO200058519-A2.
 PD 05-OCT-2000.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 2.2e-07;
 RESULT 1078
 ID AAC72094 standard; DNA; 792 BP.
 DE Single nucleotide polymorphism containing sequence #641.
 PN WO200058519-A2.
 PD 05-OCT-2000.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 2.2e-07;
 RESULT 1079
 ID AAC72112 standard; DNA; 792 BP.
 DE Single nucleotide polymorphism containing sequence #647.
 PN WO200058519-A2.
 PD 05-OCT-2000.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 2.2e-07;
 RESULT 1080
 ID AAC72106 standard; DNA; 792 BP.
 DE Single nucleotide polymorphism containing sequence #645.
 PN WO200058519-A2.
 PD 05-OCT-2000.
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 2.2e-07;
 RESULT 1081
 ID AAI92780 standard; cDNA; 2235 BP.
 DE Human polynucleotide SEQ ID NO 12840.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 88.9%; Pred. No. 3.9e-07;
 RESULT 1082
 ID ADR08411 standard; cDNA; 3923 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1917.
 PN EP1447413-A2.
 PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 66.6; DB 13; Length 3923;
Best Local Similarity 88.9%; Pred. No. 5.3e-07;
RESULT 1083
ID ABK35504 standard; DNA; 7260 BP.
DE Human endometrial cancer related gene, IGF1.
PN WO200209573-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 2.7%; Score 66.6; DB 6; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1084
ID ABK35561 standard; DNA; 7260 BP.
DE Gene IGF1 differentially expressed in breast cancer tissue.
PN WO200210436-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK/J) BAAK J.
Query Match 2.7%; Score 66.6; DB 6; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1085
ID ABT11091 standard; cDNA; 7260 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 1225.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 66.6; DB 6; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1086
ID ABK84583 standard; cDNA; 7260 BP.
DE Human cDNA differentially expressed in granulocytic cells #1154.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 66.6; DB 6; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1087
ID ABK64812 standard; DNA; 7260 BP.
DE Human benign prostatic hyperplasia gene #707.
PN WO200212440-A2.
PD 14-FEB-2002.
PA (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
Query Match 2.7%; Score 66.6; DB 6; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1088
ID ABN97244 standard; DNA; 7260 BP.
DE Gene #3742 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 66.6; DB 6; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1089
ID ADA26452 standard; DNA; 7260 BP.
DE Human insulin-like growth factor-I (IGF-I) DNA.
PN US2003072761-A1.
PD 17-APR-2003.
PA (LEBO/J) LEBOWITZ J.
Query Match 2.7%; Score 66.6; DB 9; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1090
ID ADG33110 standard; DNA; 7260 BP.
DE Human DNA differentially expressed in patients with SLE SeqID434.
PN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.7%; Score 66.6; DB 10; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1091
ID ADP65015 standard; DNA; 7260 BP.
DE Human insulin-like growth factor 1 (somatomedin C) (IGF1), DNA sequence.
PN WO2003072827-A1.

PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 2.7%; Score 66.6; DB 11; Length 7260;
Best Local Similarity 88.9%; Pred. No. 7.5e-07;
RESULT 1092
ID ABD32850 standard; cDNA; 7476 BP.
DE Human cancer-associated cDNA HRI7-016.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.6; DB 13; Length 7476;
Best Local Similarity 88.9%; Pred. No. 7.6e-07;
RESULT 1093
ID AAS42100 standard; DNA; 12595 BP.
DE Genomic sequence #416 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.6; DB 4; Length 12595;
Best Local Similarity 88.9%; Pred. No. 1e-06;
RESULT 1094
ID ACN44670 standard; DNA; 22021 BP.
DE Human genomic sequence hCG20786.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.6; DB 11; Length 22021;
Best Local Similarity 88.9%; Pred. No. 1.4e-06;
RESULT 1095
ID AAK78286 standard; DNA; 28420 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33098.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.6; DB 4; Length 28420;
Best Local Similarity 88.9%; Pred. No. 1.6e-06;
RESULT 1096
ID ACN44954 standard; DNA; 31116 BP.
DE Human genomic sequence hCG38622.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.6; DB 11; Length 31116;
Best Local Similarity 88.9%; Pred. No. 1.7e-06;
RESULT 1097
ID ABK13076 standard; DNA; 35973 BP.
DE Human amyloid beta precursor protein binding protein 1 gene.
PN WO200202820-A1.
PD 10-JAN-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 2.7%; Score 66.6; DB 6; Length 35973;
Best Local Similarity 88.9%; Pred. No. 1.8e-06;
RESULT 1098
ID AAS96607 standard; DNA; 51552 BP.
DE DNA encoding human telomerase reverse transcriptase (TERT) #1.
PN WO200188198-A1.
PD 22-NOV-2001.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 66.6; DB 6; Length 51552;
Best Local Similarity 88.9%; Pred. No. 2.2e-06;
RESULT 1099
ID ADA02540 standard; DNA; 58822 BP.
DE Human TCOP1 carcinoma associated gene, SEQ ID NO:1058.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.6; DB 9; Length 58822;
Best Local Similarity 88.9%; Pred. No. 2.4e-06;
RESULT 1100
ID ADB72278 standard; DNA; 58822 BP.
DE Human TCOP1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 2.7%; Score 66.6; DB 10; Length 58822;
 Best Local Similarity 88.9%; Pred. No. 2.4e-06;
 RESULT 1101
 ID AD95788 standard; DNA; 58822 BP.
 DE Human TCOF1 gene genomic DNA sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 2.7%; Score 66.6; DB 10; Length 58822;
 Best Local Similarity 88.9%; Pred. No. 2.4e-06;
 RESULT 1102
 ID AB033260 standard; DNA; 59748 BP.
 DE Human cancer-associated (CA) gene HD07-044.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.7%; Score 66.6; DB 13; Length 59748;
 Best Local Similarity 88.9%; Pred. No. 2.4e-06;
 RESULT 1103
 ID AB032848 standard; DNA; 104900 BP.
 DE Human cancer-associated genomic DNA HD17-016.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.7%; Score 66.6; DB 13; Length 104900;
 Best Local Similarity 88.9%; Pred. No. 3.3e-06;
 RESULT 1104
 ID AAF94800 standard; DNA; 110000 BP.
 DE Nucleotide sequence of the human SPG4 gene.
 PN FR2798138-A1.
 PD 09-MAR-2001.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 2.7%; Score 66.6; DB 5; Length 110000;
 Best Local Similarity 88.9%; Pred. No. 3.4e-06;
 RESULT 1105
 ID ABD32817 standard; DNA; 156416 BP.
 DE Human cancer-associated genomic DNA HD17-001.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.7%; Score 66.6; DB 13; Length 156416;
 Best Local Similarity 84.3%; Pred. No. 4.1e-06;
 RESULT 1106
 ID AAK87645 standard; DNA; 86 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42457.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 66.4; DB 4; Length 86;
 Best Local Similarity 92.1%; Pred. No. 7.3e-08;
 RESULT 1107
 ID AAC12861 standard; cDNA; 163 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 16936.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match 2.7%; Score 66.4; DB 3; Length 163;
 Best Local Similarity 87.5%; Pred. No. 1e-07;
 RESULT 1108
 ID ABZ71832 standard; cDNA; 452 BP.
 DE Human cancer-associated gene SEQ ID NO 139.
 PN WO200283899-A1.
 PD 24-OCT-2002.
 PA (TAKA-) TAKARA BIO INC.
 Query Match 2.7%; Score 66.4; DB 8; Length 452;
 Best Local Similarity 79.0%; Pred. No. 1.8e-07;
 RESULT 1109
 ID ACH50650 standard; cDNA; 491 BP.
 DE Human mammary gland cDNA #55.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.
 (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.7%; Score 66.4; DB 9; Length 491;
 Best Local Similarity 71.0%; Pred. No. 1.9e-07;
 RESULT 1110
 ID RAH18185 standard; cDNA; 3441 BP.
 DE Human cDNA sequence SEQ ID NO:18094.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 2.7%; Score 66.4; DB 4; Length 3441;
 Best Local Similarity 71.0%; Pred. No. 5.6e-07;
 RESULT 1111
 ID ABK42275 standard; DNA; 5629 BP.
 DE Genomic sequence #174 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 66.4; DB 4; Length 5629;
 Best Local Similarity 71.0%; Pred. No. 7.4e-07;
 RESULT 1112
 ID ADB60431 standard; DNA; 5629 BP.
 DE Connective tissue related genomic DNA #174.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 66.4; DB 9; Length 5629;
 Best Local Similarity 71.0%; Pred. No. 7.4e-07;
 RESULT 1113
 ID ABK42274 standard; DNA; 6265 BP.
 DE Genomic sequence #173 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 66.4; DB 4; Length 6265;
 Best Local Similarity 71.0%; Pred. No. 7.9e-07;
 RESULT 1114
 ID ADB60430 standard; DNA; 6265 BP.
 DE Connective tissue related genomic DNA #173.
 PN US2003054375-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 66.4; DB 9; Length 6265;
 Best Local Similarity 71.0%; Pred. No. 7.9e-07;
 RESULT 1115
 ID AAF29338 standard; DNA; 8942 BP.
 DE Atopy related gene sequence SEQ ID 2.
 PN WO200104302-A1.
 PD 18-JAN-2001.
 PA (MITU) MITSUBISHI CHEM CORP.
 Query Match 2.7%; Score 66.4; DB 5; Length 8942;
 Best Local Similarity 87.5%; Pred. No. 9.6e-07;
 RESULT 1116
 ID ABQ73765 standard; cDNA; 9883 BP.
 DE Human colon specific nucleic acid (CSNA) SEQ ID NO:71.
 PN WO200248370-A2.
 PD 20-JUN-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 2.7%; Score 66.4; DB 6; Length 9883;
 Best Local Similarity 74.2%; Pred. No. 1e-06;
 RESULT 1117
 ID AAK69531 standard; DNA; 10989 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24343.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 66.4; DB 4; Length 10989;
 Best Local Similarity 86.9%; Pred. No. 1.1e-06;
 RESULT 1118
 ID AAK64938 standard; DNA; 19183 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19750.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.4; DB 4; Length 19183;
Best Local Similarity 79.0%; Pred. No. 1.5e-06;
RESULT 1119
ID AAL36434 standard; DNA; 19183 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2799.
PN WO200153367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.4; DB 4; Length 19183;
Best Local Similarity 79.0%; Pred. No. 1.5e-06;
RESULT 1120
ID ABX59422 standard; cDNA; 19183 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1766.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 66.4; DB 8; Length 19183;
Best Local Similarity 79.0%; Pred. No. 1.5e-06;
RESULT 1121
ID ADJ30172 standard; DNA; 19183 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2799.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.4; DB 12; Length 19183;
Best Local Similarity 79.0%; Pred. No. 1.5e-06;
RESULT 1122
ID ABZ76729 standard; DNA; 19969 BP.
DE Human lactadherin related secreted protein encoding DNA SEQ ID NO:3.
PN WO2003006485-A2.
PD 23-JAN-2003.
PA (APPL-) APPLERA CORP.
Query Match 2.7%; Score 66.4; DB 8; Length 19969;
Best Local Similarity 92.1%; Pred. No. 1.5e-06;
RESULT 1123
ID ACN44094 standard; DNA; 35236 BP.
DE Human genomic sequence hCG23314.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.4; DB 11; Length 35236;
Best Local Similarity 92.1%; Pred. No. 2e-06;
RESULT 1124
ID ACN44270 standard; DNA; 46404 BP.
DE Human genomic sequence hCG37971.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.4; DB 11; Length 46404;
Best Local Similarity 79.0%; Pred. No. 2.4e-06;
RESULT 1125
ID AAD02697 standard; DNA; 160552 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (REGC-) UNIV CALIFORNIA.
Query Match 2.7%; Score 66.4; DB 4; Length 160552;
Best Local Similarity 79.0%; Pred. No. 4.8e-06;
RESULT 1126
ID ABD33462 standard; DNA; 196063 BP.
DE Human cancer-associated (CA) gene HD07-088.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.4; DB 13; Length 196063;
Best Local Similarity 79.0%; Pred. No. 5.3e-06;
RESULT 1127
ID AAK74780 standard; DNA; 138 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29592.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 138;
Best Local Similarity 89.9%; Pred. No. 1.1e-07;
RESULT 1128
ID ADN41724 standard; DNA; 146 BP.
DE Novel human secreted protein polynucleotide seqid 846.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAPL/) LAPLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 2.7%; Score 66.2; DB 12; Length 146;
Best Local Similarity 89.9%; Pred. No. 1.1e-07;
RESULT 1129
ID ADN41721 standard; DNA; 146 BP.
DE Novel human secreted protein polynucleotide seqid 843.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAPL/) LAPLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 2.7%; Score 66.2; DB 12; Length 146;
Best Local Similarity 89.9%; Pred. No. 1.1e-07;
RESULT 1130
ID ADN41722 standard; DNA; 146 BP.
DE Novel human secreted protein polynucleotide seqid 844.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAPL/) LAPLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 2.7%; Score 66.2; DB 12; Length 146;
Best Local Similarity 89.9%; Pred. No. 1.1e-07;
RESULT 1131
ID AAK95774 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNPB8RG680660.
PN WO200164876-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 4; Length 401;

Wed May 11 07:24:22 2005

us-09-978-544a-58.rng.spddi

```
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1132
ID AAK95773 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG680652.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 4; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1133
ID AAK97266 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG680652.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 4; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1134
ID AAK97267 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG680660.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 4; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1135
ID ABT00543 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 572.
PN US2002045577-A1.
PD 18-APR-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 6; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1136
ID ABT00544 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 573.
PN US2002045577-A1.
PD 18-APR-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 6; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1137
ID ABT02037 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 573.
PN US2002094954-A1.
PD 18-JUL-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 6; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1138
ID ABT02036 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 572.
PN US2002094954-A1.
PD 18-JUL-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 6; Length 401;
Best Local Similarity 72.2%; Pred. No. 1.9e-07;
RESULT 1139
ID AA181619 standard; cDNA; 404 BP.
DE Human polynucleotide SEQ ID NO 1679.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 66.2; DB 4; Length 404;
Best Local Similarity 85.1%; Pred. No. 1.9e-07;
RESULT 1140
ID AAK96627 standard; DNA; 426 BP.
DE Human neuregulin gene insertion/deletion DNP8NRG49.
PN WO200164876-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 4; Length 426;
Best Local Similarity 72.2%; Pred. No. 2e-07;
RESULT 1141
ID AAK98120 standard; DNA; 426 BP.
DE Human neuregulin gene insertion/deletion DNP8NRG49.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 4; Length 426;
Best Local Similarity 72.2%; Pred. No. 2e-07;
RESULT 1142
ID ABT01397 standard; DNA; 426 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 1426.
PN US2002045577-A1.
PD 18-APR-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 6; Length 426;
Best Local Similarity 72.2%; Pred. No. 2e-07;
RESULT 1143
ID APT02890 standard; DNA; 426 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 1426.
PN US2002094954-A1.
PD 18-JUL-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 6; Length 426;
Best Local Similarity 72.2%; Pred. No. 2e-07;
RESULT 1144
ID ADH77652 standard; DNA; 426 BP.
DE Human neuregulin gene insertion/deletion region #52.
PN US2002165144-A1.
PD 07-NOV-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.7%; Score 66.2; DB 12; Length 426;
Best Local Similarity 72.2%; Pred. No. 2e-07;
RESULT 1145
ID ACH26075 standard; cDNA; 471 BP.
DE Human adult ovary cDNA #4455.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.7%; Score 66.2; DB 9; Length 471;
Best Local Similarity 89.9%; Pred. No. 2.1e-07;
RESULT 1146
ID ACH40021 standard; cDNA; 475 BP.
DE Human foetal brain cDNA #1388.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.7%; Score 66.2; DB 9; Length 475;
Best Local Similarity 89.9%; Pred. No. 2.1e-07;
RESULT 1147
ID ACH40222 standard; cDNA; 543 BP.
DE Human foetal brain cDNA #1589.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.7%; Score 66.2; DB 9; Length 543;
Best Local Similarity 89.9%; Pred. No. 2.3e-07;
RESULT 1148
ID AAH10353 standard; cDNA; 544 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7188.
PN EP1074617-A2.
PD 07-FEB-2001.
```


PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 66.2; DB 4; Length 544;
Best Local Similarity 89.9%; Pred. No. 2.3e-07;
RESULT 1149
ID ABX61812 standard; DNA; 601 BP.
DE Novel human transporter protein related polynucleotide #8.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.7%; Score 66.2; DB 8; Length 601;
Best Local Similarity 89.9%; Pred. No. 2.4e-07;
RESULT 1150
ID ABX61811 standard; DNA; 601 BP.
DE Novel human transporter protein related polynucleotide #7.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.7%; Score 66.2; DB 8; Length 601;
Best Local Similarity 89.9%; Pred. No. 2.4e-07;
RESULT 1151
ID ABX61810 standard; DNA; 601 BP.
DE Novel human transporter protein related polynucleotide #6.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.7%; Score 66.2; DB 8; Length 601;
Best Local Similarity 89.9%; Pred. No. 2.4e-07;
RESULT 1152
ID AAH06411 standard; cDNA; 763 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:3246.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 66.2; DB 4; Length 763;
Best Local Similarity 88.8%; Pred. No. 2.8e-07;
RESULT 1153
ID AAC72064 standard; DNA; 792 BP.
DE Single nucleotide polymorphism containing sequence #631.
PN WO200058519-A2.
PD 05-OCT-2000.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (APFY-) AFFYMETRIX INC.
Query Match 2.7%; Score 66.2; DB 3; Length 792;
Best Local Similarity 87.7%; Pred. No. 2.8e-07;
RESULT 1154
ID ABV76349 standard; cDNA; 1157 BP.
DE Human signal peptidase motif-containing protein 9.68-encoding cDNA.
PN CN1351026-A.
PD 29-MAY-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 66.2; DB 6; Length 1157;
Best Local Similarity 89.9%; Pred. No. 3.5e-07;
RESULT 1155
ID AAH18715 standard; cDNA; 1602 BP.
DE Human cDNA sequence SEQ ID NO:18986.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 66.2; DB 4; Length 1602;
Best Local Similarity 89.9%; Pred. No. 4.2e-07;
RESULT 1156
ID AAH17499 standard; cDNA; 1679 BP.
DE Human cDNA sequence SEQ ID NO:16969.
PN EP1074617-A2.

PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 66.2; DB 4; Length 1679;
Best Local Similarity 89.9%; Pred. No. 4.3e-07;
RESULT 1157
ID ADQ85659 standard; cDNA; 2186 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2473.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.7%; Score 66.2; DB 12; Length 2186;
Best Local Similarity 89.9%; Pred. No. 5e-07;
RESULT 1158
ID ADQ86751 standard; cDNA; 2186 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3626.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.7%; Score 66.2; DB 12; Length 2186;
Best Local Similarity 89.9%; Pred. No. 5e-07;
RESULT 1159
ID ADQ84271 standard; cDNA; 2186 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1085.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.7%; Score 66.2; DB 13; Length 2186;
Best Local Similarity 89.9%; Pred. No. 5e-07;
RESULT 1160
ID AAH16324 standard; cDNA; 2368 BP.
DE Human cDNA sequence SEQ ID NO:15226.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 66.2; DB 4; Length 2368;
Best Local Similarity 89.9%; Pred. No. 5.2e-07;
RESULT 1161
ID ADF82145 standard; DNA; 2788 BP.
DE Leukaemia-related DNA sequence #2701.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 2.7%; Score 66.2; DB 10; Length 2788;
Best Local Similarity 89.9%; Pred. No. 5.7e-07;
RESULT 1162
ID ADA53356 standard; cDNA; 3206 BP.
DE Human coding sequence, SEQ ID 924.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 66.2; DB 10; Length 3206;
Best Local Similarity 81.1%; Pred. No. 6.2e-07;
RESULT 1163
ID ABV25122 standard; cDNA; 4870 BP.
DE Human prostate expression marker cDNA 25113.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 66.2; DB 5; Length 4870;
Best Local Similarity 89.9%; Pred. No. 7.8e-07;
RESULT 1164
ID AAK85164 standard; DNA; 5638 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39976.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 5638;
Best Local Similarity 89.9%; Pred. No. 8.4e-07;
RESULT 1165
ID AAS42158 standard; DNA; 7712 BP.
DE Genomic sequence #474 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 7712;
Best Local Similarity 89.9%; Pred. No. 1e-06;
RESULT 1166
ID AAS42157 standard; DNA; 7715 BP.
DE Genomic sequence #473 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 7715;
Best Local Similarity 89.9%; Pred. No. 1e-06;
RESULT 1167
ID AAK82834 standard; DNA; 8789 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37646.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 8789;
Best Local Similarity 89.9%; Pred. No. 1.1e-06;
RESULT 1168
ID AAS42155 standard; DNA; 9544 BP.
DE Genomic sequence #471 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 9544;
Best Local Similarity 89.9%; Pred. No. 1.1e-06;
RESULT 1169
ID AAK86473 standard; DNA; 13418 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41285.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 13418;
Best Local Similarity 89.9%; Pred. No. 1.4e-06;
RESULT 1170
ID ACN44886 standard; DNA; 26332 BP.
DE Human genomic sequence hCG39434.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.2; DB 11; Length 26332;
Best Local Similarity 89.9%; Pred. No. 2e-06;
RESULT 1171
ID AAL05917 standard; DNA; 32169 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8605.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 32169;
Best Local Similarity 89.9%; Pred. No. 2.2e-06;
RESULT 1172
ID ABJ98481 standard; DNA; 32169 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3133.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 32169;
Best Local Similarity 89.9%; Pred. No. 2.2e-06;
RESULT 1173
ID ABA19573 standard; DNA; 32169 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11904.

PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 5; Length 32169;
Best Local Similarity 89.9%; Pred. No. 2.2e-06;
RESULT 1174
ID AAL05916 standard; DNA; 32189 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8604.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 32189;
Best Local Similarity 89.9%; Pred. No. 2.2e-06;
RESULT 1175
ID ABL98480 standard; DNA; 32189 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3132.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 32189;
Best Local Similarity 89.9%; Pred. No. 2.2e-06;
RESULT 1176
ID ABA19572 standard; DNA; 32189 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11903.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 5; Length 32189;
Best Local Similarity 89.9%; Pred. No. 2.2e-06;
RESULT 1177
ID ABD32700 standard; DNA; 33362 BP.
DE Human cancer-associated genomic DNA HD14-035.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.2; DB 13; Length 33362;
Best Local Similarity 89.9%; Pred. No. 2.3e-06;
RESULT 1178
ID AAK69257 standard; DNA; 33971 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24069.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66.2; DB 4; Length 33971;
Best Local Similarity 89.9%; Pred. No. 2.3e-06;
RESULT 1179
ID ABX61804 standard; DNA; 40645 BP.
DE Genomic DNA encoding novel human GABA transporter related protein.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.7%; Score 66.2; DB 8; Length 40645;
Best Local Similarity 89.9%; Pred. No. 2.5e-06;
RESULT 1180
ID ADA49717 standard; DNA; 40645 BP.
DE Genomic DNA encoding human transporter protein.
Query Match 2.7%; Score 66.2; DB 9; Length 40645;
Best Local Similarity 89.9%; Pred. No. 2.5e-06;
RESULT 1181
ID ACN44478 standard; DNA; 54701 BP.
DE Human genomic sequence hCG24071.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 66.2; DB 11; Length 54701;
Best Local Similarity 89.9%; Pred. No. 3e-06;
RESULT 1182
ID ABS57150 standard; DNA; 63588 BP.
DE Human gene encoding a serine/threonine kinase.
Query Match 2.7%; Score 66.2; DB 8; Length 63588;

Best Local Similarity 89.9%; Pred. No. 3.2e-06;
RESULT 1183
ID AAD42934 standard; DNA; 70000 BP.
DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.
PN US6410325-B1.
PD 25-JUN-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.7%; Score 66.2; DB 6; Length 70000;
Best Local Similarity 89.9%; Pred. No. 3.4e-06;
RESULT 1184
ID ADQ19270 standard; DNA; 93443 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2089.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 66.2; DB 12; Length 93443;
Best Local Similarity 81.1%; Pred. No. 4e-06;
RESULT 1185
Query Match 2.7%; Score 66.2; DB 4; Length 110000;
Best Local Similarity 72.2%; Pred. No. 4.4e-06;
RESULT 1186
Query Match 2.7%; Score 66.2; DB 4; Length 110000;
Best Local Similarity 72.2%; Pred. No. 4.4e-06;
RESULT 1187
Query Match 2.7%; Score 66.2; DB 6; Length 110000;
Best Local Similarity 72.2%; Pred. No. 4.4e-06;
RESULT 1188
Query Match 2.7%; Score 66.2; DB 6; Length 110000;
Best Local Similarity 72.2%; Pred. No. 4.4e-06;
RESULT 1189
Query Match 2.7%; Score 66.2; DB 12; Length 110000;
Best Local Similarity 72.2%; Pred. No. 4.4e-06;
RESULT 1190
ID ABD32998 standard; DNA; 113079 BP.
DE Human cancer-associated genomic DNA HD21-021.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.2; DB 13; Length 113079;
Best Local Similarity 89.9%; Pred. No. 4.4e-06;
RESULT 1191
ID ADE43582 standard; DNA; 128034 BP.
DE Polymorphic human IDE genomic sequence, SEQ ID 187.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GHO) GEN HOSPITAL CORP.
Query Match 2.7%; Score 66.2; DB 10; Length 128034;
Best Local Similarity 81.1%; Pred. No. 4.8e-06;
RESULT 1192
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GHO) GEN HOSPITAL CORP.
Query Match 2.7%; Score 66.2; DB 10; Length 128034;
Best Local Similarity 81.1%; Pred. No. 4.8e-06;
RESULT 1193
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GHO) GEN HOSPITAL CORP.
Query Match 2.7%; Score 66.2; DB 12; Length 128034;
Best Local Similarity 81.1%; Pred. No. 4.8e-06;
RESULT 1194
ID ADH54060 standard; DNA; 128034 BP.
DE Human IDE gene variant DNA sequence SeqID187.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GHO) GEN HOSPITAL CORP.
Query Match 2.7%; Score 66.2; DB 12; Length 128034;

Best Local Similarity 81.1%; Pred. No. 4.8e-06;
RESULT 1195
ID ADQ19501 standard; DNA; 135005 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 66.2; DB 12; Length 135005;
Best Local Similarity 89.9%; Pred. No. 4.9e-06;
RESULT 1196
ID ADP65634 standard; DNA; 137908 BP.
DE Human sequence from clone 914P14 on chromosome Xq23 Contains DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 2.7%; Score 66.2; DB 11; Length 137908;
Best Local Similarity 85.1%; Pred. No. 5e-06;
RESULT 1197
ID ADB67054 standard; cDNA; 161280 BP.
DE Human lung tumour-specific related cDNA, SEQ ID No 746.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIAX CORP.
Query Match 2.7%; Score 66.2; DB 10; Length 161280;
Best Local Similarity 81.1%; Pred. No. 5.4e-06;
RESULT 1198
ID ADB88308 standard; cDNA; 161280 BP.
DE Human lung tumour antigen cDNA #640.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIAX CORP.
Query Match 2.7%; Score 66.2; DB 10; Length 161280;
Best Local Similarity 81.1%; Pred. No. 5.4e-06;
RESULT 1199
ID ACF62732 standard; DNA; 177531 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:660.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.7%; Score 66.2; DB 8; Length 177531;
Best Local Similarity 81.1%; Pred. No. 5.7e-06;
RESULT 1200
ID ADE20847 standard; DNA; 177531 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:660.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.7%; Score 66.2; DB 8; Length 177531;
Best Local Similarity 81.1%; Pred. No. 5.7e-06;
RESULT 1201
ID ADB87936 standard; DNA; 177531 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:660.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.7%; Score 66.2; DB 10; Length 177531;
Best Local Similarity 81.1%; Pred. No. 5.7e-06;
RESULT 1202
ID ADB96919 standard; DNA; 177531 BP.
DE Human MDRI related DNA sequence SEQ ID NO:660.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.7%; Score 66.2; DB 10; Length 177531;
Best Local Similarity 81.1%; Pred. No. 5.7e-06;
RESULT 1203
ID ADB92110 standard; DNA; 177531 BP.
DE Human MDRI related DNA sequence SEQ ID NO:660.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.7%; Score 66.2; DB 10; Length 177531;
Best Local Similarity 81.1%; Pred. No. 5.7e-06;

Wed May 11 07:24:22 2005

RESULT 1204
ID ADH74617 standard; DNA; 177531 BP.
DE Human BAC clone GSI-259H13 CYP3A5 genomic DNA.
PN US2003143537-A1.
PD 31-JUL-2003.
PA (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.
Query Match 2.7%; Score 66.2; DB 10; Length 177531;
Best Local Similarity 81.1%; Pred. No. 5.7e-06;
RESULT 1205
ID ADH13512 standard; DNA; 178870 BP.
DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 66.2; DB 10; Length 178870;
Best Local Similarity 89.9%; Pred. No. 5.7e-06;
RESULT 1206
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 2.7%; Score 66.2; DB 10; Length 202100;
Best Local Similarity 81.1%; Pred. No. 6.1e-06;
RESULT 1207
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 2.7%; Score 66.2; DB 12; Length 202100;
Best Local Similarity 81.1%; Pred. No. 6.1e-06;
RESULT 1208
ID ADQ18927 standard; DNA; 210204 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1746.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 66.2; DB 12; Length 210204;
Best Local Similarity 81.1%; Pred. No. 6.3e-06;
RESULT 1209
ID ADL13684 standard; DNA; 247509 BP.
DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 66.2; DB 10; Length 247509;
Best Local Similarity 89.9%; Pred. No. 6.9e-06;
RESULT 1210
ID ADQ97557 standard; DNA; 254396 BP.
DE Human cancer associated sequence HD09-013, SEQ ID 534.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.2; DB 12; Length 254396;
Best Local Similarity 89.9%; Pred. No. 7e-06;
RESULT 1211
ID ADF75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.7%; Score 66.2; DB 11; Length 304905;
Best Local Similarity 89.9%; Pred. No. 7.7e-06;
RESULT 1212
ID ABD32548 standard; DNA; 310268 BP.
DE Human cancer-associated genomic DNA HD14-033.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.2; DB 13; Length 310268;
Best Local Similarity 89.9%; Pred. No. 7.8e-06;

RESULT 1213
ID ABD33100 standard; DNA; 313287 BP.
DE Human cancer-associated (CA) gene HD07-008.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 66.2; DB 13; Length 313287;
Best Local Similarity 89.9%; Pred. No. 7.8e-06;
RESULT 1214
ID AAH16545 standard; cDNA; 2076 BP.
DE Human cDNA sequence SEQ ID NO:15602.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 66; DB 4; Length 2076;
Best Local Similarity 72.1%; Pred. No. 5.5e-07;
RESULT 1215
ID AAS73725 standard; cDNA; 3685 BP.
DE DNA encoding novel human diagnostic protein #9529.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 66; DB 5; Length 3685;
Best Local Similarity 87.8%; Pred. No. 7.5e-07;
RESULT 1216
ID AAK66109 standard; DNA; 11684 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20921.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 4; Length 11684;
Best Local Similarity 93.2%; Pred. No. 1.4e-06;
RESULT 1217
ID AAS36099 standard; DNA; 17792 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1599.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 4; Length 17792;
Best Local Similarity 79.6%; Pred. No. 1.8e-06;
RESULT 1218
ID AAS32727 standard; DNA; 17792 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 681.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 4; Length 17792;
Best Local Similarity 79.6%; Pred. No. 1.8e-06;
RESULT 1219
ID ADE46793 standard; DNA; 17792 BP.
DE Human cardiovascular system related genomic DNA #359.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 10; Length 17792;
Best Local Similarity 79.6%; Pred. No. 1.8e-06;
RESULT 1220
ID ADJ08211 standard; DNA; 17792 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1599.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 13; Length 17792;
Best Local Similarity 79.6%; Pred. No. 1.8e-06;
RESULT 1221
ID AAK72318 standard; DNA; 20245 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27130.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 4; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1222

ID ABK69845 standard; DNA; 20245 BP.
DE Human secreted protein gene 22 genomic DNA fragment #6.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 6; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1223
ID ACC50860 standard; cDNA; 20245 BP.
DE Human secreted protein BAC clone SEQ ID NO 1040.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 8; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1224
ID AB271482 standard; DNA; 20245 BP.
DE Secreted protein gene 12 genomic fragment HAU183, SEQ ID NO:592.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 8; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1225
ID ADB91838 standard; DNA; 20245 BP.
DE Human secreted protein related DNA #SEQ ID 784.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 9; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1226
ID ADC74613 standard; DNA; 20245 BP.
DE Human secreted protein-related DNA - SEQ ID 1246.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 10; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1227
ID ADD38133 standard; cDNA; 20245 BP.
DE cDNA clone in ATCC deposit #27.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 10; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1228
ID ADA57727 standard; DNA; 20245 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 66; DB 10; Length 20245;
Best Local Similarity 87.8%; Pred. No. 1.9e-06;
RESULT 1229
ID ABA82620 standard; DNA; 26928 BP.
DE Human HBM gene region b527d12-h_contig306G.
PN WO20017327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.7%; Score 66; DB 5; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1230
ID ABK22779 standard; cDNA; 26928 BP.
DE Human high bone mass (HBM) polynucleotide clone #2.
PN WO200192891-A2.
PD 06-DEC-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UVCN-) UNIV CREIGHTON SCHOOL MEDICINE.
Query Match 2.7%; Score 66; DB 6; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1231

ID ACC45361 standard; DNA; 26928 BP.
DE Human HBM gene fragment #2.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 2.7%; Score 66; DB 8; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1232
ID ADB98061 standard; DNA; 26928 BP.
DE HBM-related clone contig b527d12-h contig306G.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 2.7%; Score 66; DB 10; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1233
ID ADE82430 standard; DNA; 26928 BP.
DE Human DNA sequence related to the invention #2.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 2.7%; Score 66; DB 10; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1234
ID ADR16924 standard; DNA; 26928 BP.
DE BAC clone containing segments of the human Zmax1 gene #2.
PN US6780609-B1.
PD 24-AUG-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.7%; Score 66; DB 13; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1235
ID ADR47575 standard; DNA; 26928 BP.
DE BAC clone containing segments of the human Zmax1 gene #2.
PN US2004176582-A1.
PD 09-SEP-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (UVCN-) UNIV CREIGHTON.
Query Match 2.7%; Score 66; DB 13; Length 26928;
Best Local Similarity 76.4%; Pred. No. 2.3e-06;
RESULT 1236
ID AAF97846 standard; DNA; 51474 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:60.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 2.7%; Score 66; DB 5; Length 51474;
Best Local Similarity 72.1%; Pred. No. 3.3e-06;
RESULT 1237
ID AAK85881 standard; DNA; 173 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40693.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 173;
Best Local Similarity 90.9%; Pred. No. 1.6e-07;
RESULT 1238
ID AAK85883 standard; DNA; 225 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40695.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 225;
Best Local Similarity 90.9%; Pred. No. 1.8e-07;
RESULT 1239
ID ABK42566 standard; DNA; 290 BP.
DE Genomic sequence #465 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 290;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1240
ID ABK42567 standard; DNA; 290 BP.
DE Genomic sequence #466 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 290;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1241
ID ADB60723 standard; DNA; 290 BP.
DE Connective tissue related genomic DNA #466.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 9; Length 290;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1242
ID ADB60722 standard; DNA; 290 BP.
DE Connective tissue related genomic DNA #465.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 9; Length 290;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1243
ID ABK42569 standard; DNA; 291 BP.
DE Genomic sequence #468 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 291;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1244
ID ABK42568 standard; DNA; 291 BP.
DE Genomic sequence #467 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 291;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1245
ID ADB60725 standard; DNA; 291 BP.
DE Connective tissue related genomic DNA #468.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 9; Length 291;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1246
ID ADB60724 standard; DNA; 291 BP.
DE Connective tissue related genomic DNA #467.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 9; Length 291;
Best Local Similarity 85.9%; Pred. No. 2.1e-07;
RESULT 1247
ID AAK83966 standard; DNA; 883 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38778.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 883;
Best Local Similarity 85.9%; Pred. No. 3.9e-07;
RESULT 1248
ID AAS21879 standard; DNA; 1867 BP.
DE Human collagen gene COL9A1 5' UTR.
PN US6265157-B1.
PD 24-JUL-2001.
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.

PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
Query Match 2.7%; Score 65.8; DB 5; Length 1867;
Best Local Similarity 90.9%; Pred. No. 5.9e-07;
RESULT 1249
ID AAI61210 standard; cDNA; 1887 BP.
DE Human polynucleotide SEQ ID NO 5199.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSQ INC.
Query Match 2.7%; Score 65.8; DB 4; Length 1887;
Best Local Similarity 90.9%; Pred. No. 5.9e-07;
RESULT 1250
ID AAK74093 standard; DNA; 9333 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28905.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 9333;
Best Local Similarity 90.9%; Pred. No. 1.4e-06;
RESULT 1251
ID AAK67211 standard; DNA; 12026 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22023.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 12026;
Best Local Similarity 90.9%; Pred. No. 1.7e-06;
RESULT 1252
ID AAS21771 standard; DNA; 24183 BP.
DE Human gene for collagen COL9A1.
PN US6265157-B1.
PD 24-JUL-2001.
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
Query Match 2.7%; Score 65.8; DB 5; Length 24183;
Best Local Similarity 90.9%; Pred. No. 2.4e-06;
RESULT 1253
ID ACN43982 standard; DNA; 24898 BP.
DE Human genomic sequence hCG23625.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 65.8; DB 11; Length 24898;
Best Local Similarity 90.9%; Pred. No. 2.5e-06;
RESULT 1254
ID ABD33528 standard; DNA; 31926 BP.
DE Human cancer-associated (CA) gene HD07-104.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 65.8; DB 13; Length 31926;
Best Local Similarity 90.9%; Pred. No. 2.8e-06;
RESULT 1255
ID ADR67012 standard; DNA; 32229 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:58.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 65.8; DB 13; Length 32229;
Best Local Similarity 90.9%; Pred. No. 2.9e-06;
RESULT 1256
ID AAK64739 standard; DNA; 58708 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19551.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.8; DB 4; Length 58708;
Best Local Similarity 85.9%; Pred. No. 4e-06;
RESULT 1257
ID ACN45150 standard; DNA; 217409 BP.
DE Human genomic sequence hCG34092.

PN WO20003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 2.7%; Score 65.8; DB 11; Length 217409;
 Best Local Similarity 90.9%; Pred. No. 8.2e-06;
 RESULT 1258
 ID ADQ97557 standard; DNA; 254396 BP.
 DE Human cancer associated sequence HD09-013, SEQ ID 534.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.7%; Score 65.8; DB 12; Length 254396;
 Best Local Similarity 85.9%; Pred. No. 9e-06;
 RESULT 1259
 ID AAH51601 standard; DNA; 319608 BP.
 DE Human chromosome 13q31-q33 genomic nucleotide sequence.
 PN WO200058510-A2.
 PD 05-OCT-2000.
 PA (GSET) GENSET.
 Query Match 2.7%; Score 65.8; DB 3; Length 319608;
 Best Local Similarity 85.9%; Pred. No. 1e-05;
 RESULT 1260
 ID AAS09301 standard; DNA; 319608 BP.
 DE Human schizophrenia associated gene g35030 and biallelic markers AI-A71.
 Query Match 2.7%; Score 65.8; DB 5; Length 319608;
 Best Local Similarity 85.9%; Pred. No. 1e-05;
 RESULT 1261
 ID ABA15279 standard; DNA; 92 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7610.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 92;
 Best Local Similarity 88.8%; Pred. No. 1.3e-07;
 RESULT 1262
 ID ADA57641 standard; DNA; 101 BP.
 DE BAC fragment containing human secreted protein gene #49.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 10; Length 101;
 Best Local Similarity 88.8%; Pred. No. 1.3e-07;
 RESULT 1263
 ID AAK67159 standard; DNA; 109 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21971.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 109;
 Best Local Similarity 88.8%; Pred. No. 1.4e-07;
 RESULT 1264
 ID AAK67355 standard; DNA; 109 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22167.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 109;
 Best Local Similarity 88.8%; Pred. No. 1.4e-07;
 RESULT 1265
 ID AAC15312 standard; cDNA; 124 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 19387.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GSET) GENSET.
 Query Match 2.7%; Score 65.6; DB 3; Length 124;
 Best Local Similarity 88.8%; Pred. No. 1.5e-07;
 RESULT 1266
 ID AAK86351 standard; DNA; 128 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41163.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 128;

Best Local Similarity 88.8%; Pred. No. 1.5e-07;
 RESULT 1267
 ID AAK85587 standard; DNA; 132 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40399.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 132;
 Best Local Similarity 88.8%; Pred. No. 1.5e-07;
 RESULT 1268
 ID AAK85588 standard; DNA; 132 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40400.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 132;
 Best Local Similarity 88.8%; Pred. No. 1.5e-07;
 RESULT 1269
 ID AAK80586 standard; DNA; 142 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35398.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 142;
 Best Local Similarity 88.8%; Pred. No. 1.6e-07;
 RESULT 1270
 ID AAS32528 standard; DNA; 145 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 482.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 145;
 Best Local Similarity 88.8%; Pred. No. 1.6e-07;
 RESULT 1271
 ID ABA17343 standard; DNA; 151 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 9674.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 151;
 Best Local Similarity 88.8%; Pred. No. 1.7e-07;
 RESULT 1272
 ID AAK90410 standard; DNA; 152 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3986.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 152;
 Best Local Similarity 88.8%; Pred. No. 1.7e-07;
 RESULT 1273
 ID AAS33446 standard; DNA; 152 BP.
 DE DNA encoding human secreted protein, Seq ID NO 729.
 PN WO200155326-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 152;
 Best Local Similarity 88.8%; Pred. No. 1.7e-07;
 RESULT 1274
 ID AAL05193 standard; DNA; 152 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7881.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 152;
 Best Local Similarity 88.8%; Pred. No. 1.7e-07;
 RESULT 1275
 ID ABL98078 standard; DNA; 152 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2730.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 152;
 Best Local Similarity 88.8%; Pred. No. 1.7e-07;

RESULT 1276
ID AAS39966 standard; DNA; 152 BP.
DE Genomic sequence #385 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 152;
Best Local Similarity 88.8%; Pred. No. 1.7e-07;
RESULT 1277
ID ADB32926 standard; DNA; 152 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 863.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 65.6; DB 9; Length 152;
Best Local Similarity 88.8%; Pred. No. 1.7e-07;
RESULT 1278
ID AAK67885 standard; DNA; 156 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22697.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 156;
Best Local Similarity 88.8%; Pred. No. 1.7e-07;
RESULT 1279
ID AAC21709 standard; cDNA; 180 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 25784.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (G8ST) GENSET.
Query Match 2.7%; Score 65.6; DB 3; Length 180;
Best Local Similarity 88.8%; Pred. No. 1.8e-07;
RESULT 1280
ID AAK70933 standard; DNA; 187 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25745.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 187;
Best Local Similarity 88.8%; Pred. No. 1.9e-07;
RESULT 1281
ID AAS28218 standard; DNA; 251 BP.
DE Genomic sequence #58 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 251;
Best Local Similarity 88.8%; Pred. No. 2.2e-07;
RESULT 1282
ID ADG41414 standard; DNA; 251 BP.
DE Human respiratory system associated genomic DNA seq id 652.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 251;
Best Local Similarity 88.8%; Pred. No. 2.2e-07;
RESULT 1283
ID AD197188 standard; DNA; 251 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID652.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 11; Length 251;
Best Local Similarity 88.8%; Pred. No. 2.2e-07;
RESULT 1284
ID AAK65636 standard; DNA; 262 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20448.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 262;

Best Local Similarity 88.8%; Pred. No. 2.2e-07;
RESULT 1285
ID AAK74855 standard; DNA; 265 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29667.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 265;
Best Local Similarity 88.8%; Pred. No. 2.3e-07;
RESULT 1286
ID AAK70645 standard; DNA; 278 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25457.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 278;
Best Local Similarity 88.8%; Pred. No. 2.3e-07;
RESULT 1287
ID AAO63862 standard; cDNA; 283 BP.
DE AP2 sequence obt'd. by PCR for tumour specific DNA.
PN WO9411531-A1.
PD 26-MAY-1994.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
Query Match 2.7%; Score 65.6; DB 2; Length 283;
Best Local Similarity 88.8%; Pred. No. 2.3e-07;
RESULT 1288
ID ADB97627 standard; DNA; 283 BP.
DE APdelta2 DNA fragment #2.
PN US6566053-B1.
PD 20-MAY-2003.
PA (STRA-) STRATAGENE.
Query Match 2.7%; Score 65.6; DB 9; Length 283;
Best Local Similarity 88.8%; Pred. No. 2.3e-07;
RESULT 1289
ID ADO04061 standard; DNA; 283 BP.
DE Human AP-PCR gene fragment (APdelta2) #2.
PN US2004091889-A1.
PD 13-MAY-2004.
PA (STRA-) STRATAGENE.
Query Match 2.7%; Score 65.6; DB 12; Length 283;
Best Local Similarity 88.8%; Pred. No. 2.3e-07;
RESULT 1290
ID AAS35966 standard; DNA; 290 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1466.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 290;
Best Local Similarity 88.8%; Pred. No. 2.4e-07;
RESULT 1291
ID ADE46660 standard; DNA; 290 BP.
DE Human cardiovascular system related genomic DNA #226.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 290;
Best Local Similarity 88.8%; Pred. No. 2.4e-07;
RESULT 1292
ID ADJ08078 standard; DNA; 290 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1466.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 13; Length 290;
Best Local Similarity 88.8%; Pred. No. 2.4e-07;
RESULT 1293
ID ABA18165 standard; DNA; 302 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10496.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 302;
Best Local Similarity 88.8%; Pred. No. 2.4e-07;

RESULT 1294
 ID ABL77338 standard; cDNA; 307 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:316.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 6; Length 307;
 Best Local Similarity 88.8%; Pred. No. 2.4e-07;
 RESULT 1295
 ID AAF17603 standard; cDNA; 308 BP.
 DE Human breast cancer associated 13053 coding sequence.
 PN WO200060076-A2.
 PD 12-OCT-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 4; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1296
 ID AAS47033 standard; cDNA; 308 BP.
 DE Human breast cancer cDNA clone 13053.
 PN WO200179286-A2.
 PD 25-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 4; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1297
 ID ABA18098 standard; DNA; 308 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 10429.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1298
 ID ABK95068 standard; cDNA; 308 BP.
 DE Human breast tumour cDNA 13053.
 PN US6387697-B1.
 PD 14-MAY-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 6; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1299
 ID ABT08688 standard; cDNA; 308 BP.
 DE Human breast antigen-related nucleotide #87.
 PN US2002102602-A1.
 PD 01-AUG-2002.
 PA (YUQI-) YUQIU J.
 PA (DILL-) DILLON D C.
 PA (MITC-) MITCHAM J L.
 PA (XUJJ-) XU J.
 Query Match 2.7%; Score 65.6; DB 6; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1300
 ID ABS63634 standard; cDNA; 308 BP.
 DE Human breast tumour polynucleotide #87.
 PN US2002085998-A1.
 PD 04-JUL-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 6; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1301
 ID ABT32846 standard; DNA; 308 BP.
 DE Human tumour-related DNA sequence - SEQ ID No 88.
 PN WO200283956-A1.
 PD 24-OCT-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 10; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1302
 ID ADL92750 standard; cDNA; 308 BP.
 DE Human breast cancer-associated polypeptide cDNA #87.
 PN US2003166022-A1.
 PD 04-SEP-2003.
 PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 65.6; DB 11; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1303
 ID ADE44040 standard; cDNA; 308 BP.
 DE Human cDNA associated with breast cancer #87.
 PN US2003104366-A1.
 PD 05-JUN-2003.
 PA (JIAN-) JIANG Y.
 PA (DILL-) DILLON D C.
 PA (MITC-) MITCHAM J L.
 PA (XUJJ-) XU J.
 PA (HARL-) HARLOCKER S L.
 Query Match 2.7%; Score 65.6; DB 12; Length 308;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1304
 ID AAK77558 standard; DNA; 309 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32370.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 309;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1305
 ID AD173224 standard; DNA; 316 BP.
 DE Human ovarian cancer DNA marker #5966.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 316;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1306
 ID ADL38356 standard; DNA; 316 BP.
 DE Human ovarian cancer DNA marker #12246.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 316;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1307
 ID ABA14683 standard; DNA; 321 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7014.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 321;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1308
 ID ABA19007 standard; DNA; 321 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11338.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 321;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1309
 ID ABA14684 standard; DNA; 321 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 7015.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 321;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1310
 ID ABA19008 standard; DNA; 321 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11339.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 321;
 Best Local Similarity 88.8%; Pred. No. 2.5e-07;
 RESULT 1311
 ID ABA19006 standard; DNA; 336 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11337.

PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 336;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1312
ID ABZ73926 standard; DNA; 336 BP.
DE Secreted protein gene 105 genomic fragment HB8SG96, SEQ ID NO:1073.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 336;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1313
ID ADC20676 standard; DNA; 336 BP.
DE Human secreted protein-related DNA sequence #94.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 336;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1314
ID ABZ67514 standard; DNA; 336 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1037.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 336;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1315
ID ABL77353 standard; cDNA; 337 BP.
DE Human ovarian cancer related CDNA clone SEQ ID NO:331.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 65.6; DB 6; Length 337;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1316
ID AAC32285 standard; cDNA; 340 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 36360.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.7%; Score 65.6; DB 3; Length 340;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1317
ID AAK65488 standard; DNA; 340 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20300.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 340;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1318
ID AAK65487 standard; DNA; 340 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20299.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 340;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1319
ID AAS35760 standard; DNA; 347 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1260.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1320
ID AAS35765 standard; DNA; 347 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1265.
PN WO200155321-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1321
ID AAS35761 standard; DNA; 347 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1261.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1322
ID ADE46454 standard; DNA; 347 BP.
DE Human cardiovascular system related genomic DNA #20.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1323
ID ADE46459 standard; DNA; 347 BP.
DE Human cardiovascular system related genomic DNA #25.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1324
ID ADE46455 standard; DNA; 347 BP.
DE Human cardiovascular system related genomic DNA #21.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1325
ID ADJ07873 standard; DNA; 347 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1261.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 13; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1326
ID ADJ07877 standard; DNA; 347 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1265.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 13; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1327
ID ADJ07872 standard; DNA; 347 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1260.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 13; Length 347;
Best Local Similarity 88.8%; Pred. No. 2.6e-07;
RESULT 1328
ID ABL4843 standard; cDNA; 390 BP.
DE Human ovarian cancer related CDNA clone SEQ ID NO:7821.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.7%; Score 65.6; DB 6; Length 390;
Best Local Similarity 88.8%; Pred. No. 2.8e-07;
RESULT 1329
ID ADL44740 standard; DNA; 394 BP.
DE Human ovarian cancer DNA marker #18630.
PN WO200170979-A2.
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 394;
 Best Local Similarity 88.8%; Pred. No. 2.8e-07;
 RESULT 1330
 ID AAI94018 standard; cDNA; 395 BP.
 DE Human polynucleotide SEQ ID NO 4078.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 395;
 Best Local Similarity 88.8%; Pred. No. 2.8e-07;
 RESULT 1331
 ID ACH17123 standard; cDNA; 426 BP.
 DE Human adult heart cDNA #1437.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.7%; Score 65.6; DB 9; Length 426;
 Best Local Similarity 88.8%; Pred. No. 2.9e-07;
 RESULT 1332
 ID AAH08498 standard; cDNA; 431 BP.
 DE Human cDNA clone (5'-primer) SEQ ID NO:5333.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 2.7%; Score 65.6; DB 4; Length 431;
 Best Local Similarity 88.8%; Pred. No. 3e-07;
 RESULT 1333
 ID ABL77343 standard; cDNA; 439 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:321.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 6; Length 439;
 Best Local Similarity 88.8%; Pred. No. 3e-07;
 RESULT 1334
 ID ACH47464 standard; cDNA; 458 BP.
 DE Human infant brain cDNA #1527.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.7%; Score 65.6; DB 9; Length 458;
 Best Local Similarity 88.8%; Pred. No. 3.1e-07;
 RESULT 1335
 ID ABV45845 standard; cDNA; 463 BP.
 DE Human prostate expression marker cDNA 45836.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 463;
 Best Local Similarity 88.8%; Pred. No. 3.1e-07;
 RESULT 1336
 ID ACH23761 standard; cDNA; 474 BP.
 DE Human adult ovary cDNA #2141.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.7%; Score 65.6; DB 9; Length 474;
 Best Local Similarity 88.8%; Pred. No. 3.1e-07;
 RESULT 1337
 ID ABV49100 standard; cDNA; 475 BP.

DE Human prostate expression marker cDNA 49091.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 475;
 Best Local Similarity 88.8%; Pred. No. 3.1e-07;
 RESULT 1338
 ID ACH23575 standard; cDNA; 481 BP.
 DE Human adult ovary cDNA #1955.
 PN US2003073623-A1.
 PD 17-APR-2003.
 PA (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 Query Match 2.7%; Score 65.6; DB 9; Length 481;
 Best Local Similarity 88.8%; Pred. No. 3.1e-07;
 RESULT 1339
 ID ABV38047 standard; cDNA; 485 BP.
 DE Human prostate expression marker cDNA 38038.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 485;
 Best Local Similarity 88.8%; Pred. No. 3.2e-07;
 RESULT 1340
 ID ABV50171 standard; cDNA; 494 BP.
 DE Human prostate expression marker cDNA 50162.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 5; Length 494;
 Best Local Similarity 88.8%; Pred. No. 3.2e-07;
 RESULT 1341
 ID ABL77725 standard; cDNA; 495 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:703.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 2.7%; Score 65.6; DB 6; Length 495;
 Best Local Similarity 88.8%; Pred. No. 3.2e-07;
 RESULT 1342
 ID ACN92171 standard; DNA; 503 BP.
 DE Breast cancer related marker, seq id 13321.
 PN US200309974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 2.7%; Score 65.6; DB 11; Length 503;
 Best Local Similarity 88.8%; Pred. No. 3.2e-07;
 RESULT 1343
 ID AAL15384 standard; cDNA; 515 BP.
 DE Human breast cancer expressed polynucleotide 7841.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 515;
 Best Local Similarity 88.8%; Pred. No. 3.3e-07;
 RESULT 1344
 ID AAL24230 standard; cDNA; 515 BP.
 DE Human breast cancer expressed polynucleotide 16687.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.7%; Score 65.6; DB 4; Length 515;
 Best Local Similarity 88.8%; Pred. No. 3.3e-07;
 RESULT 1345
 ID ABN65221 standard; cDNA; 525 BP.
 DE Human cancer related polynucleotide SEQ ID NO 5188.
 PN WO200214500-A2.
 PD 21-FEB-2002.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.


```
Query Match      2.7%; Score 65.6; DB 6; Length 525;
Best Local Similarity 88.8%; Pred. No. 3.3e-07;
RESULT 1346
ID ACH45689 standard; cDNA; 526 BP.
DE Human foetal brain cDNA #6414.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match      2.7%; Score 65.6; DB 9; Length 526;
Best Local Similarity 88.8%; Pred. No. 3.3e-07;
RESULT 1347
ID AAH71264 standard; cDNA; 532 BP.
DE Human cervical cancer marker nucleic acid 2538.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      2.7%; Score 65.6; DB 4; Length 532;
Best Local Similarity 88.8%; Pred. No. 3.3e-07;
RESULT 1348
ID AAK80661 standard; DNA; 535 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35473.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      2.7%; Score 65.6; DB 4; Length 535;
Best Local Similarity 88.8%; Pred. No. 3.3e-07;
RESULT 1349
ID AAH13272 standard; cDNA; 539 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:10107.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match      2.7%; Score 65.6; DB 4; Length 539;
Best Local Similarity 88.8%; Pred. No. 3.3e-07;
RESULT 1350
ID AAH09165 standard; cDNA; 548 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6000.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match      2.7%; Score 65.6; DB 4; Length 548;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1351
ID ABV57130 standard; cDNA; 561 BP.
DE Human prostate expression marker cDNA 57121.
PN WO200160860-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      2.7%; Score 65.6; DB 5; Length 561;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1352
ID AAX77064 standard; DNA; 566 BP.
DE Egr gene.
PN WO925385-A1.
PD 27-MAY-1999.
PA (INAR-) INARX PHARM CORP.
Query Match      2.7%; Score 65.6; DB 2; Length 566;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1353
ID AAH69839 standard; cDNA; 567 BP.
DE Human cervical cancer marker nucleic acid 1113.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      2.7%; Score 65.6; DB 4; Length 567;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1354
ID AAL03007 standard; DNA; 569 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5695.
PN EP1074617-A2.

PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      2.7%; Score 65.6; DB 4; Length 569;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1355
ID AAH13412 standard; cDNA; 569 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:10247.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match      2.7%; Score 65.6; DB 4; Length 569;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1356
ID ABL97354 standard; DNA; 569 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2006.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      2.7%; Score 65.6; DB 4; Length 569;
Best Local Similarity 88.8%; Pred. No. 3.4e-07;
RESULT 1357
ID AAK82986 standard; DNA; 584 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37798.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      2.7%; Score 65.6; DB 4; Length 584;
Best Local Similarity 88.8%; Pred. No. 3.5e-07;
RESULT 1358
ID ABV08133 standard; cDNA; 586 BP.
DE Human prostate expression marker cDNA 8124.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      2.7%; Score 65.6; DB 5; Length 586;
Best Local Similarity 88.8%; Pred. No. 3.5e-07;
RESULT 1359
ID AAK78289 standard; DNA; 605 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33101.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      2.7%; Score 65.6; DB 4; Length 605;
Best Local Similarity 88.8%; Pred. No. 3.6e-07;
RESULT 1360
ID AAK66436 standard; DNA; 606 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21248.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      2.7%; Score 65.6; DB 4; Length 606;
Best Local Similarity 88.8%; Pred. No. 3.6e-07;
RESULT 1361
ID ABV50740 standard; cDNA; 620 BP.
DE Human prostate expression marker cDNA 50731.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      2.7%; Score 65.6; DB 5; Length 620;
Best Local Similarity 88.8%; Pred. No. 3.6e-07;
RESULT 1362
ID AAS44682 standard; DNA; 642 BP.
DE Human full-length polynucleotide sequence #107.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSE INC.
Query Match      2.7%; Score 65.6; DB 4; Length 642;
Best Local Similarity 88.8%; Pred. No. 3.7e-07;
RESULT 1363
ID AAH08431 standard; cDNA; 685 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:5266.
PN EP1074617-A2.
```


PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 2.7%; Score 65.6; DB 4; Length 685;
Query Match 88.8%; Pred. No. 3.8e-07;
Best Local Similarity 88.8%; Pred. No. 3.8e-07;
RESULT 1364
ID AKN85379 standard; DNA; 707 BP.
DE Breast cancer related marker, seq id 6529.
PN US2003099974-A1.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.7%; Score 65.6; DB 11; Length 707;
Best Local Similarity 88.8%; Pred. No. 3.9e-07;
RESULT 1365
ID AAK67739 standard; DNA; 713 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22551.
PN WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 713;
Best Local Similarity 88.8%; Pred. No. 3.9e-07;
RESULT 1366
ID AAK67738 standard; DNA; 723 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22550.
PN WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 723;
Best Local Similarity 88.8%; Pred. No. 3.9e-07;
RESULT 1367
ID AAK67737 standard; DNA; 786 BP.
DE Human CDNA clone (5'-primer); SEQ ID NO:908.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 2.7%; Score 65.6; DB 4; Length 786;
Query Match 88.8%; Pred. No. 4.1e-07;
Best Local Similarity 88.8%; Pred. No. 4.1e-07;
RESULT 1368
ID AAK65399 standard; DNA; 815 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20211.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 815;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1369
ID AAD31368 standard; DNA; 819 BP.
DE Amplicon 3. Gscnl2.668.05 of 92Kb gene fragment of human chromosome 17.
PN WO200210455-A2.
PD 07-FEB-2002.
PA (CELL-) CELLTECH R & D INC.
PA (STRA/) STRAHLING HAMPTON K.
Query Match 2.7%; Score 65.6; DB 6; Length 819;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1370
ID ABL51013 standard; DNA; 821 BP.
DE Human EDAL-II exon 5 SEQ ID NO:7.
PN US6355782-B1.
PD 12-MAR-2002.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 2.7%; Score 65.6; DB 6; Length 821;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1371
ID ACD07899 standard; DNA; 821 BP.
DE DNA encoding human EDAL-II exon 5.
PN US2003023991-A1.
PD 30-JAN-2003.
PA (ZONA/) ZONANA J.
PA (FERG/) FERGUSON B M.
PA (HEAD/) HEADON D.
PA (OVER/) OVERBEEK P.
Query Match 2.7%; Score 65.6; DB 9; Length 821;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;

RESULT 1372
ID AAX20483 standard; DNA; 824 BP.
DE Human secreted protein gene 72.
PN WO9906423-A1.
PD 11-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 2; Length 824;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1373
ID ABO54154 standard; CDNA; 824 BP.
DE Human ovarian antigen HRDEL61 cDNA, SEQ ID NO:34.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 6; Length 824;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1374
ID ADD90267 standard; CDNA; 824 BP.
DE Novel human secreted protein cDNA seq id 82.
PN US200319683-A1.
PD 23-OCT-2003.
PA (RUBE/) RUBEN S M.
PA (FENG/) FENG P.
PA (LAPL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (KIYAW/) KYAW H.
PA (LIYI/) LI Y.
PA (ZENG/) ZENG Z.
PA (CART/) CARTER K C.
PA (ENDR/) ENDRESS G A.
PA (WEIY/) WEI Y.
PA (FANP/) FAN P.
PA (ROSE/) ROSEN C A.
Query Match 2.7%; Score 65.6; DB 10; Length 824;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1375
ID ADG90086 standard; CDNA; 824 BP.
DE Human CDNA from secreted protein gene 72.
PN US2003166541-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 824;
Best Local Similarity 88.8%; Pred. No. 4.2e-07;
RESULT 1376
ID AAI94605 standard; CDNA; 834 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 680.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM-) HISAMITSU PHARM CO LTD.
Query Match 2.7%; Score 65.6; DB 4; Length 834;
Best Local Similarity 88.8%; Pred. No. 4.3e-07;
RESULT 1377
ID ABVI6047 standard; CDNA; 855 BP.
DE Human prostate expression marker cDNA 16038.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.7%; Score 65.6; DB 5; Length 855;
Best Local Similarity 88.8%; Pred. No. 4.3e-07;
RESULT 1378
ID ABZ80046 standard; DNA; 877 BP.
DE Human AGE receptor binding related nucleotide sequence SEQ ID NO:48.
PN WO2003008446-A1.
PD 30-JAN-2003.
PA (MITS-) MITSUBISHI PHARMA CORP.
Query Match 2.7%; Score 65.6; DB 10; Length 877;
Best Local Similarity 88.8%; Pred. No. 4.4e-07;
RESULT 1379
ID AAK87123 standard; DNA; 898 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41935.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 898;
Best Local Similarity 88.8%; Pred. No. 4.4e-07;
RESULT 1380
ID AAK72553 standard; DNA; 898 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27365.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 898;
Best Local Similarity 88.8%; Pred. No. 4.4e-07;
RESULT 1381
ID ADC87114 standard; DNA; 931 BP.
DE Human GPCR Gene SEQ ID NO:1567.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.7%; Score 65.6; DB 10; Length 931;
Best Local Similarity 88.8%; Pred. No. 4.5e-07;
RESULT 1382
ID AAK82253 standard; DNA; 1002 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37065.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1002;
Best Local Similarity 88.8%; Pred. No. 4.7e-07;
RESULT 1383
ID AAC81263 standard; DNA; 1024 BP.
DE Human tyrosine phosphatase HD-FTP gene exon 2, SEQ ID NO:41.
PN WO200063392-A1.
PD 26-OCT-2000.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.7%; Score 65.6; DB 3; Length 1024;
Best Local Similarity 88.8%; Pred. No. 4.8e-07;
RESULT 1384
ID ABA20555 standard; DNA; 1064 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12886.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 1064;
Best Local Similarity 88.8%; Pred. No. 4.9e-07;
RESULT 1385
ID AAC79002 standard; DNA; 1092 BP.
DE Human secreted protein gene 6 clone H5JAN83.
PN WO200058358-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 3; Length 1092;
Best Local Similarity 88.8%; Pred. No. 5e-07;
RESULT 1386
ID AAK66435 standard; DNA; 1100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21247.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1100;
Best Local Similarity 88.8%; Pred. No. 5e-07;
RESULT 1387
ID AAF88859 standard; cDNA; 1268 BP.
DE Phosphoenolpyruvate dependent saccharophosphotransferase 9.46 cDNA.
PN CN1352250-A.
PD 05-JUN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 65.6; DB 6; Length 1268;
Best Local Similarity 88.8%; Pred. No. 5.4e-07;
RESULT 1388
ID ABA16111 standard; DNA; 1314 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8442.
PN WO200159063-A2.

PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 1314;
Best Local Similarity 88.8%; Pred. No. 5.5e-07;
RESULT 1389
ID AAC69568 standard; DNA; 1355 BP.
DE Human secreted protein gene 57 clone HNHOD46.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 3; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1390
ID ADA40020 standard; cDNA; 1355 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1391
ID ACC50566 standard; cDNA; 1355 BP.
DE Human secreted protein coding sequence, SEQ ID 233.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1392
ID ABZ71311 standard; cDNA; 1355 BP.
DE Secreted protein-encoding gene 122 cDNA clone HNHOD46, SEQ ID NO:132.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1393
ID ADB91231 standard; cDNA; 1355 BP.
DE Human secreted protein cDNA #SEQ ID 177.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 9; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1394
ID ADC73629 standard; DNA; 1355 BP.
DE Human secreted protein-related DNA - SEQ ID 262.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1395
ID ADD37644 standard; cDNA; 1355 BP.
DE Human secreted protein encoding sequence #126.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1396
ID ADA56206 standard; DNA; 1355 BP.
DE Gene encoding human secreted protein #385.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 1355;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1397
ID AAK76040 standard; DNA; 1369 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30852.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1369;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1398
ID AAK76042 standard; DNA; 1371 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30854.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1371;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1399
ID AAK76041 standard; DNA; 1371 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30853.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1371;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1400
ID ABA21255 standard; DNA; 1380 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13586.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 1380;
Best Local Similarity 88.8%; Pred. No. 5.6e-07;
RESULT 1401
ID ABK83662 standard; cDNA; 1413 BP.
DE Human CDNA differentially expressed in granulocytic cells #233.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 65.6; DB 6; Length 1413;
Best Local Similarity 88.8%; Pred. No. 5.7e-07;
RESULT 1402
ID ABA96911 standard; cDNA; 1440 BP.
DE Human arginase 9-encoding cDNA.
PN WO200198502-A1.
PD 27-DEC-2001.
PA (BTOW-) BLOWDOWN GENE DEV INC SHANGHAI.
Query Match 2.7%; Score 65.6; DB 6; Length 1440;
Best Local Similarity 88.8%; Pred. No. 5.8e-07;
RESULT 1403
ID AAO5583 standard; cDNA; 1604 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HWD4H38, SEQ ID NO:15.
PN WO200134627-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1604;
Best Local Similarity 88.8%; Pred. No. 6.1e-07;
RESULT 1404
ID ADA40239 standard; cDNA; 1604 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 1604;
Best Local Similarity 88.8%; Pred. No. 6.1e-07;
RESULT 1405
ID ACC50676 standard; cDNA; 1604 BP.
DE Human secreted protein coding sequence, SEQ ID 343.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 1604;
Best Local Similarity 88.8%; Pred. No. 6.1e-07;
RESULT 1406
ID ADA56401 standard; DNA; 1604 BP.
DE Gene encoding human secreted protein #580.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.7%; Score 65.6; DB 10; Length 1604;
Best Local Similarity 88.8%; Pred. No. 6.1e-07;
RESULT 1407
ID ADG35139 standard; cDNA; 1636 BP.
DE Human breast cancer antigen polynucleotide seq id 23.
PN US2003108888-A1.
PD 12-JUN-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 2.7%; Score 65.6; DB 10; Length 1636;
Best Local Similarity 88.8%; Pred. No. 6.2e-07;
RESULT 1408
ID ABA19996 standard; DNA; 1643 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12327.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 1643;
Best Local Similarity 88.8%; Pred. No. 6.2e-07;
RESULT 1409
ID ABA19995 standard; DNA; 1643 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12326.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 1643;
Best Local Similarity 88.8%; Pred. No. 6.2e-07;
RESULT 1410
ID AAH17199 standard; cDNA; 1701 BP.
DE Human CDNA sequence SEQ ID NO:16569.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 65.6; DB 4; Length 1701;
Best Local Similarity 88.8%; Pred. No. 6.3e-07;
RESULT 1411
ID AAK90383 standard; DNA; 1708 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3959.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1708;
Best Local Similarity 88.8%; Pred. No. 6.3e-07;
RESULT 1412
ID AAS39939 standard; DNA; 1708 BP.
DE Genomic sequence #358 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 1708;
Best Local Similarity 88.8%; Pred. No. 6.3e-07;
RESULT 1413
ID ADB32899 standard; DNA; 1708 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 836.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.7%; Score 65.6; DB 9; Length 1708;
Best Local Similarity 88.8%; Pred. No. 6.3e-07;
RESULT 1414
ID AAK90518 standard; DNA; 1714 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4094.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1714;
Best Local Similarity 88.8%; Pred. No. 6.4e-07;
RESULT 1415
ID ADQ25421 standard; DNA; 1714 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8241.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 65.6; DB 12; Length 1714;
Best Local Similarity 88.8%; Pred. No. 6.4e-07;
RESULT 1416
ID ADQ23971 standard; DNA; 1714 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6791.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 65.6; DB 12; Length 1714;
Best Local Similarity 88.8%; Pred. No. 6.4e-07;
RESULT 1417
ID ADA19372 standard; cDNA; 1734 BP.
DE Human insulin resistance marker IRM330 (G protein gamma-4) cDNA #1.
FN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 2.7%; Score 65.6; DB 10; Length 1734;
Best Local Similarity 88.8%; Pred. No. 6.4e-07;
RESULT 1418
ID ADR07263 standard; cDNA; 1840 BP.
DE Full length human cDNA useful for treating neurological disease Seq 769.
FN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 13; Length 1840;
Best Local Similarity 88.8%; Pred. No. 6.6e-07;
RESULT 1419
ID AAK82508 standard; DNA; 1845 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37320.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1845;
Best Local Similarity 88.8%; Pred. No. 6.6e-07;
RESULT 1420
ID AAK82510 standard; DNA; 1845 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37322.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1845;
Best Local Similarity 88.8%; Pred. No. 6.6e-07;
RESULT 1421
ID AAK82509 standard; DNA; 1845 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37321.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1845;
Best Local Similarity 88.8%; Pred. No. 6.6e-07;
RESULT 1422
ID ADQ23477 standard; DNA; 1863 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6297.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 65.6; DB 12; Length 1863;
Best Local Similarity 88.8%; Pred. No. 6.7e-07;
RESULT 1423
ID AAU51671 standard; cDNA; 1886 BP.
DE Signal peptidase 11-77 coding sequence.
FN CNI360046-A.
PD 24-JUL-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 65.6; DB 6; Length 1886;
Best Local Similarity 88.8%; Pred. No. 6.7e-07;
RESULT 1424
ID ADA19373 standard; cDNA; 1930 BP.
DE Human insulin resistance marker IRM330 (G protein gamma-4) cDNA #2.
FN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 2.7%; Score 65.6; DB 10; Length 1930;
Best Local Similarity 88.8%; Pred. No. 6.8e-07;
RESULT 1425
ID ADB63149 standard; cDNA; 1939 BP.
DE Human cDNA encoding clone SPLEN20041810.
FN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 10; Length 1939;
Best Local Similarity 88.8%; Pred. No. 6.8e-07;
RESULT 1426
ID AAH13715 standard; cDNA; 1962 BP.
DE Human cDNA sequence SEQ ID NO:10603.
FN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 65.6; DB 4; Length 1962;
Best Local Similarity 88.8%; Pred. No. 6.9e-07;
RESULT 1427
ID AAD07582 standard; cDNA; 1997 BP.
DE Human secreted protein-encoding gene 12 cDNA clone HNH185, SEQ ID NO:22.
FN WO200132676-A1.
PD 10-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 1997;
Best Local Similarity 88.8%; Pred. No. 6.9e-07;
RESULT 1428
ID AAH16700 standard; cDNA; 2012 BP.
DE Human cDNA sequence SEQ ID NO:15865.
FN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 65.6; DB 4; Length 2012;
Best Local Similarity 88.8%; Pred. No. 6.9e-07;
RESULT 1429
ID ABZ57045 standard; cDNA; 2043 BP.
DE Human zinc finger protein 8.91-encoding cDNA.
FN CNI364783-A.
PD 21-AUG-2002.
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
Query Match 2.7%; Score 65.6; DB 8; Length 2043;
Best Local Similarity 88.8%; Pred. No. 7e-07;
RESULT 1430
ID AAA81645 standard; DNA; 2140 BP.
DE N. meningitidis partial DNA sequence gnm_192 SEQ ID NO:192.
FN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR-) CHIRON CORP.
Query Match 2.7%; Score 65.6; DB 3; Length 2140;
Best Local Similarity 88.8%; Pred. No. 7.2e-07;
RESULT 1431
ID AAK70794 standard; DNA; 2174 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25606.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 2174;
Best Local Similarity 88.8%; Pred. No. 7.3e-07;
RESULT 1432
ID ADQ64339 standard; cDNA; 2175 BP.
DE Novel human cDNA sequence #1500.
FN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 12; Length 2175;
Best Local Similarity 88.8%; Pred. No. 7.3e-07;
RESULT 1433
ID AAH16680 standard; cDNA; 2191 BP.
DE Human cDNA sequence SEQ ID NO:15831.
FN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.

Query Match 2.7%; Score 65.6; DB 4; Length 2191;
Best Local Similarity 88.8%; Pred. No. 7.3e-07;
RESULT 1434
ID ABQ80846 standard; cDNA; 2195 BP.
DE Tyrosine specific protein phosphatase 23.87 coding sequence.
PN CN1352275-A.
PD 05-JUN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 65.6; DB 6; Length 2195;
Best Local Similarity 88.8%; Pred. No. 7.3e-07;
RESULT 1435
ID ABL41381 standard; cDNA; 2195 BP.
DE Human protein phosphatase 8.8 encoding cDNA SEQ ID NO 1.
PN CN1327061-A.
PD 19-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 2.7%; Score 65.6; DB 6; Length 2195;
Best Local Similarity 88.8%; Pred. No. 7.3e-07;
RESULT 1436
ID ADQ64167 standard; cDNA; 2242 BP.
DE Novel human cDNA sequence #1328.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 12; Length 2242;
Best Local Similarity 88.8%; Pred. No. 7.4e-07;
RESULT 1437
ID AB236122 standard; cDNA; 2332 BP.
DE Human secretory polynucleotide SPTM SEQ ID NO 286.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 65.6; DB 8; Length 2332;
Best Local Similarity 88.8%; Pred. No. 7.5e-07;
RESULT 1438
ID ADM01346 standard; cDNA; 2405 BP.
DE Human cDNA of the invention SEQ ID NO:31.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 11; Length 2405;
Best Local Similarity 88.8%; Pred. No. 7.7e-07;
RESULT 1439
ID ADR83499 standard; DNA; 2428 BP.
DE Human VENT-like homeobox 2 DNA, target gene of mirna.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 13; Length 2428;
Best Local Similarity 88.8%; Pred. No. 7.7e-07;
RESULT 1440
ID AAC75794 standard; cDNA; 2468 BP.
DE Human ORFX ORF1349 polynucleotide sequence SEQ ID NO:2697.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 2.7%; Score 65.6; DB 3; Length 2468;
Best Local Similarity 88.8%; Pred. No. 7.8e-07;
RESULT 1441
ID AAF18152 standard; DNA; 2529 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 171.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.7%; Score 65.6; DB 3; Length 2529;
Best Local Similarity 88.8%; Pred. No. 7.9e-07;
RESULT 1442
ID AB274188 standard; DNA; 2604 BP.
DE Secreted protein gene 215 genomic fragment HNGAM58, SEQ ID NO:1335.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.7%; Score 65.6; DB 8; Length 2604;
Best Local Similarity 88.8%; Pred. No. 8e-07;
RESULT 1443
ID ADA98717 standard; DNA; 2604 BP.
DE Human secreted protein-related DNA sequence #310.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 8; Length 2604;
Best Local Similarity 88.8%; Pred. No. 8e-07;
RESULT 1444
ID AB267754 standard; DNA; 2604 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1277.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 10; Length 2604;
Best Local Similarity 88.8%; Pred. No. 8e-07;
RESULT 1445
ID AAS74215 standard; cDNA; 2629 BP.
DE DNA encoding novel human diagnostic protein #10019.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.7%; Score 65.6; DB 5; Length 2629;
Best Local Similarity 88.8%; Pred. No. 8.1e-07;
RESULT 1446
ID ADT66674 standard; cDNA; 2630 BP.
DE Human RAB21 cDNA.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEF-) GRUENENTHAL GMBH.
Query Match 2.7%; Score 65.6; DB 13; Length 2630;
Best Local Similarity 88.8%; Pred. No. 8.1e-07;
RESULT 1447
ID ADQ64717 standard; cDNA; 2636 BP.
DE Novel human cDNA sequence #1878.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 12; Length 2636;
Best Local Similarity 88.8%; Pred. No. 8.1e-07;
RESULT 1448
ID AAH17727 standard; cDNA; 2642 BP.
DE Human cDNA sequence SEQ ID NO:17334.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 65.6; DB 4; Length 2642;
Best Local Similarity 88.8%; Pred. No. 8.1e-07;
RESULT 1449
ID ADF76471 standard; cDNA; 2642 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 145.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.7%; Score 65.6; DB 10; Length 2642;
Best Local Similarity 88.8%; Pred. No. 8.1e-07;
RESULT 1450
ID ADR07439 standard; cDNA; 2651 BP.
DE Full length human cDNA useful for treating neurological disease Seq 945.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 13; Length 2651;
Best Local Similarity 88.8%; Pred. No. 8.1e-07;
RESULT 1451
ID ADA52774 standard; cDNA; 2684 BP.
DE Human coding sequence, SEQ ID 342.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Best Local Similarity 88.8%; Pred. No. 8.5e-07;
RESULT 1461
ID ADR07894 standard; cDNA; 2891 BP.
DE Full length human CDNA useful for treating neurological disease Seq 1400.
PD EPI447413-A2.
PN 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 13; Length 2891;
Best Local Similarity 88.8%; Pred. No. 8.5e-07;
RESULT 1462
ID AAK70730 standard; DNA; 2914 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25542.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 2914;
Best Local Similarity 88.8%; Pred. No. 8.5e-07;
RESULT 1463
ID ACN88617 standard; DNA; 2978 BP.
DE Breast cancer related marker, seq id 9767.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.7%; Score 65.6; DB 11; Length 2978;
Best Local Similarity 88.8%; Pred. No. 8.6e-07;
RESULT 1464
ID ACN45127 standard; cDNA; 2981 BP.
DE Human mRNA sequence HCT5626.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 65.6; DB 11; Length 2981;
Best Local Similarity 88.8%; Pred. No. 8.6e-07;
RESULT 1465
ID AAK85238 standard; DNA; 3015 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40050.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 3015;
Best Local Similarity 88.8%; Pred. No. 8.7e-07;
RESULT 1466
ID ADI40354 standard; DNA; 3085 BP.
DE Human purified secretory polynucleotide (sptm), seq id 47.
PN WO2003062385-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (JONE-) JONES A. L.
PA (DAHL-) DAHL C. R.
PA (GIET-) GIETZEN D.
PA (CHIN-) CHINN J.
PA (DUFO-) DUFOUR G. E.
PA (JACK-) JACKSON J. L.
PA (YUJY-) YU J. Y.
PA (TUAS-) TUASON O.
PA (YAPP-) YAP P. E.
PA (AMSH-) AMSHEY S. R.
PA (DAMT-) DAM T. C.
PA (LIUT-) LIU T. F.
PA (GERS-) GERSTIN E. H.
PA (PERA-) PERALTA C. H.
PA (LEWI-) LEWIS S. A.
PA (CHEN-) CHEN A. J.
PA (MARW-) MARWAHA R.
PA (LANE-) LAN R. Y.
PA (URAS-) URASHKA M. E.
PA (KRIS-) KRISTNAM S. R.
PA (KOLL-) KOLLURU V.
PA (PANE-) PANESAR I. S.
Query Match 2.7%; Score 65.6; DB 10; Length 3085;
Best Local Similarity 88.8%; Pred. No. 8.8e-07;
RESULT 1467
ID AAA35180 standard; DNA; 3108 BP.

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:54.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 2.7%; Score 65.6; DB 3; Length 3108;
Best Local Similarity 88.8%; Pred. No. 8.8e-07;
RESULT 1468
ID AAF21302 standard; DNA; 3108 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2869.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
Query Match 2.7%; Score 65.6; DB 3; Length 3108;
Best Local Similarity 88.8%; Pred. No. 8.8e-07;
RESULT 1469
ID ABZ96996 standard; DNA; 3108 BP.
DE Human nucleic acid sequence.
PN WO2000285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 65.6; DB 10; Length 3108;
Best Local Similarity 88.8%; Pred. No. 8.8e-07;
RESULT 1470
ID ABD20845 standard; DNA; 3108 BP.
DE Human pulmonary and inflammatory target DNA #456.
PN WO2000285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 2.7%; Score 65.6; DB 11; Length 3108;
Best Local Similarity 88.8%; Pred. No. 8.8e-07;
RESULT 1471
ID AAH18730 standard; cDNA; 3164 BP.
DE Human cDNA sequence SEQ ID NO:19006.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 65.6; DB 4; Length 3164;
Best Local Similarity 88.8%; Pred. No. 8.9e-07;
RESULT 1472
ID ADA53534 standard; cDNA; 3255 BP.
DE Human coding sequence, SEQ ID 1102.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 10; Length 3255;
Best Local Similarity 88.8%; Pred. No. 9.1e-07;
RESULT 1473
ID ABA01586 standard; cDNA; 3314 BP.
DE Human neuroprotein Y 11 encoding cDNA SEQ ID NO:1.
PN WO200175020-A2.
PD 11-OCT-2001.
PA (BLOW-) BLOWDOWN GENE DEV INC SHANGHAI.
Query Match 2.7%; Score 65.6; DB 6; Length 3314;
Best Local Similarity 88.8%; Pred. No. 9.2e-07;
RESULT 1474
ID ABA14359 standard; DNA; 3343 BP.
DE Human nervous system related polynucleotide SEQ ID NO 6690.
PN WO2000159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 5; Length 3343;
Best Local Similarity 88.8%; Pred. No. 9.2e-07;
RESULT 1475
ID AAK72154 standard; DNA; 3426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26966.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 3426;
Best Local Similarity 88.8%; Pred. No. 9.3e-07;
RESULT 1476

ID AAK70074 standard; DNA; 3454 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24886.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 3454;
Best Local Similarity 88.8%; Pred. No. 9.4e-07;
RESULT 1477
ID AAH18248 standard; cDNA; 3543 BP.
DE Human cDNA sequence SEQ ID NO:18200.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.7%; Score 65.6; DB 4; Length 3543;
Best Local Similarity 88.8%; Pred. No. 9.5e-07;
RESULT 1478
ID ADB62232 standard; cDNA; 3572 BP.
DE Human cDNA encoding clone CTONG20084660.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.7%; Score 65.6; DB 10; Length 3572;
Best Local Similarity 88.8%; Pred. No. 9.6e-07;
RESULT 1479
ID ADQ24785 standard; DNA; 3654 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7605.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.7%; Score 65.6; DB 12; Length 3654;
Best Local Similarity 88.8%; Pred. No. 9.7e-07;
RESULT 1480
ID ADF60998 standard; DNA; 3693 BP.
DE Pain associated human 336 gene.
PN US2003153525-A1.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.7%; Score 65.6; DB 10; Length 3693;
Best Local Similarity 88.8%; Pred. No. 9.7e-07;
RESULT 1481
ID ADX61652 standard; DNA; 3693 BP.
DE Ovarian cancer-related DNA #807 with altered ovarian cancer expression.
PN WO2003068054-A2.
PD 21-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 2.7%; Score 65.6; DB 10; Length 3693;
Best Local Similarity 88.8%; Pred. No. 9.7e-07;
RESULT 1482
ID AAK70878 standard; DNA; 3774 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25690.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 65.6; DB 4; Length 3774;
Best Local Similarity 88.8%; Pred. No. 9.9e-07;
RESULT 1483
ID AAF24498 standard; cDNA; 3809 BP.
DE Human PG-3 coding sequence.
PN WO200114550-A1.
PD 01-MAR-2001.
PA (GEST) GENSET.
Query Match 2.7%; Score 65.6; DB 4; Length 3809;
Best Local Similarity 88.8%; Pred. No. 9.9e-07;
RESULT 1484
ID ABQ81803 standard; cDNA; 3809 BP.
DE Human PG-3 encoding cDNA SEQ ID NO:2.
PN WO200266641-A1.
PD 29-AUG-2002.
PA (GEST) GENSET.
Query Match 2.7%; Score 65.6; DB 6; Length 3809;
Best Local Similarity 88.8%; Pred. No. 9.9e-07;
RESULT 1485

Wed May 11 07:24:22 2005

RESULT 1485
ID ABL7249 standard; DNA; 3863 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5586.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM. 2.7%; Score 65.6; DB 6; Length 3863;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1486
ID AAI58900 standard; cDNA; 3883 BP.
DE Human polynucleotide SEQ ID NO 1103.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC. 2.7%; Score 65.6; DB 4; Length 3883;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1487
ID ADQ99122 standard; cDNA; 3883 BP.
DE DNA encoding human GPCR-like protein seqid 792.
PN US659662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC. 2.7%; Score 65.6; DB 5; Length 3883;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1488
ID ADB4882 standard; cDNA; 3883 BP.
DE Novel human cDNA SEQ ID NO 792.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T. 2.7%; Score 65.6; DB 9; Length 3883;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1489
ID AAH98627 standard; cDNA; 3884 BP.
DE Human EST-derived coding sequence SEQ ID NO: 484.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC. 2.7%; Score 65.6; DB 4; Length 3884;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1490
ID ABN87725 standard; cDNA; 3895 BP.
DE Human prostate specific gene cDNA sequence SEQ ID NO:76.
PN WO200236808-A2.
PD 10-MAY-2002.
PA (DIAD-) DIADEXUS INC. 2.7%; Score 65.6; DB 6; Length 3895;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1491
ID AAH18220 standard; cDNA; 3921 BP.
DE Human cDNA sequence SEQ ID NO:18151.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST. 2.7%; Score 65.6; DB 4; Length 3921;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1492
ID AAL03517 standard; DNA; 3961 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6205.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.7%; Score 65.6; DB 4; Length 3961;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1493
ID AAL03518 standard; DNA; 3961 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6206.
PN WO200155320-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC. 2.7%; Score 65.6; DB 4; Length 3961;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1494
ID ABZ68882 standard; cDNA; 4018 BP.
DE Nucleotide sequence of human chemokine receptor CCR6.
PN WO2003014153-A2.
PD 20-FEB-2003.
PA (TOPI-) TOPIGEN PHARM INC. 2.7%; Score 65.6; DB 8; Length 4018;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1495
ID AAK70341 standard; DNA; 4063 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25153.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.7%; Score 65.6; DB 4; Length 4063;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1496
ID AAK82280 standard; DNA; 4063 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37092.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC. 2.7%; Score 65.6; DB 4; Length 4063;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1497
ID ABK34686 standard; cDNA; 4153 BP.
DE Human cDNA for novel secreted protein, SEQ ID 455.
PN WO200177290-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC. 2.7%; Score 65.6; DB 6; Length 4153;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1498
ID ADU95422 standard; DNA; 4247 BP.
DE Human nontropic protein coding sequence, SEQ ID 11.
PN JP2003310264-A.
PD 05-NOV-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO. 2.7%; Score 65.6; DB 12; Length 4247;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1499
ID ADF10544 standard; DNA; 4314 BP.
DE Reference mRNA sequences for marker probe #221.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC. 2.7%; Score 65.6; DB 12; Length 4314;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;
RESULT 1500
ID ADR14440 standard; DNA; 4314 BP.
DE Human NF-kappaB pathway-associated gene SeqID441.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO. 2.7%; Score 65.6; DB 13; Length 4314;
Query Match Best Local Similarity 88.8%; Pred. No. 1e-06;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 01:39:26 ; Search time 426 Seconds
(without alignments)
9441.240 Million cell updates/sec

Title: US-09-978-544A-58
Perfect score: 2458
Sequence: 1 gcgcggagccatctgcc.....acagagcgggactcgtctc 2458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1986.4	80.8	2184	3	US-09-484-970B-161
2	1441	58.6	141560	4	US-09-949-016-16476
3	652	26.5	2685	4	US-09-949-016-4734
4	70.8	2.9	601	4	US-09-949-016-121707
5	70.8	2.9	15192	4	US-09-949-016-15143
6	70.8	2.9	19861	4	US-09-949-016-14498
7	70.6	2.9	1000	4	US-09-866-108A-15752
8	70.4	2.9	601	4	US-09-949-016-93537
9	70.4	2.9	601	4	US-09-949-016-121416
10	70.4	2.9	601	4	US-09-949-016-121706
11	70.4	2.9	601	4	US-09-949-016-146958
12	70.4	2.9	601	4	US-09-949-016-198954
13	70.4	2.9	601	4	US-09-949-016-198955
14	70.4	2.9	23218	4	US-09-949-016-11987
15	70.4	2.9	23219	4	US-09-949-016-13396
16	70.4	2.9	55886	4	US-09-949-016-14435
17	70.4	2.9	91933	4	US-09-949-016-15129
18	70.4	2.9	91933	4	US-09-949-016-11855
19	70.4	2.9	91933	4	US-09-949-016-14628
20	70.4	2.9	92227	4	US-09-949-016-11929
21	70.4	2.9	92232	4	US-09-949-016-15421
22	70.4	2.9	105055	4	US-09-949-016-14001
23	70.4	2.9	146307	4	US-09-949-016-14881
24	70.4	2.9	146307	4	US-09-949-016-14882
25	70.4	2.9	146307	4	US-09-949-016-14883
26	70.4	2.9	146307	4	US-09-949-016-14884
27	70.4	2.9	146307	4	US-09-949-016-14885

28	70.4	2.9	146307	4	US-09-949-016-14886	Sequence 14886, A
29	70.4	2.9	146307	4	US-09-949-016-14887	Sequence 14887, A
30	70.4	2.9	146307	4	US-09-949-016-14888	Sequence 14888, A
31	70.4	2.9	148405	4	US-09-949-016-11747	Sequence 11747, A
32	70.4	2.9	148405	4	US-09-949-016-12835	Sequence 12835, A
33	70.4	2.9	148405	4	US-09-949-016-12836	Sequence 12836, A
34	70.4	2.9	148405	4	US-09-949-016-12837	Sequence 12837, A
35	70.4	2.9	374159	4	US-09-949-016-15868	Sequence 15868, A
36	70.4	2.9	767677	4	US-09-949-016-12147	Sequence 12147, A
37	70.4	2.9	767677	4	US-09-949-016-17361	Sequence 17361, A
38	70	2.8	601	4	US-09-949-016-77470	Sequence 77470, A
39	70	2.8	601	4	US-09-949-016-93538	Sequence 93538, A
40	70	2.8	601	4	US-09-949-016-93539	Sequence 93539, A
41	69.8	2.8	33885	4	US-09-949-016-16081	Sequence 16081, A
42	69.4	2.8	601	4	US-09-949-016-154293	Sequence 154293, A
43	69.4	2.8	187916	4	US-09-949-016-12980	Sequence 12980, A
44	69.4	2.8	212139	4	US-09-949-016-16065	Sequence 16065, A
45	68.8	2.8	601	4	US-09-949-016-40432	Sequence 40432, A
46	68.8	2.8	601	4	US-09-949-016-40433	Sequence 40433, A
47	68.8	2.8	601	4	US-09-949-016-59095	Sequence 59095, A
48	68.8	2.8	601	4	US-09-949-016-59096	Sequence 59096, A
49	68.8	2.8	601	4	US-09-949-016-59097	Sequence 59097, A
50	68.8	2.8	601	4	US-09-949-016-59098	Sequence 59098, A
51	68.8	2.8	601	4	US-09-949-016-80325	Sequence 80325, A
52	68.8	2.8	601	4	US-09-949-016-80326	Sequence 80326, A
53	68.8	2.8	601	4	US-09-949-016-107944	Sequence 107944, A
54	68.8	2.8	601	4	US-09-949-016-110122	Sequence 110122, A
55	68.8	2.8	601	4	US-09-949-016-122847	Sequence 122847, A
56	68.8	2.8	601	4	US-09-949-016-130731	Sequence 130731, A
57	68.8	2.8	601	4	US-09-949-016-160661	Sequence 160661, A
58	68.8	2.8	601	4	US-09-949-016-164628	Sequence 164628, A
59	68.8	2.8	601	4	US-09-949-016-178384	Sequence 178384, A
60	68.8	2.8	7720	3	US-09-318-448-5	Sequence 5, Appl1
61	68.8	2.8	11321	4	US-09-949-016-13456	Sequence 13456, A
62	68.8	2.8	14205	4	US-09-949-016-16196	Sequence 16196, A
63	68.8	2.8	17353	4	US-09-949-016-13437	Sequence 13437, A
64	68.8	2.8	18026	4	US-09-949-016-13309	Sequence 13309, A
65	68.8	2.8	18744	4	US-09-949-016-14052	Sequence 14052, A
66	68.8	2.8	20875	4	US-09-949-016-15860	Sequence 15860, A
67	68.8	2.8	22281	4	US-09-949-016-14778	Sequence 14778, A
68	68.8	2.8	24663	4	US-09-949-016-14268	Sequence 14268, A
69	68.8	2.8	29171	4	US-09-949-016-12283	Sequence 12283, A
70	68.8	2.8	23171	4	US-09-949-016-13509	Sequence 13509, A
71	68.8	2.8	41965	4	US-09-949-016-13067	Sequence 13067, A
72	68.8	2.8	43255	4	US-09-949-016-11909	Sequence 11909, A
73	68.8	2.8	44096	4	US-09-949-016-15208	Sequence 15208, A
74	68.8	2.8	45469	4	US-09-949-016-13398	Sequence 13398, A
75	68.8	2.8	48018	4	US-09-949-016-17573	Sequence 17573, A
76	68.8	2.8	50073	4	US-09-949-016-16026	Sequence 16026, A
77	68.8	2.8	51967	4	US-09-949-016-16982	Sequence 16982, A
78	68.8	2.8	55114	4	US-09-949-016-16792	Sequence 16792, A
79	68.8	2.8	55827	3	US-09-813-133A-3	Sequence 3, Appl1
80	68.8	2.8	55827	4	US-10-212-877-3	Sequence 3, Appl1
81	68.8	2.8	62776	4	US-09-949-016-17576	Sequence 17576, A
82	68.8	2.8	67156	4	US-09-949-016-12284	Sequence 12284, A
83	68.8	2.8	67157	4	US-09-949-016-16558	Sequence 16558, A
84	68.8	2.8	70563	4	US-09-949-016-16743	Sequence 16743, A
85	68.8	2.8	71574	4	US-09-949-016-15580	Sequence 15580, A
86	68.8	2.8	77100	4	US-09-949-016-16418	Sequence 16418, A
87	68.8	2.8	81585	4	US-09-949-016-15427	Sequence 15427, A
88	68.8	2.8	84171	4	US-09-949-016-16356	Sequence 16356, A
89	68.8	2.8	87752	4	US-09-949-016-16807	Sequence 16807, A
90	68.8	2.8	90472	4	US-09-949-016-14038	Sequence 14038, A
91	68.8	2.8	104520	4	US-09-949-016-13303	Sequence 13303, A
92	68.8	2.8	106255	4	US-09-949-016-16858	Sequence 16858, A
93	68.8	2.8	126029	4	US-09-949-016-14731	Sequence 14731, A
94	68.8	2.8	133278	4	US-09-949-016-12524	Sequence 12524, A
95	68.8	2.8	133358	4	US-09-949-016-16964	Sequence 16964, A
96	68.8	2.8	131360	4	US-09-949-016-12651	Sequence 12651, A
97	68.8	2.8	151088	4	US-09-949-016-16240	Sequence 16240, A
98	68.8	2.8	194889	4	US-09-949-016-15654	Sequence 15654, A
99	68.8	2.8	194915	4	US-09-949-016-15584	Sequence 15584, A
100	68.8	2.8	227390	4	US-09-949-016-12201	Sequence 12201, A

c 101	68.8	2.8	227391	4	US-09-949-016-13365	Sequence 13365, A	c 174	67.2	2.7	601	4	US-09-949-016-13584	Sequence 35884, A
c 102	68.8	2.8	237863	4	US-09-949-016-13404	Sequence 13404, A	c 175	67.2	2.7	601	4	US-09-949-016-13585	Sequence 35885, A
c 103	68.8	2.8	254964	4	US-09-949-016-12583	Sequence 12583, A	c 176	67.2	2.7	601	4	US-09-949-016-13586	Sequence 35886, A
c 104	68.8	2.8	254964	4	US-09-949-016-12583	Sequence 12583, A	c 177	67.2	2.7	601	4	US-09-949-016-13590	Sequence 35960, A
c 105	68.8	2.8	325791	4	US-09-768-185A-1	Sequence 1, Appl1	c 178	67.2	2.7	601	4	US-09-949-016-35961	Sequence 35961, A
c 106	68.8	2.8	390890	4	US-09-949-016-14720	Sequence 14720, A	c 179	67.2	2.7	601	4	US-09-949-016-35962	Sequence 35962, A
c 107	68.4	2.8	601	4	US-09-949-016-42468	Sequence 42468, A	c 180	67.2	2.7	601	4	US-09-949-016-35963	Sequence 35963, A
c 108	68.4	2.8	601	4	US-09-949-016-46156	Sequence 46156, A	c 181	67.2	2.7	601	4	US-09-949-016-36047	Sequence 36047, A
c 109	68.4	2.8	601	4	US-09-949-016-79760	Sequence 79760, A	c 182	67.2	2.7	601	4	US-09-949-016-36048	Sequence 36048, A
c 110	68.4	2.8	601	4	US-09-949-016-90388	Sequence 90388, A	c 183	67.2	2.7	601	4	US-09-949-016-36049	Sequence 36049, A
c 111	68.4	2.8	601	4	US-09-949-016-143233	Sequence 143233, A	c 184	67.2	2.7	601	4	US-09-949-016-36050	Sequence 36050, A
c 112	68.4	2.8	601	4	US-09-949-016-143404	Sequence 143404, A	c 185	67.2	2.7	601	4	US-09-949-016-38083	Sequence 38083, A
c 113	68.4	2.8	601	4	US-09-949-016-146621	Sequence 146621, A	c 186	67.2	2.7	601	4	US-09-949-016-38084	Sequence 38084, A
c 114	68.4	2.8	601	4	US-09-949-016-160660	Sequence 160660, A	c 187	67.2	2.7	601	4	US-09-949-016-38242	Sequence 38242, A
c 115	68.4	2.8	601	4	US-09-949-016-183646	Sequence 183646, A	c 188	67.2	2.7	601	4	US-09-949-016-38243	Sequence 38243, A
c 116	68.4	2.8	94019	4	US-09-949-016-13203	Sequence 13203, A	c 189	67.2	2.7	601	4	US-09-949-016-40593	Sequence 40593, A
c 117	68.2	2.8	601	4	US-09-949-016-34027	Sequence 34027, A	c 190	67.2	2.7	601	4	US-09-949-016-40594	Sequence 40594, A
c 118	68.2	2.8	601	4	US-09-949-016-34028	Sequence 34028, A	c 191	67.2	2.7	601	4	US-09-949-016-42469	Sequence 42469, A
c 119	68.2	2.8	601	4	US-09-949-016-138225	Sequence 138225, A	c 192	67.2	2.7	601	4	US-09-949-016-42470	Sequence 42470, A
c 120	68.2	2.8	601	4	US-09-949-016-138226	Sequence 138226, A	c 193	67.2	2.7	601	4	US-09-949-016-45773	Sequence 45773, A
c 121	68.2	2.8	601	4	US-09-949-016-138227	Sequence 138227, A	c 194	67.2	2.7	601	4	US-09-949-016-45774	Sequence 45774, A
c 122	68.2	2.8	601	4	US-09-949-016-140141	Sequence 140141, A	c 195	67.2	2.7	601	4	US-09-949-016-45775	Sequence 45775, A
c 123	68.2	2.8	601	4	US-09-949-016-140142	Sequence 140142, A	c 196	67.2	2.7	601	4	US-09-949-016-45929	Sequence 45929, A
c 124	68.2	2.8	39113	4	US-09-949-016-15634	Sequence 15634, A	c 197	67.2	2.7	601	4	US-09-949-016-45930	Sequence 45930, A
c 125	68.2	2.8	43255	4	US-09-949-016-11909	Sequence 11909, A	c 198	67.2	2.7	601	4	US-09-949-016-45931	Sequence 45931, A
c 126	68.2	2.8	55674	4	US-09-949-016-12563	Sequence 12563, A	c 199	67.2	2.7	601	4	US-09-949-016-46994	Sequence 46994, A
c 127	68.2	2.8	55675	4	US-09-949-016-15706	Sequence 15706, A	c 200	67.2	2.7	601	4	US-09-949-016-49957	Sequence 49957, A
c 128	68	2.8	601	4	US-09-949-016-19952	Sequence 19952, A	c 201	67.2	2.7	601	4	US-09-949-016-53844	Sequence 53844, A
c 129	68	2.8	601	4	US-09-949-016-56179	Sequence 56179, A	c 202	67.2	2.7	601	4	US-09-949-016-57225	Sequence 57225, A
c 130	68	2.8	9968	4	US-09-949-016-17571	Sequence 17571, A	c 203	67.2	2.7	601	4	US-09-949-016-60352	Sequence 60352, A
c 131	68	2.8	24663	4	US-09-949-016-14268	Sequence 14268, A	c 204	67.2	2.7	601	4	US-09-949-016-61846	Sequence 61846, A
c 132	68	2.8	40641	4	US-09-949-016-13376	Sequence 13376, A	c 205	67.2	2.7	601	4	US-09-949-016-61768	Sequence 61768, A
c 133	68	2.8	55130	4	US-09-949-016-11850	Sequence 11850, A	c 206	67.2	2.7	601	4	US-09-949-016-66698	Sequence 66698, A
c 134	68	2.8	134631	4	US-09-949-016-11757	Sequence 11757, A	c 207	67.2	2.7	601	4	US-09-949-016-70763	Sequence 70763, A
c 135	68	2.8	134140	4	US-09-949-016-12672	Sequence 12672, A	c 208	67.2	2.7	601	4	US-09-949-016-73155	Sequence 73155, A
c 136	68	2.8	134241	4	US-09-949-016-12424	Sequence 12424, A	c 209	67.2	2.7	601	4	US-09-949-016-80340	Sequence 80340, A
c 137	68	2.8	134242	4	US-09-949-016-15813	Sequence 15813, A	c 210	67.2	2.7	601	4	US-09-949-016-80341	Sequence 80341, A
c 138	68	2.8	134242	4	US-09-949-016-15814	Sequence 15814, A	c 211	67.2	2.7	601	4	US-09-949-016-80355	Sequence 80355, A
c 139	68	2.8	134242	4	US-09-949-016-15815	Sequence 15815, A	c 212	67.2	2.7	601	4	US-09-949-016-80356	Sequence 80356, A
c 140	67.8	2.8	601	4	US-09-949-016-177021	Sequence 177021, A	c 213	67.2	2.7	601	4	US-09-949-016-87581	Sequence 87581, A
c 141	67.8	2.8	601	4	US-09-949-016-177022	Sequence 177022, A	c 214	67.2	2.7	601	4	US-09-949-016-89865	Sequence 89865, A
c 142	67.8	2.8	601	4	US-09-949-016-177023	Sequence 177023, A	c 215	67.2	2.7	601	4	US-09-949-016-89866	Sequence 89866, A
c 143	67.8	2.8	17328	4	US-09-949-016-15736	Sequence 15736, A	c 216	67.2	2.7	601	4	US-09-949-016-104937	Sequence 104937, A
c 144	67.8	2.8	20099	4	US-09-949-016-13784	Sequence 13784, A	c 217	67.2	2.7	601	4	US-09-949-016-104938	Sequence 104938, A
c 145	67.8	2.8	26896	4	US-09-949-016-16800	Sequence 16800, A	c 218	67.2	2.7	601	4	US-09-949-016-104939	Sequence 104939, A
c 146	67.8	2.8	29133	4	US-09-949-016-12694	Sequence 12694, A	c 219	67.2	2.7	601	4	US-09-949-016-104940	Sequence 104940, A
c 147	67.8	2.8	29393	4	US-09-949-016-17024	Sequence 17024, A	c 220	67.2	2.7	601	4	US-09-949-016-104962	Sequence 104962, A
c 148	67.8	2.8	38479	4	US-09-949-016-16730	Sequence 16730, A	c 221	67.2	2.7	601	4	US-09-949-016-104963	Sequence 104963, A
c 149	67.8	2.8	54033	4	US-09-949-016-12091	Sequence 12091, A	c 222	67.2	2.7	601	4	US-09-949-016-104964	Sequence 104964, A
c 150	67.8	2.8	54033	4	US-09-949-016-14325	Sequence 14325, A	c 223	67.2	2.7	601	4	US-09-949-016-104965	Sequence 104965, A
c 151	67.8	2.8	199471	4	US-09-949-016-14083	Sequence 14083, A	c 224	67.2	2.7	601	4	US-09-949-016-126996	Sequence 126996, A
c 152	67.6	2.8	601	4	US-09-949-016-50942	Sequence 50942, A	c 225	67.2	2.7	601	4	US-09-949-016-126997	Sequence 126997, A
c 153	67.6	2.8	601	4	US-09-949-016-50996	Sequence 50996, A	c 226	67.2	2.7	601	4	US-09-949-016-126997	Sequence 126997, A
c 154	67.6	2.8	17527	4	US-09-949-016-13145	Sequence 13145, A	c 227	67.2	2.7	601	4	US-09-949-016-126998	Sequence 126998, A
c 155	67.6	2.8	36180	4	US-09-949-016-11745	Sequence 11745, A	c 228	67.2	2.7	601	4	US-09-949-016-126998	Sequence 126998, A
c 156	67.6	2.8	36181	4	US-09-949-016-11745	Sequence 11745, A	c 229	67.2	2.7	601	4	US-09-949-016-131818	Sequence 131818, A
c 157	67.6	2.8	36741	3	US-09-301-665-3	Sequence 3, Appl1	c 230	67.2	2.7	601	4	US-09-949-016-136956	Sequence 136956, A
c 158	67.6	2.8	44166	4	US-09-949-016-15829	Sequence 15829, A	c 231	67.2	2.7	601	4	US-09-949-016-138815	Sequence 138815, A
c 159	67.6	2.8	54180	4	US-09-949-016-14894	Sequence 14894, A	c 232	67.2	2.7	601	4	US-09-949-016-138816	Sequence 138816, A
c 160	67.6	2.8	77586	4	US-09-949-016-13220	Sequence 13220, A	c 233	67.2	2.7	601	4	US-09-949-016-138817	Sequence 138817, A
c 161	67.6	2.8	77586	4	US-09-949-016-13221	Sequence 13221, A	c 234	67.2	2.7	601	4	US-09-949-016-138823	Sequence 138823, A
c 162	67.4	2.7	4704	2	US-08-476-062A-52	Sequence 52, Appl1	c 235	67.2	2.7	601	4	US-09-949-016-138824	Sequence 138824, A
c 163	67.4	2.7	4704	2	US-09-023-655-1358	Sequence 1358, Ap	c 236	67.2	2.7	601	4	US-09-949-016-138825	Sequence 138825, A
c 164	67.4	2.7	44308	4	US-09-949-016-15604	Sequence 15604, A	c 237	67.2	2.7	601	4	US-09-949-016-138832	Sequence 138832, A
c 165	67.2	2.7	351	4	US-09-621-976-9805	Sequence 9805, Ap	c 238	67.2	2.7	601	4	US-09-949-016-138833	Sequence 138833, A
c 166	67.2	2.7	601	4	US-09-949-016-28844	Sequence 28844, A	c 239	67.2	2.7	601	4	US-09-949-016-138834	Sequence 138834, A
c 167	67.2	2.7	601	4	US-09-949-016-30652	Sequence 30652, A	c 240	67.2	2.7	601	4	US-09-949-016-138841	Sequence 138841, A
c 168	67.2	2.7	601	4	US-09-949-016-33510	Sequence 33510, A	c 241	67.2	2.7	601	4	US-09-949-016-138842	Sequence 138842, A
c 169	67.2	2.7	601	4	US-09-949-016-35805	Sequence 35805, A	c 242	67.2	2.7	601	4	US-09-949-016-138843	Sequence 138843, A
c 170	67.2	2.7	601	4	US-09-949-016-35806	Sequence 35806, A	c 243	67.2	2.7	601	4	US-09-949-016-139425	Sequence 139425, A
c 171	67.2	2.7	601	4	US-09-949-016-35807	Sequence 35807, A	c 244	67.2	2.7	601	4	US-09-949-016-139426	Sequence 139426, A
c 172	67.2	2.7	601	4	US-09-949-016-35808	Sequence 35808, A	c 245	67.2	2.7	601	4	US-09-949-016-140304	Sequence 140304, A
c 173	67.2	2.7	601	4	US-09-949-016-35883	Sequence 35883, A	c 246	67.2	2.7	601	4		

c 247	67.2	2.7	601	4	US-09-949-016-143232	Sequence 143232,	320	67.2	2.7	22683	4	US-09-949-016-14055	Sequence 14055, A
c 248	67.2	2.7	601	4	US-09-949-016-143403	Sequence 143403,	c 321	67.2	2.7	22257	4	US-09-949-016-12894	Sequence 12894, A
c 249	67.2	2.7	601	4	US-09-949-016-145425	Sequence 145425,	c 322	67.2	2.7	23260	4	US-09-949-016-14300	Sequence 14300, A
c 250	67.2	2.7	601	4	US-09-949-016-151101	Sequence 151101,	c 323	67.2	2.7	22496	4	US-09-949-016-11823	Sequence 11823, A
c 251	67.2	2.7	601	4	US-09-949-016-159655	Sequence 159655,	c 324	67.2	2.7	24496	4	US-09-949-016-14253	Sequence 14253, A
c 252	67.2	2.7	601	4	US-09-949-016-161576	Sequence 161576,	c 325	67.2	2.7	24741	4	US-09-949-016-15547	Sequence 15547, A
c 253	67.2	2.7	601	4	US-09-949-016-163471	Sequence 163471,	c 326	67.2	2.7	24841	4	US-09-949-016-14009	Sequence 14009, A
c 254	67.2	2.7	601	4	US-09-949-016-164973	Sequence 164973,	c 327	67.2	2.7	25122	4	US-09-949-016-16312	Sequence 16312, A
c 255	67.2	2.7	601	4	US-09-949-016-167790	Sequence 167790,	c 328	67.2	2.7	25160	4	US-09-949-016-12691	Sequence 12691, A
c 256	67.2	2.7	601	4	US-09-949-016-179088	Sequence 179088,	c 329	67.2	2.7	25162	4	US-09-949-016-13065	Sequence 13065, A
c 257	67.2	2.7	601	4	US-09-949-016-179952	Sequence 179952,	c 330	67.2	2.7	25162	4	US-09-949-016-13066	Sequence 13066, A
c 258	67.2	2.7	601	4	US-09-949-016-183645	Sequence 183645,	c 331	67.2	2.7	25260	4	US-09-949-016-11985	Sequence 11985, A
c 259	67.2	2.7	601	4	US-09-949-016-183647	Sequence 183647,	c 332	67.2	2.7	25260	4	US-09-949-016-12907	Sequence 12907, A
c 260	67.2	2.7	601	4	US-09-949-016-190968	Sequence 190968,	c 333	67.2	2.7	26133	4	US-09-949-016-15959	Sequence 15959, A
c 261	67.2	2.7	601	4	US-09-949-016-195744	Sequence 195744,	c 334	67.2	2.7	26433	4	US-09-949-016-15401	Sequence 15401, A
c 262	67.2	2.7	601	4	US-09-949-016-197123	Sequence 197123,	c 335	67.2	2.7	26640	4	US-09-949-016-17431	Sequence 17431, A
c 263	67.2	2.7	601	4	US-09-949-016-197124	Sequence 197124,	c 336	67.2	2.7	26777	4	US-09-949-016-13015	Sequence 13015, A
c 264	67.2	2.7	601	4	US-09-949-016-197125	Sequence 197125,	c 337	67.2	2.7	27667	4	US-09-949-016-13401	Sequence 13401, A
c 265	67.2	2.7	601	4	US-09-949-016-197126	Sequence 197126,	c 338	67.2	2.7	27702	4	US-09-949-016-11795	Sequence 11795, A
c 266	67.2	2.7	601	4	US-09-949-016-197241	Sequence 197241,	c 339	67.2	2.7	30006	4	US-09-949-016-16385	Sequence 16385, A
c 267	67.2	2.7	601	4	US-09-949-016-197242	Sequence 197242,	c 340	67.2	2.7	30337	4	US-09-949-016-13053	Sequence 13053, A
c 268	67.2	2.7	601	4	US-09-949-016-197243	Sequence 197243,	c 341	67.2	2.7	30364	4	US-09-949-016-15620	Sequence 15620, A
c 269	67.2	2.7	601	4	US-09-949-016-197244	Sequence 197244,	c 342	67.2	2.7	31623	4	US-09-949-016-15945	Sequence 15945, A
c 270	67.2	2.7	601	4	US-09-949-016-197359	Sequence 197359,	c 343	67.2	2.7	31820	4	US-09-949-016-13356	Sequence 13356, A
c 271	67.2	2.7	601	4	US-09-949-016-197360	Sequence 197360,	c 344	67.2	2.7	32068	4	US-09-949-016-12971	Sequence 12971, A
c 272	67.2	2.7	601	4	US-09-949-016-197361	Sequence 197361,	c 345	67.2	2.7	32068	4	US-09-949-016-12972	Sequence 12972, A
c 273	67.2	2.7	601	4	US-09-949-016-197362	Sequence 197362,	c 346	67.2	2.7	32068	4	US-09-949-016-12973	Sequence 12973, A
c 274	67.2	2.7	601	4	US-09-949-016-197477	Sequence 197477,	c 347	67.2	2.7	32068	4	US-09-949-016-12974	Sequence 12974, A
c 275	67.2	2.7	601	4	US-09-949-016-197478	Sequence 197478,	c 348	67.2	2.7	32068	4	US-09-949-016-12975	Sequence 12975, A
c 276	67.2	2.7	601	4	US-09-949-016-197479	Sequence 197479,	c 349	67.2	2.7	32068	4	US-09-949-016-14436	Sequence 14436, A
c 277	67.2	2.7	601	4	US-09-949-016-197480	Sequence 197480,	c 350	67.2	2.7	32068	4	US-09-949-016-14437	Sequence 14437, A
c 278	67.2	2.7	601	4	US-09-949-016-201851	Sequence 201851,	c 351	67.2	2.7	32068	4	US-09-949-016-14438	Sequence 14438, A
c 279	67.2	2.7	601	4	US-09-949-016-202374	Sequence 202374,	c 352	67.2	2.7	32068	4	US-09-949-016-14439	Sequence 14439, A
c 280	67.2	2.7	601	4	US-09-949-016-205378	Sequence 205378,	c 353	67.2	2.7	32068	4	US-09-949-016-14440	Sequence 14440, A
c 281	67.2	2.7	2713	2	US-08-916-901-6	Sequence 6, Appli	c 354	67.2	2.7	32068	4	US-09-949-016-14441	Sequence 14441, A
c 282	67.2	2.7	2713	3	US-09-154-602-6	Sequence 6, Appli	c 355	67.2	2.7	32068	4	US-09-949-016-14557	Sequence 14557, A
c 283	67.2	2.7	3144	4	US-09-949-016-13259	Sequence 3259, Ap	c 356	67.2	2.7	32202	4	US-09-949-016-14575	Sequence 14575, A
c 284	67.2	2.7	4524	4	US-09-949-016-12658	Sequence 12658, A	c 357	67.2	2.7	32278	4	US-09-949-016-12681	Sequence 12681, A
c 285	67.2	2.7	4525	4	US-09-949-016-15792	Sequence 15792, A	c 358	67.2	2.7	34544	4	US-09-949-016-16124	Sequence 16124, A
c 286	67.2	2.7	6029	4	US-09-949-016-13342	Sequence 13342, A	c 359	67.2	2.7	34548	4	US-09-949-016-16873	Sequence 16873, A
c 287	67.2	2.7	10465	4	US-09-949-016-13136	Sequence 13136, A	c 360	67.2	2.7	35688	4	US-09-949-016-16873	Sequence 16873, A
c 288	67.2	2.7	10993	4	US-09-949-016-12142	Sequence 12142, A	c 361	67.2	2.7	36093	4	US-09-949-016-14664	Sequence 14664, A
c 289	67.2	2.7	12565	3	US-09-345-217-3	Sequence 3, Appli	c 362	67.2	2.7	36093	4	US-09-949-016-14665	Sequence 14665, A
c 290	67.2	2.7	12565	4	US-09-845-129-3	Sequence 3, Appli	c 363	67.2	2.7	36171	4	US-09-949-016-13876	Sequence 13876, A
c 291	67.2	2.7	12565	4	US-09-578-534-17	Sequence 17, Appli	c 364	67.2	2.7	36242	4	US-09-949-016-12996	Sequence 12996, A
c 292	67.2	2.7	12565	4	US-09-632-657-3	Sequence 3, Appli	c 365	67.2	2.7	36242	4	US-09-949-016-12997	Sequence 12997, A
c 293	67.2	2.7	12565	4	US-09-584-950-3	Sequence 3, Appli	c 366	67.2	2.7	36242	4	US-09-949-016-12998	Sequence 12998, A
c 294	67.2	2.7	12565	4	US-09-054-272-49	Sequence 49, Appli	c 367	67.2	2.7	36242	4	US-09-949-016-12999	Sequence 12999, A
c 295	67.2	2.7	13675	4	US-09-949-016-11746	Sequence 11746, A	c 368	67.2	2.7	36274	4	US-09-949-016-13000	Sequence 13000, A
c 296	67.2	2.7	13743	4	US-09-949-016-16538	Sequence 16538, A	c 369	67.2	2.7	36907	4	US-09-949-016-12633	Sequence 12633, A
c 297	67.2	2.7	15007	4	US-09-949-016-15279	Sequence 15279, A	c 370	67.2	2.7	36907	4	US-09-949-016-12633	Sequence 12633, A
c 298	67.2	2.7	15133	4	US-09-949-016-15001	Sequence 15001, A	c 371	67.2	2.7	36913	4	US-09-949-016-15585	Sequence 15585, A
c 299	67.2	2.7	15454	4	US-09-949-016-16679	Sequence 16679, A	c 372	67.2	2.7	37004	4	US-09-949-016-15317	Sequence 15317, A
c 300	67.2	2.7	16629	4	US-09-949-016-12862	Sequence 12862, A	c 373	67.2	2.7	37288	4	US-09-949-016-14593	Sequence 14593, A
c 301	67.2	2.7	16631	4	US-09-949-016-13745	Sequence 13745, A	c 374	67.2	2.7	37288	4	US-09-949-016-14594	Sequence 14594, A
c 302	67.2	2.7	17086	4	US-09-949-016-13684	Sequence 13684, A	c 375	67.2	2.7	37428	4	US-09-949-016-12299	Sequence 12299, A
c 303	67.2	2.7	18068	4	US-09-949-016-13291	Sequence 13291, A	c 376	67.2	2.7	37492	4	US-09-949-016-13198	Sequence 13198, A
c 304	67.2	2.7	18080	4	US-09-949-016-15660	Sequence 15660, A	c 377	67.2	2.7	37565	4	US-09-949-016-15847	Sequence 15847, A
c 305	67.2	2.7	18200	4	US-09-949-016-15661	Sequence 15661, A	c 378	67.2	2.7	38343	4	US-09-949-016-15714	Sequence 15714, A
c 306	67.2	2.7	18572	4	US-09-949-016-17183	Sequence 17183, A	c 379	67.2	2.7	38772	4	US-09-949-016-12382	Sequence 12382, A
c 307	67.2	2.7	18798	4	US-09-949-016-14339	Sequence 14339, A	c 380	67.2	2.7	38772	4	US-09-949-016-12729	Sequence 12729, A
c 308	67.2	2.7	19091	4	US-09-949-016-15805	Sequence 15805, A	c 381	67.2	2.7	40493	4	US-09-949-016-15453	Sequence 15453, A
c 309	67.2	2.7	19677	4	US-09-949-016-17427	Sequence 17427, A	c 382	67.2	2.7	40575	4	US-09-949-016-17246	Sequence 17246, A
c 310	67.2	2.7	19719	4	US-09-949-016-15662	Sequence 15662, A	c 383	67.2	2.7	40624	4	US-09-949-016-11904	Sequence 11904, A
c 311	67.2	2.7	19719	4	US-09-949-016-15663	Sequence 15663, A	c 384	67.2	2.7	40625	4	US-09-949-016-14016	Sequence 14016, A
c 312	67.2	2.7	21017	4	US-09-949-016-12965	Sequence 12965, A	c 385	67.2	2.7	41895	4	US-09-949-016-15135	Sequence 15135, A
c 313	67.2	2.7	21234	3	US-09-810-671-3	Sequence 3, Appli	c 386	67.2	2.7	43507	4	US-09-949-016-13297	Sequence 13297, A
c 314	67.2	2.7	21234	4	US-10-109-854-3	Sequence 3, Appli	c 387	67.2	2.7	43550	4	US-09-949-016-12400	Sequence 12400, A
c 315	67.2	2.7	21234	4	US-10-339-656-3	Sequence 3, Appli	c 388	67.2	2.7	43555	4	US-09-949-016-13993	Sequence 13993, A
c 316	67.2	2.7	21284	4	US-09-820-002-3	Sequence 3, Appli	c 389	67.2	2.7	44378	4	US-09-949-016-12540	Sequence 12540, A
c 317	67.2	2.7	22170	4	US-09-949-016-13669	Sequence 13669, A	c 390	67.2	2.7	44676	4	US-09-949-016-17511	Sequence 17511, A
c 318	67.2	2.7	22471	4	US-09-949-016-15902	Sequence 15902, A	c 391	67.2	2.7	44789	4	US-09-949-016-13409	Sequence 13409, A
c 319	67.2	2.7	22683	4	US-09-949-016-14054	Sequence 14054, A	c 392	67.2	2.7	45299	4	US-09-949-016-12965	Sequence 12965, A

393	67.2	2.7	45300	4	US-09-949-016-13045	Sequence 13045, A	466	67.2	2.7	120727	4	US-09-949-016-15787	Sequence 15787, A
c 394	67.2	2.7	45365	4	US-09-949-016-11893	Sequence 11893, A	467	67.2	2.7	120727	4	US-09-949-016-15788	Sequence 15788, A
395	67.2	2.7	45427	4	US-09-949-016-16243	Sequence 16243, A	468	67.2	2.7	124480	4	US-09-949-016-15921	Sequence 15921, A
c 396	67.2	2.7	45456	4	US-09-949-016-16243	Sequence 16243, A	469	67.2	2.7	126254	4	US-09-949-016-15341	Sequence 15341, A
c 397	67.2	2.7	45484	4	US-09-949-016-12967	Sequence 12967, A	c 470	67.2	2.7	128516	4	US-09-949-016-13501	Sequence 13501, A
c 398	67.2	2.7	47471	4	US-09-949-016-12967	Sequence 12967, A	c 471	67.2	2.7	131978	4	US-09-949-016-13517	Sequence 13517, A
c 399	67.2	2.7	49848	4	US-09-949-016-15675	Sequence 15675, A	c 472	67.2	2.7	133157	4	US-09-949-016-12541	Sequence 12541, A
c 400	67.2	2.7	51273	4	US-09-949-016-13018	Sequence 13018, A	c 473	67.2	2.7	133753	4	US-09-949-016-17404	Sequence 17404, A
c 401	67.2	2.7	51273	4	US-09-949-016-13018	Sequence 13018, A	c 474	67.2	2.7	133753	4	US-09-949-016-15300	Sequence 15300, A
c 402	67.2	2.7	52821	4	US-09-949-016-15857	Sequence 15857, A	c 475	67.2	2.7	142428	4	US-09-949-016-12241	Sequence 12241, A
c 403	67.2	2.7	52821	4	US-09-949-016-15857	Sequence 15857, A	c 476	67.2	2.7	142428	4	US-09-949-016-13530	Sequence 13530, A
c 404	67.2	2.7	53442	4	US-09-949-016-11921	Sequence 11921, A	c 477	67.2	2.7	145287	4	US-09-949-016-13531	Sequence 13531, A
c 405	67.2	2.7	53453	4	US-09-949-016-11921	Sequence 11921, A	c 478	67.2	2.7	146039	4	US-09-949-016-12541	Sequence 12541, A
c 406	67.2	2.7	56326	4	US-09-949-016-14648	Sequence 14648, A	c 479	67.2	2.7	148609	4	US-09-949-016-12860	Sequence 12860, A
c 407	67.2	2.7	56326	4	US-09-949-016-14648	Sequence 14648, A	c 480	67.2	2.7	148609	4	US-09-949-016-16787	Sequence 16787, A
c 408	67.2	2.7	57299	4	US-09-949-016-12141	Sequence 12141, A	c 481	67.2	2.7	152626	4	US-09-949-016-13870	Sequence 13870, A
c 409	67.2	2.7	57751	4	US-09-949-016-13611	Sequence 13611, A	c 482	67.2	2.7	152626	4	US-09-949-016-16191	Sequence 16191, A
c 410	67.2	2.7	57859	4	US-09-949-016-12334	Sequence 12334, A	c 483	67.2	2.7	156617	4	US-09-949-016-16038	Sequence 16038, A
c 411	67.2	2.7	57859	4	US-09-949-016-14658	Sequence 14658, A	c 484	67.2	2.7	156617	4	US-09-949-016-13444	Sequence 13444, A
c 412	67.2	2.7	59240	4	US-09-949-016-11933	Sequence 11933, A	c 485	67.2	2.7	172751	4	US-09-949-016-15841	Sequence 15841, A
c 413	67.2	2.7	59479	4	US-09-949-016-16910	Sequence 16910, A	c 486	67.2	2.7	172751	4	US-09-949-016-17202	Sequence 17202, A
c 414	67.2	2.7	62873	4	US-09-949-016-15676	Sequence 15676, A	c 487	67.2	2.7	189560	4	US-09-949-016-17539	Sequence 17539, A
c 415	67.2	2.7	66219	4	US-09-949-016-12038	Sequence 12038, A	c 488	67.2	2.7	239527	4	US-09-949-016-15980	Sequence 15980, A
c 416	67.2	2.7	66227	4	US-09-949-016-15303	Sequence 15303, A	c 489	67.2	2.7	240157	4	US-09-949-016-16264	Sequence 16264, A
c 417	67.2	2.7	66804	4	US-09-949-016-13703	Sequence 13703, A	c 490	67.2	2.7	246240	2	US-08-724-394A-20	Sequence 20, Appl
c 418	67.2	2.7	67755	4	US-09-949-016-13703	Sequence 13703, A	c 491	67.2	2.7	246240	2	US-08-724-394A-21	Sequence 21, Appl
c 419	67.2	2.7	68778	4	US-09-949-016-16406	Sequence 16406, A	c 492	67.2	2.7	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 420	67.2	2.7	69813	4	US-09-949-016-12455	Sequence 12455, A	c 493	67.2	2.7	251672	4	US-09-949-016-117296	Sequence 117296, A
c 421	67.2	2.7	69813	4	US-09-949-016-13905	Sequence 13905, A	c 494	67.2	2.7	251672	4	US-09-949-016-11973	Sequence 11973, A
c 422	67.2	2.7	69813	4	US-09-949-016-13905	Sequence 13905, A	c 495	67.2	2.7	256387	4	US-09-949-016-14608	Sequence 14608, A
c 423	67.2	2.7	69833	4	US-09-949-016-12861	Sequence 12861, A	c 496	67.2	2.7	260247	4	US-09-949-016-13358	Sequence 13358, A
c 424	67.2	2.7	70947	4	US-09-949-016-13165	Sequence 13165, A	c 497	67.2	2.7	280353	4	US-09-949-016-13506	Sequence 13506, A
c 425	67.2	2.7	74527	4	US-09-949-016-12339	Sequence 12339, A	c 498	67.2	2.7	304533	4	US-09-949-016-15371	Sequence 15371, A
c 426	67.2	2.7	74528	4	US-09-949-016-13275	Sequence 13275, A	c 499	67.2	2.7	304533	4	US-09-949-016-15372	Sequence 15372, A
c 427	67.2	2.7	74881	4	US-09-949-016-15545	Sequence 15545, A	c 500	67.2	2.7	325791	4	US-09-768-185A-1	Sequence 1, Appl
c 428	67.2	2.7	74914	4	US-09-949-016-12286	Sequence 12286, A	c 501	67.2	2.7	325791	4	US-09-949-016-17371	Sequence 17371, A
c 429	67.2	2.7	77036	4	US-09-949-016-16156	Sequence 16156, A	c 502	67.2	2.7	373694	4	US-09-949-016-12062	Sequence 12062, A
c 430	67.2	2.7	80411	4	US-09-949-016-15777	Sequence 15777, A	c 503	67.2	2.7	385136	4	US-09-949-016-16073	Sequence 16073, A
c 431	67.2	2.7	84571	4	US-09-949-016-17547	Sequence 17547, A	c 504	67.2	2.7	636591	4	US-09-949-016-11808	Sequence 11808, A
c 432	67.2	2.7	84870	4	US-09-949-016-17334	Sequence 17334, A	c 505	67.2	2.7	636591	4	US-09-949-016-13388	Sequence 13388, A
c 433	67.2	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A	c 506	67.2	2.7	670690	4	US-09-949-016-12505	Sequence 12505, A
c 434	67.2	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A	c 507	67.2	2.7	670690	4	US-09-949-016-14207	Sequence 14207, A
c 435	67.2	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A	c 508	67.2	2.7	678533	4	US-09-949-016-14577	Sequence 14577, A
c 436	67.2	2.7	85152	4	US-09-949-016-12665	Sequence 12665, A	c 509	67.2	2.7	678533	4	US-09-949-016-14578	Sequence 14578, A
c 437	67.2	2.7	85152	4	US-09-949-016-12666	Sequence 12666, A	c 510	67.2	2.7	678533	4	US-09-949-016-14578	Sequence 14578, A
c 438	67.2	2.7	85152	4	US-09-949-016-12667	Sequence 12667, A	c 511	67.2	2.7	678533	4	US-09-949-016-19907	Sequence 19907, A
c 439	67.2	2.7	85152	4	US-09-949-016-12668	Sequence 12668, A	c 512	67.2	2.7	601	4	US-09-949-016-19908	Sequence 19908, A
c 440	67.2	2.7	85152	4	US-09-949-016-17011	Sequence 17011, A	c 513	67.2	2.7	601	4	US-09-949-016-14322	Sequence 14322, A
c 441	67.2	2.7	87780	4	US-09-949-016-17028	Sequence 17028, A	c 514	67.2	2.7	5414	4	US-09-949-016-14322	Sequence 14322, A
c 442	67.2	2.7	88557	4	US-09-949-016-13502	Sequence 13502, A	c 515	67.2	2.7	24394	4	US-09-949-016-17487	Sequence 17487, A
c 443	67.2	2.7	88758	4	US-09-949-016-13089	Sequence 13089, A	c 516	67.2	2.7	37059	4	US-09-949-016-15865	Sequence 15865, A
c 444	67.2	2.7	89689	4	US-09-949-016-16976	Sequence 16976, A	c 517	67.2	2.7	48996	4	US-09-949-016-12744	Sequence 12744, A
c 445	67.2	2.7	90428	4	US-09-949-016-16324	Sequence 16324, A	c 518	67.2	2.7	48996	4	US-09-949-016-10592	Sequence 10592, A
c 446	67.2	2.7	94593	4	US-09-949-016-16324	Sequence 16324, A	c 519	66.8	2.7	601	4	US-09-949-016-46659	Sequence 46659, A
c 447	67.2	2.7	98302	4	US-09-949-016-16847	Sequence 16847, A	c 520	66.8	2.7	601	4	US-09-949-016-46659	Sequence 46659, A
c 448	67.2	2.7	98500	3	US-09-798-096-10	Sequence 10, Appl	c 521	66.8	2.7	601	4	US-09-949-016-77627	Sequence 77627, A
c 449	67.2	2.7	101356	4	US-09-949-016-12364	Sequence 12364, A	c 522	66.8	2.7	601	4	US-09-949-016-77627	Sequence 77627, A
c 450	67.2	2.7	101357	4	US-09-949-016-16924	Sequence 16924, A	c 523	66.8	2.7	601	4	US-09-949-016-77627	Sequence 77627, A
c 451	67.2	2.7	101558	4	US-09-949-016-12243	Sequence 12243, A	c 524	66.8	2.7	601	4	US-09-949-016-140303	Sequence 140303, A
c 452	67.2	2.7	106924	4	US-09-949-016-13834	Sequence 13834, A	c 525	66.8	2.7	601	4	US-09-949-016-160827	Sequence 160827, A
c 453	67.2	2.7	110243	4	US-09-949-016-13698	Sequence 13698, A	c 526	66.8	2.7	601	4	US-09-949-016-195745	Sequence 195745, A
c 454	67.2	2.7	113283	4	US-09-949-016-16976	Sequence 16976, A	c 527	66.8	2.7	601	4	US-09-949-016-195745	Sequence 195745, A
c 455	67.2	2.7	113283	4	US-09-949-016-16977	Sequence 16977, A	c 528	66.8	2.7	601	4	US-09-949-016-196612	Sequence 196612, A
c 456	67.2	2.7	113283	4	US-09-949-016-16977	Sequence 16977, A	c 529	66.8	2.7	601	4	US-09-949-016-198275	Sequence 198275, A
c 457	67.2	2.7	113701	4	US-09-949-016-13214	Sequence 13214, A	c 530	66.8	2.7	601	4	US-09-949-016-204246	Sequence 204246, A
c 458	67.2	2.7	113701	4	US-09-949-016-13214	Sequence 13214, A	c 531	66.8	2.7	601	4	US-09-949-016-12160	Sequence 12160, A
c 459	67.2	2.7	1154793	4	US-10-148-806-3	Sequence 3, Appl	c 532	66.8	2.7	119032	4	US-09-949-016-17268	Sequence 17268, A
c 460	67.2	2.7	115963	4	US-09-949-016-16205	Sequence 16205, A	c 533	66.8	2.7	119032	4	US-09-949-016-26757	Sequence 26757, A
c 461	67.2	2.7	115963	4	US-09-949-016-12298	Sequence 12298, A	c 534	66.6	2.7	601	4	US-09-949-016-29827	Sequence 29827, A
c 462	67.2	2.7	116652	4	US-09-949-016-13413	Sequence 13413, A	c 535	66.6	2.7	601	4	US-09-949-016-65845	Sequence 65845, A
c 463	67.2	2.7	117001	4	US-09-949-016-15684	Sequence 15684, A	c 536	66.6	2.7	601	4	US-09-949-016-65846	Sequence 65846, A
c 464	67.2	2.7	119649	4	US-09-949-016-12537	Sequence 12537, A	c 537	66.6	2.7	601	4	US-09-949-016-65847	Sequence 65847, A
c 465	67.2	2.7	119649	4	US-09-949-016-12537	Sequence 12537, A	c 538	66.6	2.7	601	4	US-09-949-016-65847	Sequence 65847, A

C 539	66.6	2.7	601	4	US-09-949-016-146889	Sequence 146889,	C 612	66.2	2.7	304533	4	US-09-949-016-15372	Sequence 15372, A
C 540	66.6	2.7	601	4	US-09-949-016-161273	Sequence 161273,	C 613	66.2	2.7	422592	4	US-09-949-016-14182	Sequence 14182, A
C 541	66.6	2.7	601	4	US-09-949-016-162252	Sequence 162252,	C 614	66	2.7	24496	4	US-09-949-016-11823	Sequence 11823, A
C 542	66.6	2.7	601	4	US-09-949-016-163068	Sequence 163068,	C 615	66	2.7	24497	4	US-09-949-016-14253	Sequence 14253, A
C 543	66.6	2.7	601	4	US-09-949-016-163068	Sequence 163068,	C 616	66	2.7	26928	4	US-09-544-398B-6	Sequence 6, Appl1
C 544	66.6	2.7	6021	4	US-09-949-016-131178	Sequence 131178, A	C 617	66	2.7	26928	4	US-09-543-771B-6	Sequence 6, Appl1
C 545	66.6	2.7	7260	4	US-09-917-254-31	Sequence 31, Appl	C 618	66	2.7	28315	4	US-09-949-016-16916	Sequence 16916, A
C 546	66.6	2.7	7260	4	US-09-919-497-24	Sequence 24, Appl	C 619	65.8	2.7	601	4	US-09-949-016-39131	Sequence 39131, A
C 547	66.6	2.7	15116	4	US-09-949-016-12354	Sequence 12354, A	C 620	65.8	2.7	601	4	US-09-949-016-87997	Sequence 87997, A
C 548	66.6	2.7	15117	4	US-09-949-016-16260	Sequence 16260, A	C 621	65.8	2.7	601	4	US-09-949-016-89154	Sequence 89154, A
C 549	66.6	2.7	32104	4	US-09-949-016-14722	Sequence 14722, A	C 622	65.8	2.7	601	4	US-09-949-016-89155	Sequence 89155, A
C 550	66.6	2.7	39489	4	US-09-949-016-13886	Sequence 13886, A	C 623	65.8	2.7	1867	3	US-08-943-731-111	Sequence 111, App
C 551	66.6	2.7	49352	4	US-09-949-016-12197	Sequence 12197, A	C 624	65.8	2.7	4897	4	US-09-949-016-16426	Sequence 16426, A
C 552	66.6	2.7	49360	4	US-09-949-016-17583	Sequence 17583, A	C 625	65.8	2.7	24183	3	US-08-943-731-3	Sequence 3, Appl1
C 553	66.6	2.7	48691	4	US-09-949-016-16308	Sequence 16308, A	C 626	65.8	2.7	64024	4	US-09-949-016-12823	Sequence 12823, A
C 554	66.6	2.7	51552	4	US-09-733-294A-30	Sequence 30, Appl	C 627	65.8	2.7	64024	4	US-09-949-016-17593	Sequence 17593, A
C 555	66.6	2.7	70828	4	US-09-949-016-12122	Sequence 12122, A	C 628	65.8	2.7	71935	4	US-09-949-016-12214	Sequence 12214, A
C 556	66.6	2.7	88240	4	US-09-949-016-16279	Sequence 16279, A	C 629	65.8	2.7	97195	4	US-09-949-016-12212	Sequence 12212, A
C 557	66.6	2.7	96074	4	US-09-949-016-13760	Sequence 12760, A	C 630	65.8	2.7	97196	4	US-09-949-016-16971	Sequence 16971, A
C 558	66.6	2.7	96074	4	US-09-949-016-13760	Sequence 12760, A	C 631	65.8	2.7	113701	4	US-09-949-016-13214	Sequence 13214, A
C 559	66.6	2.7	96074	4	US-09-949-016-13760	Sequence 12760, A	C 632	65.8	2.7	237510	4	US-09-949-016-14273	Sequence 14273, A
C 560	66.6	2.7	129899	4	US-09-949-016-17103	Sequence 17103, A	C 633	65.8	2.7	319608	4	US-09-539-333D-1	Sequence 1, Appl1
C 561	66.6	2.7	148156	4	US-09-949-016-14684	Sequence 14684, A	C 634	65.8	2.7	319608	4	US-09-679-409-1	Sequence 1, Appl1
C 562	66.6	2.7	235452	4	US-09-949-016-13675	Sequence 13675, A	C 635	65.6	2.7	124	4	US-09-513-999C-19387	Sequence 19387, A
C 563	66.4	2.7	163	4	US-09-513-999C-16936	Sequence 16936, A	C 636	65.6	2.7	180	4	US-09-513-999C-25784	Sequence 25784, A
C 564	66.4	2.7	601	4	US-09-949-016-16569	Sequence 16569, A	C 637	65.6	2.7	283	4	US-08-579-445-26	Sequence 26, Appl
C 565	66.4	2.7	601	4	US-09-949-016-105755	Sequence 105755,	C 638	65.6	2.7	308	3	US-09-222-575-88	Sequence 88, Appl
C 566	66.4	2.7	16965	4	US-09-949-016-16705	Sequence 16705, A	C 639	65.6	2.7	308	4	US-09-389-681-88	Sequence 88, Appl
C 567	66.4	2.7	19327	4	US-09-949-016-13666	Sequence 13666, A	C 640	65.6	2.7	308	4	US-09-620-405B-88	Sequence 88, Appl
C 568	66.4	2.7	22911	4	US-09-949-016-16683	Sequence 16683, A	C 641	65.6	2.7	308	4	US-09-339-338-88	Sequence 88, Appl
C 569	66.4	2.7	62883	4	US-09-949-016-12661	Sequence 12661, A	C 642	65.6	2.7	308	4	US-09-433-826B-88	Sequence 88, Appl
C 570	66.4	2.7	86857	4	US-09-949-016-14688	Sequence 14688, A	C 643	65.6	2.7	308	4	US-09-604-287A-88	Sequence 88, Appl
C 571	66.4	2.7	146428	4	US-09-949-016-12620	Sequence 12620, A	C 644	65.6	2.7	308	4	US-09-285-480-88	Sequence 88, Appl
C 572	66.4	2.7	146428	4	US-09-949-016-12620	Sequence 12620, A	C 645	65.6	2.7	308	4	US-09-834-759-88	Sequence 88, Appl
C 573	66.2	2.7	601	4	US-09-949-016-12081	Sequence 12081, A	C 646	65.6	2.7	308	4	US-09-590-751A-88	Sequence 88, Appl
C 574	66.2	2.7	601	4	US-09-949-016-86050	Sequence 86050, A	C 647	65.6	2.7	308	4	US-09-551-621-88	Sequence 88, Appl
C 575	66.2	2.7	601	4	US-09-949-016-86052	Sequence 86052, A	C 648	65.6	2.7	340	4	US-09-513-999C-36360	Sequence 36360, A
C 576	66.2	2.7	601	4	US-09-949-016-177507	Sequence 177507,	C 649	65.6	2.7	410	4	US-09-621-976-15464	Sequence 15464, A
C 577	66.2	2.7	601	4	US-09-949-016-177508	Sequence 177508,	C 650	65.6	2.7	464	4	US-09-621-976-15464	Sequence 15464, A
C 578	66.2	2.7	11667	4	US-09-949-016-13934	Sequence 184358, A	C 651	65.6	2.7	541	4	US-09-949-016-130275	Sequence 130275, A
C 579	66.2	2.7	11667	4	US-09-949-016-13934	Sequence 184358, A	C 652	65.6	2.7	601	4	US-09-949-016-19402	Sequence 19402, A
C 580	66.2	2.7	1961	4	US-09-949-016-13400	Sequence 13400, A	C 653	65.6	2.7	601	4	US-09-949-016-21009	Sequence 21009, A
C 581	66.2	2.7	17514	4	US-09-949-016-13121	Sequence 13121, A	C 654	65.6	2.7	601	4	US-09-949-016-22147	Sequence 22147, A
C 582	66.2	2.7	17580	4	US-09-949-016-16055	Sequence 16055, A	C 655	65.6	2.7	601	4	US-09-949-016-24952	Sequence 24952, A
C 583	66.2	2.7	24553	4	US-09-949-016-16901	Sequence 16901, A	C 656	65.6	2.7	601	4	US-09-949-016-24953	Sequence 24953, A
C 584	66.2	2.7	26314	4	US-09-949-016-16389	Sequence 16389, A	C 657	65.6	2.7	601	4	US-09-949-016-25832	Sequence 25832, A
C 585	66.2	2.7	26314	4	US-09-949-016-16389	Sequence 16389, A	C 658	65.6	2.7	601	4	US-09-949-016-27664	Sequence 27664, A
C 586	66.2	2.7	26314	4	US-09-949-016-16389	Sequence 16389, A	C 659	65.6	2.7	601	4	US-09-949-016-28487	Sequence 28487, A
C 587	66.2	2.7	38702	4	US-09-949-016-13788	Sequence 17585, A	C 660	65.6	2.7	601	4	US-09-949-016-28744	Sequence 28744, A
C 588	66.2	2.7	38702	4	US-09-949-016-13788	Sequence 17585, A	C 661	65.6	2.7	601	4	US-09-949-016-31490	Sequence 31490, A
C 589	66.2	2.7	39686	4	US-09-949-016-13633	Sequence 13633, A	C 662	65.6	2.7	601	4	US-09-949-016-31491	Sequence 31491, A
C 590	66.2	2.7	40168	4	US-09-949-016-13225	Sequence 13225, A	C 663	65.6	2.7	601	4	US-09-949-016-31491	Sequence 31491, A
C 591	66.2	2.7	43992	4	US-09-949-016-12172	Sequence 12172, A	C 664	65.6	2.7	601	4	US-09-949-016-35838	Sequence 35838, A
C 592	66.2	2.7	43992	4	US-09-949-016-12172	Sequence 12172, A	C 665	65.6	2.7	601	4	US-09-949-016-35915	Sequence 35915, A
C 593	66.2	2.7	43164	4	US-09-949-016-12985	Sequence 12985, A	C 666	65.6	2.7	601	4	US-09-949-016-36002	Sequence 36002, A
C 594	66.2	2.7	43164	4	US-09-949-016-12986	Sequence 12986, A	C 667	65.6	2.7	601	4	US-09-949-016-36121	Sequence 36121, A
C 595	66.2	2.7	43164	4	US-09-949-016-12986	Sequence 12986, A	C 668	65.6	2.7	601	4	US-09-949-016-36689	Sequence 36689, A
C 596	66.2	2.7	49487	4	US-09-949-016-13263	Sequence 13263, A	C 669	65.6	2.7	601	4	US-09-949-016-36944	Sequence 36944, A
C 597	66.2	2.7	51508	4	US-09-949-016-11770	Sequence 11770, A	C 670	65.6	2.7	601	4	US-09-949-016-40479	Sequence 40479, A
C 598	66.2	2.7	53558	4	US-09-949-016-16681	Sequence 16681, A	C 671	65.6	2.7	601	4	US-09-949-016-41232	Sequence 41232, A
C 599	66.2	2.7	63588	4	US-09-873-404-3	Sequence 3, Appl1	C 672	65.6	2.7	601	4	US-09-949-016-41557	Sequence 41557, A
C 600	66.2	2.7	63588	4	US-10-243-735-3	Sequence 3, Appl1	C 673	65.6	2.7	601	4	US-09-949-016-43155	Sequence 43155, A
C 601	66.2	2.7	63588	4	US-10-243-735-3	Sequence 3, Appl1	C 674	65.6	2.7	601	4	US-09-949-016-43384	Sequence 43384, A
C 602	66.2	2.7	70000	3	US-09-851-896-3	Sequence 3, Appl1	C 675	65.6	2.7	601	4	US-09-949-016-43613	Sequence 43613, A
C 603	66.2	2.7	76399	4	US-09-949-016-16819	Sequence 16819, A	C 676	65.6	2.7	601	4	US-09-949-016-45481	Sequence 45481, A
C 604	66.2	2.7	80355	4	US-09-949-016-12735	Sequence 12735, A	C 677	65.6	2.7	601	4	US-09-949-016-46388	Sequence 46388, A
C 605	66.2	2.7	80357	4	US-09-949-016-13572	Sequence 13572, A	C 678	65.6	2.7	601	4	US-09-949-016-46671	Sequence 46671, A
C 606	66.2	2.7	98302	4	US-09-949-016-16847	Sequence 16847, A	C 679	65.6	2.7	601	4	US-09-949-016-47364	Sequence 47364, A
C 607	66.2	2.7	140224	4	US-09-949-016-17002	Sequence 17002, A	C 680	65.6	2.7	601	4	US-09-949-016-47366	Sequence 47366, A
C 608	66.2	2.7	146095	4	US-09-949-016-12872	Sequence 12872, A	C 681	65.6	2.7	601	4	US-09-949-016-47974	Sequence 47974, A
C 609	66.2	2.7	146104	4	US-09-949-016-13239	Sequence 13239, A	C 682	65.6	2.7	601	4	US-09-949-016-52283	Sequence 52283, A
C 610	66.2	2.7	166698	4	US-09-949-016-16038	Sequence 16038, A	C 683	65.6	2.7	601	4	US-09-949-016-52284	Sequence 52284, A
C 611	66.2	2.7	304533	4	US-09-949-016-15371	Sequence 15371, A	C 684	65.6	2.7	601	4	US-09-949-016-52286	Sequence 52286, A

C 831	65.6	2.7	601	4	US-09-949-016-201294	Sequence 201294, App1	904	65.6	2.7	21536	4	US-09-949-016-13367	Sequence 13367, A
C 832	65.6	2.7	601	4	US-09-949-016-201342	Sequence 201342, App1	905	65.6	2.7	21536	4	US-09-949-016-13368	Sequence 13368, A
C 833	65.6	2.7	601	4	US-09-949-016-201408	Sequence 201408, App1	906	65.6	2.7	21536	4	US-09-949-016-13369	Sequence 13369, A
C 834	65.6	2.7	601	4	US-09-949-016-201456	Sequence 201456, App1	C 907	65.6	2.7	21614	4	US-09-949-016-13078	Sequence 13078, A
C 835	65.6	2.7	601	4	US-09-949-016-201858	Sequence 201858, App1	C 908	65.6	2.7	22311	4	US-09-949-016-12344	Sequence 12344, A
C 836	65.6	2.7	601	4	US-09-949-016-203303	Sequence 203303, App1	C 909	65.6	2.7	22312	4	US-09-949-016-17217	Sequence 17217, A
C 837	65.6	2.7	601	4	US-09-949-016-203304	Sequence 203304, App1	C 910	65.6	2.7	22686	4	US-09-949-016-12279	Sequence 12279, A
C 838	65.6	2.7	601	4	US-09-949-016-203305	Sequence 203305, App1	C 911	65.6	2.7	22686	4	US-09-949-016-15293	Sequence 15293, A
C 839	65.6	2.7	601	4	US-09-949-016-203771	Sequence 203771, App1	C 912	65.6	2.7	21300	4	US-09-949-016-15933	Sequence 15933, A
C 840	65.6	2.7	601	4	US-09-949-016-203772	Sequence 203772, App1	C 913	65.6	2.7	21300	4	US-09-949-016-13726	Sequence 13726, A
C 841	65.6	2.7	601	4	US-09-949-016-204143	Sequence 204143, App1	C 914	65.6	2.7	23501	4	US-09-949-016-17517	Sequence 17517, A
C 842	65.6	2.7	601	4	US-09-949-016-204338	Sequence 204338, App1	C 915	65.6	2.7	23501	4	US-09-949-016-14160	Sequence 14160, A
C 843	65.6	2.7	601	4	US-09-949-016-205341	Sequence 205341, App1	C 916	65.6	2.7	24020	4	US-09-949-016-17353	Sequence 17353, A
C 844	65.6	2.7	819	4	US-09-918-686-5	Sequence 5, App1	C 917	65.6	2.7	24144	4	US-09-949-016-15209	Sequence 15209, A
C 845	65.6	2.7	821	3	US-09-342-681C-7	Sequence 7, App1	C 918	65.6	2.7	24508	4	US-09-949-016-16005	Sequence 16005, A
C 846	65.6	2.7	3883	3	US-09-620-312D-792	Sequence 792, App1	C 919	65.6	2.7	24563	4	US-09-949-016-11864	Sequence 11864, A
C 847	65.6	2.7	4793	3	US-09-561-497-10	Sequence 10, App1	C 920	65.6	2.7	24563	4	US-09-949-016-13492	Sequence 13492, A
C 848	65.6	2.7	5096	4	US-09-949-016-15105	Sequence 15105, App1	C 921	65.6	2.7	24593	4	US-09-949-016-13433	Sequence 13433, A
C 849	65.6	2.7	6759	4	US-09-949-016-13689	Sequence 13689, App1	C 922	65.6	2.7	24645	4	US-09-949-016-14062	Sequence 14062, A
C 850	65.6	2.7	6799	4	US-09-620-312D-299	Sequence 299, App1	C 923	65.6	2.7	24707	4	US-09-949-016-12979	Sequence 12979, A
C 851	65.6	2.7	7480	4	US-09-949-016-11999	Sequence 11999, App1	C 924	65.6	2.7	24715	4	US-09-949-016-15380	Sequence 15380, A
C 852	65.6	2.7	7567	4	US-09-949-016-16486	Sequence 16486, App1	C 925	65.6	2.7	24839	4	US-09-949-016-12952	Sequence 12952, A
C 853	65.6	2.7	7620	1	US-07-767-135-1	Sequence 1, App1	C 926	65.6	2.7	24993	4	US-09-949-016-17400	Sequence 17400, A
C 854	65.6	2.7	7620	1	US-07-841-652-1	Sequence 1, App1	C 927	65.6	2.7	25041	4	US-09-326-480A-4	Sequence 4, App1
C 855	65.6	2.7	7971	4	US-09-949-016-14508	Sequence 14508, App1	C 928	65.6	2.7	25041	4	US-09-949-016-13397	Sequence 13397, A
C 856	65.6	2.7	8798	4	US-09-949-016-14609	Sequence 14609, App1	C 929	65.6	2.7	25067	4	US-09-949-016-17222	Sequence 17222, A
C 857	65.6	2.7	9038	4	US-09-949-016-13523	Sequence 13523, App1	C 930	65.6	2.7	26007	4	US-09-949-016-17449	Sequence 17449, A
C 858	65.6	2.7	9589	4	US-09-949-016-12889	Sequence 12889, App1	C 931	65.6	2.7	26050	4	US-09-949-016-14045	Sequence 14045, A
C 859	65.6	2.7	9695	4	US-09-949-016-13860	Sequence 13860, App1	C 932	65.6	2.7	26104	4	US-09-949-016-14045	Sequence 14045, A
C 860	65.6	2.7	9968	4	US-09-949-016-17571	Sequence 17571, App1	C 933	65.6	2.7	26257	4	US-09-949-016-16791	Sequence 16791, A
C 861	65.6	2.7	10827	4	US-09-949-016-12297	Sequence 12297, App1	C 934	65.6	2.7	26314	4	US-09-949-016-16389	Sequence 16389, A
C 862	65.6	2.7	11026	4	US-09-949-016-16680	Sequence 16680, App1	C 935	65.6	2.7	26438	4	US-09-949-016-17351	Sequence 17351, A
C 863	65.6	2.7	11406	4	US-09-949-016-17355	Sequence 17355, App1	C 936	65.6	2.7	26587	4	US-09-949-016-16636	Sequence 16636, A
C 864	65.6	2.7	11988	4	US-09-949-016-11977	Sequence 11977, App1	C 937	65.6	2.7	27184	4	US-09-949-016-17415	Sequence 17415, A
C 865	65.6	2.7	11989	4	US-09-949-016-13676	Sequence 13676, App1	C 938	65.6	2.7	27578	4	US-09-949-016-12167	Sequence 12167, A
C 866	65.6	2.7	12113	4	US-09-949-016-13144	Sequence 13144, App1	C 939	65.6	2.7	27579	4	US-09-949-016-15005	Sequence 15005, A
C 867	65.6	2.7	12434	4	US-09-949-016-14506	Sequence 14506, App1	C 940	65.6	2.7	27780	4	US-09-949-016-12013	Sequence 12013, A
C 868	65.6	2.7	12440	4	US-09-949-016-14109	Sequence 14109, App1	C 941	65.6	2.7	27791	4	US-09-949-016-17498	Sequence 17498, A
C 869	65.6	2.7	12440	4	US-09-949-016-14110	Sequence 14110, App1	C 942	65.6	2.7	28136	4	US-09-949-016-16317	Sequence 16317, A
C 870	65.6	2.7	12440	4	US-09-949-016-14899	Sequence 14899, App1	C 943	65.6	2.7	28165	4	US-09-949-016-17259	Sequence 17259, A
C 871	65.6	2.7	12440	4	US-09-949-016-14900	Sequence 14900, App1	C 944	65.6	2.7	28198	4	US-09-949-016-12349	Sequence 12349, A
C 872	65.6	2.7	12476	4	US-09-949-016-14623	Sequence 14623, App1	C 945	65.6	2.7	28257	4	US-09-949-016-13076	Sequence 13076, A
C 873	65.6	2.7	14721	4	US-09-949-016-13507	Sequence 13507, App1	C 946	65.6	2.7	28321	4	US-09-949-016-16936	Sequence 16936, A
C 874	65.6	2.7	14754	4	US-09-949-016-13636	Sequence 13636, App1	C 947	65.6	2.7	28325	4	US-09-949-016-16622	Sequence 16622, A
C 875	65.6	2.7	15024	4	US-09-949-016-15704	Sequence 15704, App1	C 948	65.6	2.7	28932	4	US-09-949-016-16653	Sequence 16653, A
C 876	65.6	2.7	15230	4	US-09-949-016-13450	Sequence 13450, App1	C 949	65.6	2.7	28932	4	US-09-949-016-16284	Sequence 16284, A
C 877	65.6	2.7	15273	4	US-09-949-016-12356	Sequence 12356, App1	C 950	65.6	2.7	29300	4	US-09-949-016-15326	Sequence 15326, A
C 878	65.6	2.7	15273	4	US-09-949-016-13341	Sequence 13341, App1	C 951	65.6	2.7	30402	4	US-09-949-016-12451	Sequence 12451, A
C 879	65.6	2.7	15358	4	US-09-949-016-13382	Sequence 13382, App1	C 952	65.6	2.7	30569	4	US-09-949-016-12592	Sequence 12592, A
C 880	65.6	2.7	15671	4	US-09-949-016-13623	Sequence 13623, App1	C 953	65.6	2.7	30569	4	US-09-949-016-12592	Sequence 12592, A
C 881	65.6	2.7	15677	4	US-09-949-016-13976	Sequence 13976, App1	C 954	65.6	2.7	31111	4	US-09-949-016-15628	Sequence 15628, A
C 882	65.6	2.7	15788	4	US-09-920-759-13	Sequence 13, App1	C 955	65.6	2.7	31391	4	US-09-949-016-17200	Sequence 17200, A
C 883	65.6	2.7	16158	4	US-09-949-016-17568	Sequence 17568, App1	C 956	65.6	2.7	32010	4	US-09-949-016-13127	Sequence 13127, A
C 884	65.6	2.7	16621	4	US-09-949-016-13708	Sequence 13708, App1	C 957	65.6	2.7	33353	4	US-09-949-016-17285	Sequence 17285, A
C 885	65.6	2.7	17082	4	US-09-949-016-14893	Sequence 14893, App1	C 958	65.6	2.7	33845	4	US-09-949-016-16081	Sequence 16081, A
C 886	65.6	2.7	17628	4	US-09-949-016-16718	Sequence 16718, App1	C 959	65.6	2.7	34047	4	US-09-949-016-17555	Sequence 17555, A
C 887	65.6	2.7	17730	4	US-09-949-016-12123	Sequence 12123, App1	C 960	65.6	2.7	34230	4	US-09-949-016-12052	Sequence 12052, A
C 888	65.6	2.7	17731	4	US-09-949-016-13472	Sequence 13472, App1	C 961	65.6	2.7	34422	4	US-09-949-016-12701	Sequence 12701, A
C 889	65.6	2.7	18157	4	US-09-949-016-16193	Sequence 16193, App1	C 962	65.6	2.7	34422	4	US-09-949-016-16075	Sequence 16075, A
C 890	65.6	2.7	18291	4	US-09-949-016-14787	Sequence 14787, App1	C 963	65.6	2.7	34629	4	US-09-949-016-13295	Sequence 13295, A
C 891	65.6	2.7	18448	4	US-09-949-016-15345	Sequence 15345, App1	C 964	65.6	2.7	35489	4	US-09-949-016-17209	Sequence 17209, A
C 892	65.6	2.7	18601	4	US-09-949-016-17560	Sequence 17560, App1	C 965	65.6	2.7	35493	4	US-09-949-016-16780	Sequence 16780, A
C 893	65.6	2.7	18947	4	US-09-949-016-15106	Sequence 15106, App1	C 966	65.6	2.7	35784	4	US-09-949-016-16785	Sequence 16785, A
C 894	65.6	2.7	19826	4	US-09-949-016-16973	Sequence 16973, App1	C 967	65.6	2.7	35784	4	US-09-949-016-16785	Sequence 16785, A
C 895	65.6	2.7	20116	4	US-09-949-016-16861	Sequence 16861, App1	C 968	65.6	2.7	36180	4	US-09-949-016-11745	Sequence 11745, A
C 896	65.6	2.7	20347	4	US-09-949-016-16752	Sequence 16752, App1	C 969	65.6	2.7	36181	4	US-09-949-016-16163	Sequence 16163, A
C 897	65.6	2.7	21210	4	US-09-949-016-12266	Sequence 12266, App1	C 970	65.6	2.7	36228	4	US-09-949-016-12256	Sequence 12256, A
C 898	65.6	2.7	21211	4	US-09-949-016-17328	Sequence 17328, App1	C 971	65.6	2.7	36228	4	US-09-949-016-15468	Sequence 15468, A
C 899	65.6	2.7	21535	4	US-09-949-016-12826	Sequence 12826, App1	C 972	65.6	2.7	36592	4	US-09-949-016-16313	Sequence 16313, A
C 900	65.6	2.7	21535	4	US-09-949-016-12827	Sequence 12827, App1	C 973	65.6	2.7	36592	4	US-09-949-016-13476	Sequence 13476, A
C 901	65.6	2.7	21535	4	US-09-949-016-12828	Sequence 12828, App1	C 974	65.6	2.7	36741	3	US-09-301-665-3	Sequence 3, App1
C 902	65.6	2.7	21535	4	US-09-949-016-12829	Sequence 12829, App1	C 975	65.6	2.7	36952	4	US-09-949-016-14786	Sequence 14786, A
C 903	65.6	2.7	21536	4	US-09-949-016-13366	Sequence 13366, App1	C 976	65.6	2.7	37195	4	US-09-949-016-13264	Sequence 13264, A

us-09-978-544a-58.rn1

Wed May 11 07:24:22 2005

977	65.6	2.7	37335	4	US-09-949-016-17132	Sequence 17132, A	c1050	65.6	2.7	54779	4	US-09-949-001-27	Sequence 27, Appl
978	65.6	2.7	37692	4	US-09-949-016-12089	Sequence 12089, A	c1051	65.6	2.7	54780	4	US-09-949-001-39	Sequence 39, Appl
c 979	65.6	2.7	37822	4	US-09-949-016-16391	Sequence 16391, A	c1052	65.6	2.7	54878	4	US-09-949-016-12255	Sequence 12255, A
980	65.6	2.7	38559	4	US-09-949-016-13384	Sequence 13384, A	c1053	65.6	2.7	54878	4	US-09-949-016-12255	Sequence 12255, A
981	65.6	2.7	38559	4	US-09-949-016-13385	Sequence 13385, A	c1054	65.6	2.7	55114	4	US-09-949-016-16792	Sequence 16792, A
982	65.6	2.7	38559	4	US-09-949-016-13386	Sequence 13386, A	c1055	65.6	2.7	55927	4	US-09-949-016-15017	Sequence 15017, A
c 983	65.6	2.7	38653	4	US-09-949-016-15987	Sequence 15987, A	c1056	65.6	2.7	55927	4	US-09-949-016-15017	Sequence 15017, A
984	65.6	2.7	38920	4	US-09-949-016-17546	Sequence 17546, A	c1057	65.6	2.7	56241	4	US-09-949-016-15174	Sequence 15174, A
c 985	65.6	2.7	39299	4	US-09-949-016-16625	Sequence 16625, A	c1058	65.6	2.7	56241	4	US-09-949-016-15175	Sequence 15175, A
986	65.6	2.7	39949	4	US-09-949-016-14210	Sequence 14210, A	c1059	65.6	2.7	57507	4	US-09-949-016-15019	Sequence 15019, A
c 987	65.6	2.7	40000	3	US-09-949-016-16504	Sequence 16504, A	c1060	65.6	2.7	57507	4	US-09-949-016-15019	Sequence 15019, A
c 988	65.6	2.7	40435	4	US-09-949-016-15504	Sequence 15504, A	c1061	65.6	2.7	57914	4	US-09-949-016-11935	Sequence 11935, A
989	65.6	2.7	40493	4	US-09-949-016-15453	Sequence 15453, A	c1062	65.6	2.7	57936	4	US-09-949-016-16232	Sequence 16232, A
c 990	65.6	2.7	40548	4	US-09-949-016-13317	Sequence 13317, A	c1063	65.6	2.7	58593	4	US-09-949-016-16232	Sequence 16232, A
c 991	65.6	2.7	40617	4	US-09-949-016-15197	Sequence 15197, A	c1064	65.6	2.7	58782	4	US-09-949-016-16851	Sequence 16851, A
c 992	65.6	2.7	40742	4	US-09-949-016-17151	Sequence 17151, A	c1065	65.6	2.7	58782	4	US-09-949-016-16851	Sequence 16851, A
c 993	65.6	2.7	40742	4	US-09-949-016-13097	Sequence 13097, A	c1066	65.6	2.7	60376	4	US-09-949-016-12423	Sequence 12423, A
c 994	65.6	2.7	41106	4	US-09-949-016-15796	Sequence 15796, A	c1067	65.6	2.7	60376	4	US-09-949-016-12423	Sequence 12423, A
995	65.6	2.7	41612	4	US-09-949-016-12769	Sequence 12769, A	c1068	65.6	2.7	60424	4	US-09-949-016-12702	Sequence 12702, A
c 996	65.6	2.7	41612	4	US-09-949-016-12773	Sequence 12773, A	c1069	65.6	2.7	60424	4	US-09-949-016-12702	Sequence 12702, A
c 997	65.6	2.7	41671	4	US-09-949-016-16693	Sequence 16693, A	c1070	65.6	2.7	60592	4	US-09-949-016-13741	Sequence 13741, A
c 998	65.6	2.7	42053	4	US-09-949-016-15924	Sequence 15924, A	c1071	65.6	2.7	60592	4	US-09-949-016-13741	Sequence 13741, A
c 999	65.6	2.7	42404	4	US-09-949-016-16415	Sequence 16415, A	c1072	65.6	2.7	61124	4	US-09-949-016-11914	Sequence 11914, A
1000	65.6	2.7	42672	4	US-09-949-016-17253	Sequence 17253, A	c1073	65.6	2.7	61124	4	US-09-949-016-11914	Sequence 11914, A
1001	65.6	2.7	42672	4	US-09-949-016-17254	Sequence 17254, A	c1074	65.6	2.7	61198	4	US-09-949-016-15771	Sequence 15771, A
1002	65.6	2.7	43232	4	US-09-949-016-17307	Sequence 17307, A	c1075	65.6	2.7	61198	4	US-09-949-016-15771	Sequence 15771, A
1003	65.6	2.7	43537	4	US-09-949-016-13458	Sequence 13458, A	c1076	65.6	2.7	62072	4	US-09-949-016-16076	Sequence 16076, A
1004	65.6	2.7	44477	4	US-09-949-016-16767	Sequence 16767, A	c1077	65.6	2.7	62072	4	US-09-949-016-16076	Sequence 16076, A
1005	65.6	2.7	44848	4	US-09-949-016-17238	Sequence 17238, A	c1078	65.6	2.7	64137	4	US-09-949-016-14831	Sequence 14831, A
1006	65.6	2.7	44848	4	US-09-949-016-1927	Sequence 1927, A	c1079	65.6	2.7	64137	4	US-09-949-016-14831	Sequence 14831, A
c1007	65.6	2.7	45314	4	US-09-949-016-12843	Sequence 12843, A	c1080	65.6	2.7	65042	3	US-09-949-016-11957	Sequence 3, Appl
c1008	65.6	2.7	45484	4	US-09-949-016-13267	Sequence 13267, A	c1081	65.6	2.7	65042	3	US-09-949-016-11957	Sequence 3, Appl
1009	65.6	2.7	45484	4	US-09-949-016-17599	Sequence 17599, A	c1082	65.6	2.7	66065	4	US-09-949-016-13292	Sequence 13292, A
1010	65.6	2.7	45900	4	US-09-949-016-13848	Sequence 13848, A	c1083	65.6	2.7	66065	4	US-09-949-016-13292	Sequence 13292, A
c1011	65.6	2.7	46885	4	US-09-949-016-15420	Sequence 15420, A	c1084	65.6	2.7	68444	4	US-09-949-016-13968	Sequence 13968, A
c1012	65.6	2.7	47375	4	US-09-949-016-16460	Sequence 16460, A	c1085	65.6	2.7	68444	4	US-09-949-016-13968	Sequence 13968, A
c1013	65.6	2.7	47683	4	US-09-949-016-17236	Sequence 17236, A	c1086	65.6	2.7	68452	4	US-09-949-016-13305	Sequence 13305, A
c1014	65.6	2.7	48682	4	US-09-949-016-17237	Sequence 17237, A	c1087	65.6	2.7	68452	4	US-09-949-016-13305	Sequence 13305, A
c1015	65.6	2.7	48682	4	US-09-949-016-17238	Sequence 17238, A	c1088	65.6	2.7	72504	4	US-09-949-016-12140	Sequence 12140, A
c1016	65.6	2.7	48682	4	US-09-949-016-17239	Sequence 17239, A	c1089	65.6	2.7	72504	4	US-09-949-016-12140	Sequence 12140, A
c1017	65.6	2.7	49212	4	US-09-949-016-12494	Sequence 12494, A	c1090	65.6	2.7	72604	3	US-09-949-016-15671	Sequence 15671, A
c1018	65.6	2.7	49320	4	US-09-949-016-14726	Sequence 14726, A	c1091	65.6	2.7	72604	3	US-09-949-016-15671	Sequence 15671, A
c1019	65.6	2.7	49315	4	US-09-949-016-13016	Sequence 13016, A	c1092	65.6	2.7	74177	4	US-09-949-016-11988	Sequence 11988, A
c1020	65.6	2.7	49401	4	US-09-949-016-17080	Sequence 17080, A	c1093	65.6	2.7	74177	4	US-09-949-016-11988	Sequence 11988, A
c1021	65.6	2.7	49440	4	US-09-949-016-14150	Sequence 14150, A	c1094	65.6	2.7	75674	4	US-09-949-016-17597	Sequence 17597, A
c1022	65.6	2.7	49472	4	US-09-949-016-14150	Sequence 14150, A	c1095	65.6	2.7	75674	4	US-09-949-016-17597	Sequence 17597, A
c1023	65.6	2.7	49472	4	US-09-949-016-14150	Sequence 14150, A	c1096	65.6	2.7	76165	4	US-09-949-016-12288	Sequence 12288, A
1024	65.6	2.7	50186	4	US-09-949-016-15721	Sequence 15721, A	c1097	65.6	2.7	76165	4	US-09-949-016-12288	Sequence 12288, A
1025	65.6	2.7	50186	4	US-09-949-016-14066	Sequence 14066, A	c1098	65.6	2.7	76553	4	US-09-949-016-14005	Sequence 14005, A
1026	65.6	2.7	50368	4	US-09-949-016-13256	Sequence 13256, A	c1099	65.6	2.7	76553	4	US-09-949-016-14005	Sequence 14005, A
c1027	65.6	2.7	50878	4	US-09-949-016-11787	Sequence 11787, A	c1100	65.6	2.7	77636	4	US-09-949-016-17482	Sequence 17482, A
c1028	65.6	2.7	51022	4	US-09-949-016-17135	Sequence 17135, A	c1101	65.6	2.7	77636	4	US-09-949-016-17482	Sequence 17482, A
c1029	65.6	2.7	51022	4	US-09-949-016-17136	Sequence 17136, A	c1102	65.6	2.7	77626	4	US-09-949-016-16156	Sequence 16156, A
c1030	65.6	2.7	51022	4	US-09-949-016-17138	Sequence 17138, A	c1103	65.6	2.7	77626	4	US-09-949-016-16156	Sequence 16156, A
c1031	65.6	2.7	51049	4	US-09-949-016-15571	Sequence 15571, A	c1104	65.6	2.7	77626	4	US-09-949-016-16156	Sequence 16156, A
c1032	65.6	2.7	51629	4	US-09-949-016-12883	Sequence 12883, A	c1105	65.6	2.7	77626	4	US-09-949-016-16156	Sequence 16156, A
c1033	65.6	2.7	51631	4	US-09-949-016-15496	Sequence 15496, A	c1106	65.6	2.7	81927	4	US-09-949-016-14209	Sequence 14209, A
1034	65.6	2.7	51719	4	US-09-949-016-16982	Sequence 16982, A	c1107	65.6	2.7	81927	4	US-09-949-016-14209	Sequence 14209, A
1035	65.6	2.7	51967	4	US-09-949-016-16498	Sequence 16498, A	c1108	65.6	2.7	83450	4	US-09-949-016-14209	Sequence 14209, A
1036	65.6	2.7	52494	4	US-09-949-016-16118	Sequence 16118, A	c1109	65.6	2.7	83450	4	US-09-949-016-14209	Sequence 14209, A
1037	65.6	2.7	52494	4	US-09-949-016-16118	Sequence 16118, A	c1110	65.6	2.7	83708	4	US-09-949-016-16241	Sequence 16241, A
1038	65.6	2.7	52496	4	US-09-949-016-16119	Sequence 16119, A	c1111	65.6	2.7	83708	4	US-09-949-016-16241	Sequence 16241, A
c1039	65.6	2.7	52496	4	US-09-949-016-16119	Sequence 16119, A	c1112	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
c1040	65.6	2.7	52496	4	US-09-949-016-16119	Sequence 16119, A	c1113	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
c1041	65.6	2.7	52821	4	US-09-949-016-12137	Sequence 12137, A	c1114	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
1042	65.6	2.7	52824	4	US-09-949-016-12137	Sequence 12137, A	c1115	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
c1043	65.6	2.7	53737	4	US-09-949-016-16197	Sequence 16197, A	c1116	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
c1044	65.6	2.7	53789	4	US-09-949-016-13955	Sequence 13955, A	c1117	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
1045	65.6	2.7	54161	4	US-09-949-016-11905	Sequence 11905, A	c1118	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
1046	65.6	2.7	54161	4	US-09-949-016-11905	Sequence 11905, A	c1119	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
1047	65.6	2.7	54463	4	US-09-949-016-14781	Sequence 14781, A	c1120	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
c1048	65.6	2.7	54463	4	US-09-949-016-14781	Sequence 14781, A	c1121	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A
c1049	65.6	2.7	54463	4	US-09-949-016-14781	Sequence 14781, A	c1122	65.6	2.7	84875	4	US-09-949-016-17334	Sequence 17334, A

1269	65.6	2.7	203475	4	US-09-949-016-17227	Sequence 17227, A	1342	65.4	2.7	28055	4	US-09-949-016-16441	Sequence 16441, A
1270	65.6	2.7	203475	4	US-09-949-016-17228	Sequence 17228, A	1343	65.4	2.7	33663	4	US-09-949-016-15679	Sequence 15679, A
1271	65.6	2.7	203475	4	US-09-949-016-17229	Sequence 17229, A	c1344	65.4	2.7	70000	3	US-09-851-896-3	Sequence 3, Appli
1272	65.6	2.7	205044	4	US-09-949-016-15851	Sequence 15851, A	c1345	65.4	2.7	76399	4	US-09-949-016-16819	Sequence 16819, A
1273	65.6	2.7	205044	4	US-09-949-016-15852	Sequence 15852, A	c1346	65.4	2.7	77772	4	US-09-949-016-17417	Sequence 17417, A
1274	65.6	2.7	205044	4	US-09-949-016-15853	Sequence 15853, A	c1347	65.4	2.7	77997	4	US-09-949-016-17417	Sequence 17417, A
1275	65.6	2.7	205044	4	US-09-949-016-17009	Sequence 17009, A	1348	65.4	2.7	77997	4	US-09-949-016-12388	Sequence 12388, A
1276	65.6	2.7	205210	4	US-09-949-016-15094	Sequence 15094, A	1349	65.4	2.7	94156	4	US-09-949-016-14673	Sequence 14673, A
1277	65.6	2.7	205210	4	US-09-949-016-15094	Sequence 15094, A	c1350	65.4	2.7	283538	4	US-09-949-016-13506	Sequence 13506, A
1278	65.6	2.7	222452	4	US-09-949-016-12968	Sequence 12968, A	1351	65.2	2.7	601	4	US-09-949-016-19401	Sequence 19401, A
1279	65.6	2.7	223471	4	US-09-949-016-12387	Sequence 12387, A	c1352	65.2	2.7	601	4	US-09-949-016-21810	Sequence 21810, A
1280	65.6	2.7	223471	4	US-09-949-016-12724	Sequence 12724, A	1353	65.2	2.7	601	4	US-09-949-016-23558	Sequence 23558, A
1281	65.6	2.7	223471	4	US-09-949-016-12725	Sequence 12725, A	1354	65.2	2.7	601	4	US-09-949-016-30314	Sequence 30314, A
1282	65.6	2.7	225127	4	US-09-949-016-16480	Sequence 16480, A	1355	65.2	2.7	601	4	US-09-949-016-32293	Sequence 32293, A
c1283	65.6	2.7	225127	4	US-09-949-016-16480	Sequence 16480, A	1356	65.2	2.7	601	4	US-09-949-016-44090	Sequence 44090, A
1284	65.6	2.7	235452	4	US-09-949-016-13675	Sequence 13675, A	c1357	65.2	2.7	601	4	US-09-949-016-44119	Sequence 44119, A
c1285	65.6	2.7	235452	4	US-09-949-016-13675	Sequence 13675, A	1358	65.2	2.7	601	4	US-09-949-016-44148	Sequence 44148, A
1286	65.6	2.7	237241	4	US-09-949-016-13418	Sequence 13418, A	c1359	65.2	2.7	601	4	US-09-949-016-44177	Sequence 44177, A
1287	65.6	2.7	237241	4	US-09-949-016-16274	Sequence 16274, A	1360	65.2	2.7	601	4	US-09-949-016-44206	Sequence 44206, A
c1288	65.6	2.7	248968	4	US-09-949-016-12614	Sequence 12614, A	c1361	65.2	2.7	601	4	US-09-949-016-44619	Sequence 44619, A
c1289	65.6	2.7	248968	4	US-09-949-016-12614	Sequence 12614, A	1362	65.2	2.7	601	4	US-09-949-016-47365	Sequence 47365, A
1290	65.6	2.7	253335	4	US-09-949-016-12656	Sequence 12656, A	c1363	65.2	2.7	601	4	US-09-949-016-47975	Sequence 47975, A
c1291	65.6	2.7	253335	4	US-09-949-016-12656	Sequence 12656, A	1364	65.2	2.7	601	4	US-09-949-016-52285	Sequence 52285, A
c1292	65.6	2.7	253335	4	US-09-949-016-12656	Sequence 12656, A	c1365	65.2	2.7	601	4	US-09-949-016-56357	Sequence 56357, A
c1293	65.6	2.7	255679	4	US-09-949-016-17189	Sequence 17189, A	c1366	65.2	2.7	601	4	US-09-949-016-76095	Sequence 76095, A
c1294	65.6	2.7	255679	4	US-09-949-016-17189	Sequence 17189, A	c1367	65.2	2.7	601	4	US-09-949-016-83533	Sequence 83533, A
1295	65.6	2.7	264358	4	US-09-949-016-16435	Sequence 16435, A	c1368	65.2	2.7	601	4	US-09-949-016-83709	Sequence 83709, A
c1296	65.6	2.7	264358	4	US-09-949-016-16435	Sequence 16435, A	1369	65.2	2.7	601	4	US-09-949-016-88524	Sequence 88524, A
c1297	65.6	2.7	264665	4	US-09-949-016-13747	Sequence 13747, A	1370	65.2	2.7	601	4	US-09-949-016-88524	Sequence 88524, A
c1298	65.6	2.7	264665	4	US-09-949-016-13747	Sequence 13747, A	1371	65.2	2.7	601	4	US-09-949-016-120352	Sequence 120352, A
1299	65.6	2.7	275110	4	US-09-949-016-12706	Sequence 12706, A	c1372	65.2	2.7	601	4	US-09-949-016-120353	Sequence 120353, A
c1300	65.6	2.7	275110	4	US-09-949-016-12706	Sequence 12706, A	1373	65.2	2.7	601	4	US-09-949-016-120359	Sequence 120359, A
c1301	65.6	2.7	275110	4	US-09-949-016-12706	Sequence 12706, A	c1374	65.2	2.7	601	4	US-09-949-016-120359	Sequence 120359, A
c1302	65.6	2.7	276687	4	US-09-949-016-17504	Sequence 17504, A	1375	65.2	2.7	601	4	US-09-949-016-121348	Sequence 121348, A
c1303	65.6	2.7	276687	4	US-09-949-016-17504	Sequence 17504, A	c1376	65.2	2.7	601	4	US-09-949-016-121348	Sequence 121348, A
c1304	65.6	2.7	278866	4	US-09-949-016-13922	Sequence 13922, A	1377	65.2	2.7	601	4	US-09-949-016-122159	Sequence 122159, A
c1305	65.6	2.7	278866	4	US-09-949-016-13922	Sequence 13922, A	c1378	65.2	2.7	601	4	US-09-949-016-133485	Sequence 133485, A
c1306	65.6	2.7	278866	4	US-09-949-016-13922	Sequence 13922, A	1379	65.2	2.7	601	4	US-09-949-016-13729	Sequence 13729, A
c1307	65.6	2.7	278866	4	US-09-949-016-14699	Sequence 14699, A	c1379	65.2	2.7	601	4	US-09-949-016-140099	Sequence 140099, A
c1308	65.6	2.7	278866	4	US-09-949-016-14699	Sequence 14699, A	c1380	65.2	2.7	601	4	US-09-949-016-140124	Sequence 140124, A
c1309	65.6	2.7	278866	4	US-09-949-016-14700	Sequence 14700, A	1381	65.2	2.7	601	4	US-09-949-016-140124	Sequence 140124, A
c1310	65.6	2.7	278866	4	US-09-949-016-14700	Sequence 14700, A	c1382	65.2	2.7	601	4	US-09-949-016-148676	Sequence 148676, A
c1311	65.6	2.7	278866	4	US-09-949-016-14700	Sequence 14700, A	c1383	65.2	2.7	601	4	US-09-949-016-153592	Sequence 153592, A
c1312	65.6	2.7	278866	4	US-09-949-016-14700	Sequence 14700, A	1384	65.2	2.7	601	4	US-09-949-016-153592	Sequence 153592, A
c1313	65.6	2.7	285478	4	US-09-949-016-13362	Sequence 13362, A	c1385	65.2	2.7	601	4	US-09-949-016-158966	Sequence 158966, A
c1314	65.6	2.7	285478	4	US-09-949-016-12887	Sequence 12887, A	1386	65.2	2.7	601	4	US-09-949-016-163130	Sequence 163130, A
c1315	65.6	2.7	288031	4	US-09-949-016-14864	Sequence 14864, A	c1387	65.2	2.7	601	4	US-09-949-016-163130	Sequence 163130, A
c1316	65.6	2.7	288031	4	US-09-949-016-16600	Sequence 16600, A	1388	65.2	2.7	601	4	US-09-949-016-163130	Sequence 163130, A
c1317	65.6	2.7	312474	4	US-09-949-016-17434	Sequence 17434, A	c1389	65.2	2.7	601	4	US-09-949-016-17426	Sequence 17426, A
c1318	65.6	2.7	421118	4	US-09-949-016-16297	Sequence 16297, A	1390	65.2	2.7	601	4	US-09-949-016-189198	Sequence 189198, A
c1319	65.6	2.7	421118	4	US-09-949-016-16297	Sequence 16297, A	c1391	65.2	2.7	601	4	US-09-949-016-196314	Sequence 196314, A
c1320	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1392	65.2	2.7	601	4	US-09-949-016-196611	Sequence 196611, A
c1321	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1393	65.2	2.7	601	4	US-09-949-016-196611	Sequence 196611, A
c1322	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1394	65.2	2.7	5139	4	US-09-949-016-198023	Sequence 198023, A
c1323	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1395	65.2	2.7	32104	3	US-09-949-016-15353	Sequence 15353, A
c1324	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1396	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1325	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1397	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1326	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1398	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1327	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1399	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1328	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1399	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1329	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1400	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1330	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1401	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1331	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1402	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1332	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1403	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1333	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1404	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1334	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1405	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1335	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1406	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1336	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1407	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1337	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1408	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1338	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1409	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1339	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1410	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1340	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1411	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1341	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1412	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1342	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1413	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1343	65.6	2.7	524032	4	US-09-949-016-16931	Sequence 16931, A	c1414	65.2	2.7	35060	3	US-09-949-016-14722	Sequence 14722, A
c1344	65.6	2.7	524032										

QY	795	CTCTGGACTGTACAGTGTGACAGAGCAACGAAAGCTGGGAAAGCTGTGTGTGCG	854
Db	594	CTCTGGACTGTACAGTGTGACAGAGCAACGAAAGCTGGGAAAGCTGTGTGTGCG	653
QY	855	AGTAACTGTACAGTGTGACAGAGCAACGAAAGCTGGGAAAGCTGTGTGTGCG	914
Db	654	AGTAACTGTACAGTGTGACAGAGCAACGAAAGCTGGGAAAGCTGTGTGTGCG	713
QY	915	GGCTGGAGCCCTGTGATTTTCCTTTGGTGTGCTCTAATCCGAGGAAAGCAAAAGA	974
Db	714	GGCTGGAGCCCTGTGATTTTCCTTTGGTGTGCTCTAATCCGAGGAAAGCAAAAGA	773
QY	975	AAGATATGAGGAAAGAGAGACCTAATGAAATTCGAGAGATGCTGAAGCTCCAAAGC	1034
Db	774	AAGATATGAGGAAAGAGAGACCTAATGAAATTCGAGAGATGCTGAAGCTCCAAAGC	833
QY	1035	CGCTTTGTGAAACCCAGCTCTCTCTCAGGCTCTCGAGCTCAGGCTCTGTTCTTC	1094
Db	834	CGCTTTGTGAAACCCAGCTCTCTCTCAGGCTCTCGAGCTCAGGCTCTGTTCTTC	893
QY	1095	CTCCACTCGCTCCACAGCAAAATAGTCTCAGCAGCAGCGGACACTGTGTC-AACTGACG	1153
Db	894	CTCCACTCGCTCCACAGCAAAATAGTCTCAGCAGCAGCGGACACTGTGTC-AACTGACG	953
QY	1154	CAGCAGCCCGAGCGGCTGGCCACCCAGGCATACAGCTAGTGGGGCCAGAGGTGAGAG	1213
Db	954	CAGCAGCCCGAGCGGCTGGCCACCCAGGCATACAGCTAGTGGGGCCAGAGGTGAGAG	1013
QY	1214	GTTCTGMAACCAAGAAAGTCCACCATGCTAATCTGACCAAGAGCAGAAACCAACCCAGCA	1273
Db	1014	GTTCTGMAACCAAGAAAGTCCACCATGCTAATCTGACCAAGAGCAGAAACCAACCCAGCA	1073
QY	1274	TGATCCCCAGCAGCAGAGAGCTTCCAAAACCGTCTGAAATACATGAGCTTGATCTCCCA	1333
Db	1074	TGATCCCCAGCAGCAGAGAGCTTCCAAAACCGTCTGAAATACATGAGCTTGATCTCCCA	1133
QY	1334	CGTTTCTTAGAGTCCAGGCTTTGGACTCTTCCTGCTGATGGAGCTCAAGTCAACGAC	1393
Db	1134	CGTTTCTTAGAGTCCAGGCTTTGGACTCTTCCTGCTGATGGAGCTCAAGTCAACGAC	1193
QY	1394	CACACAACAGATGAGAGGTCTAATGAGTACAGTGTGAGATGCGAAGCAGATTCAGA	1453
Db	1194	CACACAACAGATGAGAGGTCTAATGAGTACAGTGTGAGATGCGAAGCAGATTCAGA	1253
QY	1454	TGAGCAATTTCTTATACATACCAACCAAGCAAGAGGATGTAAGTCTGATTCATCTGTAA	1513
Db	1254	TGAGCAATTTCTTATACATACCAACCAAGCAAGAGGATGTAAGTCTGATTCATCTGTAA	1313
QY	1514	AAAGGCATCTTATTTGTGCTTTAGACAGAGTAAGGAAAGCAGGAGTCCAAATCTATTT	1573
Db	1314	AAAGGCATCTTATTTGTGCTTTAGACAGAGTAAGGAAAGCAGGAGTCCAAATCTATTT	1373
QY	1574	GTTGACGAGCACTGTGTGAGAGGTTGGGAAAGCTGAGTGTATATACCTAAACCTT	1633
Db	1374	GTTGACGAGCACTGTGTGAGAGGTTGGGAAAGCTGAGTGTATATACCTAAACCTT	1433
QY	1634	TTAATGTGGATATTTTGTATCAGTCTTTGATTTCAAAATTTCAAGAGGAAATGGGATG	1693
Db	1434	TTAATGTGGATATTTTGTATCAGTCTTTGATTTCAAAATTTCAAGAGGAAATGGGATG	1493
QY	1694	CTGTTTGTAAATTTCTATGATTTCTGCAAACTTATGATTTATGATTTATGATTTATG	1753
Db	1494	CTGTTTGTAAATTTCTATGATTTCTGCAAACTTATGATTTATGATTTATGATTTATG	1553
QY	1754	TCAAGCAGAACCCACAGCCTTATACACCTGTCTACACCATGCTGAGTCAACCACTTC	1813
Db	1554	TCAAGCAGAACCCACAGCCTTATACACCTGTCTACACCATGCTGAGTCAACCACTTC	1613
QY	1814	TAAGAACTCCAAAAAGGAAACATGTGTCTTCTTATTTCTGACTTAACCTCATTTGTCAT	1873
Db	1614	TAAGAACTCCAAAAAGGAAACATGTGTCTTCTTATTTCTGACTTAACCTCATTTGTCAT	1673
QY	1874	AGGTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGAGATGAATGA	1933
Db	1674	AGGTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGAGATGAATGA	1733
QY	1934	GTTTCTCCACTCTACTAATCTCCTATTTGATTTGAGCCCAAAATAAATATGAAAGG	1993
Db	1734	GTTTCTCCACTCTACTAATCTCCTATTTGATTTGAGCCCAAAATAAATATGAAAGG	1793
QY	1994	AGACAAAATTTGTGACAAAGGATTTGGAAGAGCTTTCCATCTTCATGATGTTATGAGGA	2053
Db	1794	AGACAAAATTTGTGACAAAGGATTTGGAAGAGCTTTCCATCTTCATGATGTTATGAGGA	1853
QY	2054	TTGTTGACAAACATTTAGAAATATATAATGAGGCAATTTGGAATTTCCCTCAATCAGAT	2113
Db	1854	TTGTTGACAAACATTTAGAAATATATAATGAGGCAATTTGGAATTTCCCTCAATCAGAT	1913
QY	2114	GCCTCTAGGAGCTTTCTGCTAGATATTTCTGGAAGGAAATAACAATGCTCATTTAT	2173
Db	1914	GCCTCTAGGAGCTTTCTGCTAGATATTTCTGGAAGGAAATAACAATGCTCATTTAT	1973
QY	2174	CAACGCTCTTAGAAAGAAATTTCTTAGAGAAAGGATCTAGGAATGCTGAAGATTAC	2233
Db	1974	CAACGCTCTTAGAAAGAAATTTCTTAGAGAAAGGATCTAGGAATGCTGAAGATTAC	2033
QY	2234	CAACATACCATTTATGATCTCTCTTCTGAGAAATGTGAAACCAAGATTTGCAAGACTG	2293
Db	2034	CAACATACCATTTATGATCTCTCTTCTGAGAAATGTGAAACCAAGATTTGCAAGACTG	2093
QY	2294	GGTGGACTAGAAAGGAGATTTAGATCAGTTTCTCTTAATATGTCAGGAAGGTAGCCCG	2353
Db	2094	GGTGGACTAGAAAGGAGATTTAGATCAGTTTCTCTTAATATGTCAGGAAGGTAGCCCG	2153
QY	2354	GCATGTGCCAGGACCTCTAGGAAATCCAG	2385
Db	2153	GCATGTGCCAGGACCTCTAGGAAATCCAG	2184
RESULT 2			
US-09-949-016-16476			
; Sequence 16476, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CLO01307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 16476			
; LENGTH: 141560			
; TYPE: DNA			
; ORGANISM: Human			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (1)...(141560)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-949-016-16476			
Query Match 58.6%; Score 1441; DB 4; Length 141560;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 1444; Conservative			
QY	1010	GAGAGATGCTGAAGCTCCAAAGCCCGTCTTGTGTAACCCAGGCTCTCTTCTCAGGCT	1069
Db	123272	GAGAGATGCTGAAGCTCCAAAGCCCGTCTTGTGTAACCCAGGCTCTCTTCTCAGGCT	123331

QY 1070 CTGGAGCTCAGCTCTGGTTCTTCTCCACTCGCTCCACAGCAATAGTCTCAGCA 1129
DB 123332 CTCGGAGCTCAGCTCTGGTTCTTCTCCACTCGCTCCACAGCAATAGTCTCAGCA 123391
QY 1130 GCAGCGGACACTGTCAACTGACGAGCAGCCAGCCAGGGCTGGCCACCCAGGAGATCA 1189
DB 123392 GCAGCGGACACTGTCAACTGACGAGCAGCCAGCCAGGGCTGGCCACCCAGGAGATCA 123451
QY 1190 GCTTAGTGGGGCAGAGGTGAGAGTTCTGAACCAAGAAAGTCCACCAATGTAATCTGA 1249
DB 123452 GCTTAGTGGGGCAGAGGTGAGAGTTCTGAACCAAGAAAGTCCACCAATGTAATCTGA 123511
QY 1250 CCAAGCAGAAACACACCCAGCAGATGATCCAGCCAGAGCAGAGCTTCCAAACGGTCT 1309
DB 123512 CCAAGCAGAAACACACCCAGCAGATGATCCAGCCAGAGCAGAGCTTCCAAACGGTCT 123571
QY 1310 GAATTACAAATGACTTGCATCCACGCTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTC 1369
DB 123572 GAATTACAAATGACTTGCATCCACGCTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTC 123631
QY 1370 GTCAATGGAGCTCAAGTCAACGAGCAGCAACACAGATGAGAGTCACTTAAGTAGCAGTG 1429
DB 123632 GTCAATGGAGCTCAAGTCAACGAGCAGCAACACAGATGAGAGTCACTTAAGTAGCAGTG 123691
QY 1430 AGCATTTGACGGAACAGATTCAGATGAGCATTTTCTTATACAAATACCAACCAAGCAAA 1489
DB 123692 AGCATTTGACGGAACAGATTCAGATGAGCATTTTCTTATACAAATACCAACCAAGCAAA 123751
QY 1490 GGATGTAAGTCAATCATCTGTAAGAAAGCATCTTATGTGCTTTAGACCAAGATGAAG 1549
DB 123752 GGATGTAAGTCAATCATCTGTAAGAAAGCATCTTATGTGCTTTAGACCAAGATGAAG 123811
QY 1550 GAAAGCAGAGTCCAAATCTATTGTTGACCAAGGACCTGTGTTGAGAAAGTTGGGGAAG 1609
DB 123812 GAAAGCAGAGTCCAAATCTATTGTTGACCAAGGACCTGTGTTGAGAAAGTTGGGGAAG 123871
QY 1610 GTGAGGTGAATATACATAAATCTTTAATGTGGGATATTTGTATCAGTGTCTTGAATCA 1669
DB 123872 GTGAGGTGAATATACATAAATCTTTAATGTGGGATATTTGTATCAGTGTCTTGAATCA 123931
QY 1670 CAATTTTCAAGAGGAATGGGATGCTGTTGTAATTTCTATGATTTCTCAAACTTA 1729
DB 123932 CAATTTTCAAGAGGAATGGGATGCTGTTGTAATTTCTATGATTTCTCAAACTTA 123991
QY 1730 TTGGATTATTAGTATTTCAGACAGTCAAGCAGACCCACAGCCTTATTACCTCTCTAC 1789
DB 123992 TTGGATTATTAGTATTTCAGACAGTCAAGCAGACCCACAGCCTTATTACCTCTCTAC 124051
QY 1790 ACCATGTACTGAGCTAACCACTTTAAGAACTCCAAAGGAACATGTGCTCTCTAT 1849
DB 124052 ACCATGTACTGAGCTAACCACTTTAAGAACTCCAAAGGAACATGTGCTCTCTAT 124111
QY 1850 TCTGACTTAACCTTCAATTTGTCTAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAG 1909
DB 124112 TCTGACTTAACCTTCAATTTGTCTAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAG 124171
QY 1910 TGGGAGATGGAGAGAGTGAATGAGTTTCTCCACTCTATATAATCTCACTATTTTGTAT 1969
DB 124172 TGGGAGATGGAGAGAGTGAATGAGTTTCTCCACTCTATATAATCTCACTATTTTGTAT 124231
QY 1970 TGAGCCCCAAATACTATGAAGAGAGCAAAATTTGTGACAAAGATTTGGAAGCTT 2029
DB 124232 TGAGCCCCAAATACTATGAAGAGAGCAAAATTTGTGACAAAGATTTGGAAGCTT 124291
QY 2030 TCCATCTTCATGATCTATGAGATTTGTGACAAACATTTAGAAATATATATGAGCAAT 2089
DB 124292 TCCATCTTCATGATCTATGAGATTTGTGACAAACATTTAGAAATATATATGAGCAAT 124351
QY 2090 TGTGATTTCCCTCAAAATCAGATGCTCTAAGGACTTTCTGCTAGATATTCTTGGAG 2149
DB 124352 TGTGATTTCCCTCAAAATCAGATGCTCTAAGGACTTTCTGCTAGATATTCTTGGAG 124411
QY 2150 GAGAAATACACATGTCTATTTATCAAGCTCTTCTAGAAAGATTTCTTCTAGAGAAAAAGG 2209

DB 124412 GAGAAATACACATGTCTATTTATCAAGCTCTTCTAGAAAGATTTCTTCTAGAGAAAAAGG 124471
QY 2210 GATCTAGGAATGCTGAAAGATTTACCAACATACCAATTTATAGTCTCTCTTTCTGAGAAAA 2269
DB 124472 GATCTAGGAATGCTGAAAGATTTACCAACATACCAATTTATAGTCTCTCTTTCTGAGAAAA 124531
QY 2270 TGTGAAACAGAAATTTGCAAGACTGGGTGAGCTAGAAAGGAGATTTAGATCAGTTTCTCT 2329
DB 124532 TGTGAAACAGAAATTTGCAAGACTGGGTGAGCTAGAAAGGAGATTTAGATCAGTTTCTCT 124591
QY 2330 TAATATGTCAGGAAGGTAGCCGGCATGTCAGGACCTGTAGGAAAAATCCAGCAG 2389
DB 124592 TAATATGTCAGGAAGGTAGCCGGCATGTCAGGACCTGTAGGAAAAATCCAGCAG 124651
QY 2390 TGGAGTTTGCAGTACGCGAGATTTATGTCATTTGCACCTCCAGCTGGGTGACAGCGGGA 2449
DB 124652 TGGAGTTTGCAGTACGCGAGATTTATGTCATTTGCACCTCCAGCTGGGTGACAAAGCAAGA 124711
QY 2450 CTCCTCTCTC 2458
DB 124712 CTCCTCTCTC 124720

RESULT 3
US-09-949-016-4734
; Sequence 4734, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4734
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4734

Query Match 26.5%; Score 652; DB 4; Length 2685;
Best Local Similarity 100.0%; Pred. No. 1.1e-186;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 GTTTCCTACTATGTTGGAACCTTGGGGACTCACACTGAGATCAAGAGAGTGCAGAGGAA 276
DB 88 GTTTCCTACTATGTTGGAACCTTGGGGACTCACACTGAGATCAAGAGAGTGCAGAGGAA 147
QY 277 AAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCAGAAAAAGACACTCTGGATATT 336
DB 148 AAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCAGAAAAAGACACTCTGGATATT 207
QY 337 GAATGGCTGTCTCACCGATAATGAAGGGAAACCAAAAGTGGTGATCACTTACTCCAGTCT 396
DB 208 GAATGGCTGTCTCACCGATAATGAAGGGAAACCAAAAGTGGTGATCACTTACTCCAGTCT 267
QY 397 CATGTCTCAATTAATTCAGTCTGAGAAAGGCGCCAGTGGCCCTTTGCTTCCGAATTC 456
DB 268 CATGTCTCAATTAATTCAGTCTGAGAAAGGCGCCAGTGGCCCTTTGCTTCCGAATTC 327
QY 457 CTGGCAGAGATGCTCTCTTCAGATTGAACCTCTGAAGCCAGGTGATGAGGGCCGGTAC 516
DB 328 CTGGCAGAGATGCTCTCTTCAGATTGAACCTCTGAAGCCAGGTGATGAGGGCCGGTAC 387

Wed May 11 07:24:22 2005

```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15143
; LENGTH: 15192
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15143

Query Match      2.9%; Score 70.8; DB 4; Length 15192;
Best Local Similarity 83.0%; Pred. No. 8.1e-11;
Matches 93; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 517 ACCTGTAAAGCTTAAGATTTCAGGCGCTACGTGTGGAGCCATGTCATCTTAAAGTCTTA 576
Db 388 ACCTGTAAAGGTTAAGATTTCAGGCGCTACGTGTGGAGCCATGTCATCTTAAAGTCTTA 447
QY 577 GTGAGACCATCCAAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAGGAAGTACCTG 636
Db 448 GTGAGACCATCCAAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAGGAAGTACCTG 507
QY 637 ACTTTGAGTGTGAGTATCTCTGACAGAGCCCAATGTTGTTACTTACTGCGAGCGAATC 696
Db 508 ACTTTGAGTGTGAGTATCTCTGACAGAGCCCAATGTTGTTACTTACTGCGAGCGAATC 567
QY 697 CGAGAGAAAGAGGAGAGAGTGAACGCTGCTGCCCTCCCAATCTAGGATGTGATCAACCC 756
Db 568 CGAGAGAAAGAGGAGAGAGTGAACGCTGCTGCCCTCCCAATCTAGGATGTGATCAACCC 627
QY 757 CTTGACAGTGTGCTGCGAATCTTACCATGCTTCTACTCTGACGTGACCTGACAGTGCACA 816
Db 628 CTTGACAGTGTGCTGCGAATCTTACCATGCTTCTACTCTGACGTGACCTGACAGTGCACA 687
QY 817 GCAGCAAGAGAGTGGGAAAGAGCTGTGTGTGGAGTAACTGTACAGT 868
Db 688 GCAGCAAGAGAGTGGGAAAGAGCTGTGTGTGGAGTAACTGTACAGT 739

RESULT 4
US-09-949-016-121707
; Sequence 121707, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121707
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-121707

Query Match      2.9%; Score 70.8; DB 4; Length 601;
Best Local Similarity 83.0%; Pred. No. 8.1e-11;
Matches 93; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 2343 AAGGTAGCCGGCATGTGCCAGCACCTGTAG--GAAATCCAGCAGGTGGAGTTGCA 2400
Db 166 AATTAGCCGGCATGTGCCAGCACCTGTAGTCCAGCTACTGGAGCGGAGTTGCA 225
QY 2401 GTGAGCCGAGATTATGCCATTGCACTTCAGCTGGGTGCAGACGGGACTC 2452
Db 226 GTGAGCTGAGATCAGCCATTGCACTCCAGCTGGGTGCAGACGGGACTC 277

RESULT 5
US-09-949-016-15143
; Sequence 15143, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15143
; LENGTH: 15192
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15143

Query Match      2.9%; Score 70.8; DB 4; Length 15192;
Best Local Similarity 83.0%; Pred. No. 8.1e-11;
Matches 93; Conservative 0; Mismatches 17; Indels 2; Gaps 1;

QY 2343 AAGGTAGCCGGCATGTGCCAGCACCTGTAG--GAAATCCAGCAGGTGGAGTTGCA 2400
Db 166 AATTAGCCGGCATGTGCCAGCACCTGTAGTCCAGCTACTGGAGCGGAGTTGCA 225
QY 2401 GTGAGCCGAGATTATGCCATTGCACTTCAGCTGGGTGCAGACGGGACTC 2452
Db 226 GTGAGCTGAGATCAGCCATTGCACTCCAGCTGGGTGCAGACGGGACTC 277

RESULT 6
US-09-949-016-14498
; Sequence 14498, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14498
; LENGTH: 19861
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14498

Query Match      2.9%; Score 70.8; DB 4; Length 19861;
Best Local Similarity 74.3%; Pred. No. 1e-09;
Matches 104; Conservative 0; Mismatches 32; Indels 4; Gaps 1;

QY 2323 TTCTCTTAATAATGTCTCAAGGAAGTGTAGCCGGCATGTGCCAGCACCTGTAGGAAAATC 2382
Db 11332 TGCTCTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11391
QY 2383 -----CAGCAGAGTGGAGTTGCAGTGCAGCGGAGATATGCCATTGCACTCCAGCTGGGTG 2438
Db 11392 TACTCAGGAGCGGAGTTGCAGTGCAGCGGAGATATGCCATTGCACTCCAGCTGGGTG 11451
QY 2439 ACAGAGCGGAGTCCGCTC 2458
Db 11452 ACAGAGCAAGACTGTCTC 11471

RESULT 7
US-09-866-108A-15752/c
; Sequence 15752, Application US/09866108A

```


Patent No. 6886188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEWICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6886188
SEQ ID NO 15752
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-15752

Query Match 2.9%; Score 70.6; DB 4; Length 1000;
Best Local Similarity 74.5%; Pred. No. 1.3e-10;
Matches 102; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
Qy 2322 TTTTCTCTTATATGTCAGGAAGGTAGCCGGGCAATGTCAGGCACCTGTAGGAAAT 2381
Db 156 TCTACTTAAATAACAAAACAAAATAGCCGGGCGTGGTGGCGCGCTGTAGTCCAG 97
Qy 2382 CCAGCAGGTGGAGTTGTCAGTGAGCCGAGATTATGCCATTGCATCCAGCCTGGGTGACA 2441
Db 96 CTA-CAGCGGAGCTTGTCAGTAAGCCGAGATAGCCGCACTGCATCCAGCCTGGGTGACA 38
Qy 2442 GAGCGGAGCTCCGTCTC 2458
Db 37 GAGAGAGACTCCATCTC 21

RESULT 8
US-09-949-016-93537/c
Sequence 93537, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6886188
SEQ ID NO 15752
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-15752

Query Match 2.9%; Score 70.6; DB 4; Length 1000;
Best Local Similarity 74.5%; Pred. No. 1.3e-10;
Matches 102; Conservative 0; Mismatches 34; Indels 1; Gaps 1;
Qy 2322 TTTTCTCTTATATGTCAGGAAGGTAGCCGGGCAATGTCAGGCACCTGTAGGAAAT 2381
Db 156 TCTACTTAAATAACAAAACAAAATAGCCGGGCGTGGTGGCGCGCTGTAGTCCAG 97
Qy 2382 CCAGCAGGTGGAGTTGTCAGTGAGCCGAGATTATGCCATTGCATCCAGCCTGGGTGACA 2441
Db 96 CTA-CAGCGGAGCTTGTCAGTAAGCCGAGATAGCCGCACTGCATCCAGCCTGGGTGACA 38
Qy 2442 GAGCGGAGCTCCGTCTC 2458
Db 37 GAGAGAGACTCCATCTC 21

RESULT 8
US-09-949-016-93537/c
Sequence 93537, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6886188
SEQ ID NO 15752
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-15752

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 93537
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-93537

Query Match 2.9%; Score 70.4; DB 4; Length 601;
Best Local Similarity 71.6%; Pred. No. 1.1e-10;
Matches 106; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
Qy 2311 GATTAGATCAGTTTCTCTTATATGTCAGGAAGGTAGCCGGGCAATGTCAGGCACCTCCAGCACC 2370
Db 448 GGTGAACCCCGTCTCTACTTAAATAACAAAATAGCCGAGCTGTGGCAGAGAA 389
Qy 2371 TGTAAGAAAATCCAGCAGGTGGAGTTGTCAGTGAGCCGAGATTATGCCATTGCATCCAG 2430
Db 388 TG-GTGTGAACCCAGGAGCGGAGCTTACAGTGAGCCAAAGATTGCGCCACTGCATCCAG 330
Qy 2431 CCTGGGTGACAGAGCGGAGCTCCGTCTC 2458
Db 329 CCTGGGACAGAGCGAGACTCCGTCTC 302

RESULT 9
US-09-949-016-121416/c
Sequence 121416, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 121416
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-121416

Query Match 2.9%; Score 70.4; DB 4; Length 601;
Best Local Similarity 92.5%; Pred. No. 1.1e-10;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 2379 AATCCAGCAGGTGGAGTTGTCAGTGAGCCGAGATTATGCCATTGCATCCAGCCTGGGTG 2438
Db 232 AACCCAGGAGGTGGAGTTGAGGGGCGGAGATCATGCCATTCATCCAGCCTGGGTG 173
Qy 2439 ACAGAGCGGAGCTCCGTCTC 2458
Db 172 ACAGTGAGAGACTCCGTCTC 153

RESULT 10
US-09-949-016-121706
Sequence 121706, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 121706
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-121706

Query Match 2.9%; Score 70.4; DB 4; Length 601;
Best Local Similarity 82.1%; Pred. No. 1.1e-10;
Matches 92; Conservative 1; Mismatches 17; Indels 2; Gaps 1;
QY 2343 AAGGTAGCCGGCATGTGGCCAGGCACTGTAG--GAAATCCACGAGGTGGAGTTGCA 2400
DB 198 AAATAGCCGGCATGTGGCCGGCCCTGTAGTCCAGCTACTGGAGCGGAGTTGCA 257
QY 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGCTGGGTGACAGCGGGACTC 2452
DB 258 GTGACCTGAGATCAGCCATTGCACTCCAGCGCTGGGTGACAGCGAGACTC 309

RESULT 11
US-09-949-016-146958
Sequence 146958, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 146958
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-146958

Query Match 2.9%; Score 70.4; DB 4; Length 601;
Best Local Similarity 92.5%; Pred. No. 1.1e-10;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2379 AATCCAGCAGGTGGAGTTGCAGTGGCCGAGATTATGCCATTGCACTCCAGCCTGGGTG 2438
DB 205 AACCCAGGAGTGGAGTTGCAGTGGCCGAGATCATGCACTCCAGCCTGGGGG 264
QY 2439 ACAGAGCGGACTCCGCTTC 2458
DB 265 ACAGAGCGAGACTCCGCTTC 284

RESULT 12
US-09-949-016-198954/c
Sequence 198954, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198954
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-198954

Query Match 2.9%; Score 70.4; DB 4; Length 601;
Best Local Similarity 92.5%; Pred. No. 1.1e-10;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2379 AATCCAGCAGGTGGAGTTGCAGTGGCCGAGATTATGCCATTGCACTCCAGCCTGGGTG 2438
DB 426 AATCCAGGAGTGGAGTTGCAGTGGCCGAGATTGTGCCATTGCACTCCAGCCTGGGAG 367
QY 2439 ACAGAGCGGACTCCGCTTC 2458
DB 366 ACAGAGCAAGACTCCGCTTC 347

RESULT 13
US-09-949-016-198955/c
Sequence 198955, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 198955
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-198955

Query Match 2.9%; Score 70.4; DB 4; Length 601;
Best Local Similarity 92.5%; Pred. No. 1.1e-10;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2379 AATCCAGCAGGTGGAGTTGCAGTGGCCGAGATTATGCCATTGCACTCCAGCCTGGGTG 2438
DB 398 AATCCAGGAGTGGAGTTGCAGTGGCCGAGATTGTGCCATTGCACTCCAGCCTGGGAG 339
QY 2439 ACAGAGCGGACTCCGCTTC 2458
DB 338 ACAGAGCAAGACTCCGCTTC 319

RESULT 14

US-09-949-016-11987
; Sequence 11987, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11987
; LENGTH: 23218
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11987

Query Match 2.9%; Score 70.4; DB 4; Length 23218;
Best Local Similarity 92.5%; Pred. No. 1.5e-09;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2379 AATCCAGCAGGTGGAGTTGCAGTCCGAGATTTATGCCATTGCACTCCAGCCTGGGTG 2438
Db 8003 AATCCAGGAGTGGAGTTGCAGTCCGAGATCGTGCCATTGCACTCCAGCCTGGGTG 8062

Qy 2439 ACAGAGCGGAGCTCGTCTC 2458
Db 8063 ACAGAGCGGAGCTCCATCTC 8082

RESULT 15

US-09-949-016-13396
; Sequence 13396, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13396
; LENGTH: 23219
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13396

Query Match 2.9%; Score 70.4; DB 4; Length 23219;
Best Local Similarity 92.5%; Pred. No. 1.5e-09;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2379 AATCCAGCAGGTGGAGTTGCAGTCCGAGATTTATGCCATTGCACTCCAGCCTGGGTG 2438
Db 8003 AATCCAGGAGTGGAGTTGCAGTCCGAGATCGTGCCATTGCACTCCAGCCTGGGTG 8062

Qy 2439 ACAGAGCGGAGCTCGTCTC 2458

Db 8063 ACAGAGCGGAGCTCCATCTC 8082

Search completed: May 6, 2005, 07:15:02
Job time : 504 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2005, 21:33:33 ; Search time 1289 Seconds
(without alignments)
11659.897 Million cell updates/sec

Perfect score: 2458
Sequence: 1 gcgcggggagccatctgcc.....acagaggggactcgtcttc 2458

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
32	2458	100.0	2458	10	US-09-997-428-502
127	2458	100.0	2458	14	US-10-167-749-58
289	2458	100.0	2458	15	US-10-223-085-63
295	2458	100.0	2458	15	US-10-219-065-129
324	2458	100.0	2458	15	US-10-223-084-63
325	2458	100.0	2458	15	US-10-223-088-63
326	2458	100.0	2458	15	US-10-223-090-63
331	2458	100.0	2458	15	US-10-223-087-63
332	2458	100.0	2458	15	US-10-223-083-63
336	2458	100.0	2458	15	US-10-223-089-63
509	2458	100.0	2458	16	US-10-223-081-63
547	2458	100.0	2458	16	US-10-223-082-63

616	2458	100.0	2458	17	US-10-170-481A-58	Sequence 58, Appl
618	2458	100.0	2458	17	US-10-210-028-58	Sequence 58, Appl
687	2458	100.0	2458	17	US-10-162-521A-58	Sequence 58, Appl
702	2458	100.0	2458	17	US-10-305-654-63	Sequence 63, Appl
721	2458	100.0	2458	17	US-10-081-056-63	Sequence 63, Appl
722	2458	100.0	2458	19	US-10-918-851-58	Sequence 58, Appl
723	2458	100.0	2458	19	US-10-931-886-387	Sequence 387, Appl
724	2458	100.0	2458	19	US-10-805-667-58	Sequence 58, Appl
726	2458	100.0	2458	19	US-10-897-359-58	Sequence 58, Appl
727	2458	100.0	2458	19	US-10-893-802-58	Sequence 58, Appl
728	2458	100.0	2458	19	US-10-897-360-58	Sequence 58, Appl
729	2458	99.7	3120	18	US-10-723-860-7540	Sequence 7540, Ap
730	2448.4	99.6	5120	18	US-10-696-487-1	Sequence 1, Appl
731	1804.8	73.4	1948	9	US-09-796-858-23	Sequence 23, Appl
732	1441	58.6	5183	9	US-09-764-877-3153	Sequence 3153, Ap
733	1441	58.6	5183	17	US-10-242-515-3153	Sequence 3153, Ap
734	1422.4	57.9	1942	18	US-10-723-860-6121	Sequence 6121, Ap
735	1045	42.5	1949	9	US-09-796-858-25	Sequence 25, Appl
736	575.2	23.4	1233	10	US-09-814-353-20546	Sequence 20546, A
737	426	17.3	426	17	US-10-243-552-162	Sequence 162, App
738	380	15.5	392	18	US-10-243-552-768	Sequence 768, App
739	359.8	14.6	378	17	US-10-723-860-3569	Sequence 3569, Ap
740	359.8	14.6	378	17	US-10-242-535A-49733	Sequence 49733, A
741	352.6	14.3	1496	14	US-10-198-846-11539	Sequence 49733, A
742	339.4	13.8	405	10	US-10-814-353-15423	Sequence 1539, A
743	308	12.5	332	18	US-09-814-353-1750	Sequence 15423, A
744	221.6	9.0	295	10	US-09-814-353-2706	Sequence 1750, Ap
745	221.6	9.0	295	10	US-09-814-353-9039	Sequence 2706, Ap
746	190.2	7.7	241	17	US-10-242-535A-21857	Sequence 9039, Ap
747	190.2	7.7	241	17	US-10-085-783A-21857	Sequence 21857, A
748	143	5.8	232	9	US-09-783-590-7314	Sequence 7314, Ap
749	79.4	3.2	43454	13	US-10-087-192-88	Sequence 88, Appl
750	72.8	3.0	870	13	US-10-027-632-261214	Sequence 261214, S
751	72.8	3.0	870	13	US-10-027-632-261215	Sequence 261215, S
752	72.8	3.0	870	13	US-10-027-632-261216	Sequence 261216, S
753	72.8	3.0	870	13	US-10-027-632-261217	Sequence 261217, S
754	72.8	3.0	870	17	US-10-027-632-261214	Sequence 261214, S
755	72.8	3.0	870	17	US-10-027-632-261215	Sequence 261215, S
756	72.8	3.0	870	17	US-10-027-632-261216	Sequence 261216, S
757	72.8	3.0	870	17	US-10-027-632-261217	Sequence 261217, S
758	72.4	2.9	814	13	US-10-027-632-160540	Sequence 160540, S
759	72.4	2.9	814	13	US-10-027-632-160541	Sequence 160541, S
760	72.4	2.9	814	13	US-10-027-632-160542	Sequence 160542, S
761	72.4	2.9	814	17	US-10-027-632-160540	Sequence 160540, S
762	72.4	2.9	814	17	US-10-027-632-160541	Sequence 160541, S
763	72.4	2.9	814	17	US-10-027-632-160542	Sequence 160542, S
764	72.2	2.9	319	9	US-09-784-869-1566	Sequence 1566, Ap
765	72.2	2.9	319	14	US-10-091-504-1566	Sequence 1566, Ap
766	72.2	2.9	319	17	US-10-227-577-1566	Sequence 1566, Ap
767	72	2.9	22693	17	US-10-371-416-6	Sequence 6, Appl
768	71.6	2.9	31463	18	US-10-719-993-6826	Sequence 6826, Ap
769	71.6	2.9	57095	18	US-10-719-993-7030	Sequence 7030, Ap
770	71.6	2.9	68114	18	US-10-719-993-6809	Sequence 6809, Ap
771	71.6	2.9	136328	15	US-10-101-510-127	Sequence 127, App
772	70.6	2.9	1000	9	US-09-866-108-15752	Sequence 15752, A
773	70.6	2.9	1000	18	US-10-723-361-15752	Sequence 15752, A
774	70.4	2.9	201	19	US-10-741-600-48382	Sequence 48382, A
775	70.4	2.9	815	13	US-10-027-632-152840	Sequence 152840, S
776	70.4	2.9	815	17	US-10-027-632-152840	Sequence 152840, S
777	70.4	2.9	830	13	US-10-027-632-155156	Sequence 155156, S
778	70.4	2.9	830	13	US-10-027-632-169662	Sequence 169662, S
779	70.4	2.9	830	17	US-10-027-632-155156	Sequence 155156, S
780	70.4	2.9	830	17	US-10-027-632-169662	Sequence 169662, S
781	70.4	2.9	96596	17	US-10-052-482-10	Sequence 10, Appl
782	70.4	2.9	119036	19	US-10-741-600-17721	Sequence 17721, A
783	70.4	2.9	149480	10	US-09-873-367C-284	Sequence 284, App
784	70.4	2.9	149480	10	US-09-873-367C-285	Sequence 285, App
785	70.4	2.9	149480	11	US-09-968-007A-232	Sequence 232, App
786	70.4	2.9	149480	19	US-10-843-641A-284	Sequence 284, App
787	70.4	2.9	149480	19	US-10-843-641A-285	Sequence 285, App
788	70.4	2.9	149480	19	US-10-843-641A-6702	Sequence 6702, Ap
789	70.4	2.9	216929	18	US-10-741-601-5727	Sequence 5727, Ap

790	70.2	2.9	299	9	US-09-764-869-1567	Sequence 1567, Ap	863	68.8	2.8	55827	9	US-09-813-133A-3	Sequence 3, Appli
791	70.2	2.9	299	14	US-10-091-504-1567	Sequence 1567, Ap	864	68.8	2.8	55827	14	US-10-212-877-3	Sequence 3, Appli
792	70.2	2.9	299	17	US-10-227-577-1567	Sequence 1567, Ap	865	68.8	2.8	55827	17	US-10-954-110-3	Sequence 3, Appli
793	70.2	2.9	530	13	US-10-027-632-135976	Sequence 135976, c	866	68.8	2.8	56510	19	US-10-741-600-17637	Sequence 17637, A
794	70.2	2.9	530	17	US-10-027-632-135976	Sequence 135976, c	867	68.8	2.8	61458	17	US-10-085-117-292	Sequence 292, App
795	70.2	2.9	67858	19	US-10-741-600-17974	Sequence 17974, A	868	68.8	2.8	68355	19	US-10-484-577-665	Sequence 665, App
796	70	2.8	659	17	US-10-012-697-885	Sequence 885, App	869	68.8	2.8	86001	18	US-10-317-500-4	Sequence 4, Appli
797	70	2.8	1843	13	US-10-027-632-97500	Sequence 97500, A	870	68.8	2.8	96588	11	US-09-997-722-292	Sequence 292, App
798	70	2.8	1843	17	US-10-027-632-97500	Sequence 97500, A	871	68.8	2.8	106938	18	US-10-322-281-566	Sequence 566, App
799	70	2.8	34641	9	US-09-954-456-1110	Sequence 1110, Ap	872	68.8	2.8	113604	14	US-10-227-195A-1	Sequence 1, Appli
800	70	2.8	34641	9	US-09-954-456-11787	Sequence 11787, Ap	873	68.8	2.8	113604	14	US-10-227-195A-2	Sequence 2, Appli
801	70	2.8	34641	10	US-09-931-733-6	Sequence 6, Appli	874	68.8	2.8	113604	17	US-10-227-152B-1	Sequence 1, Appli
802	70	2.8	34641	19	US-10-843-641A-4137	Sequence 4137, Ap	875	68.8	2.8	113604	17	US-10-227-152B-2	Sequence 2, Appli
803	70	2.8	34641	19	US-10-843-641A-4814	Sequence 4814, Ap	876	68.8	2.8	118951	14	US-10-161-572-11	Sequence 11, Appl
804	69.8	2.8	276276	13	US-10-087-192-754	Sequence 754, App	877	68.8	2.8	130877	18	US-10-322-281-54	Sequence 54, Appl
805	69.4	2.8	201	19	US-10-741-600-48401	Sequence 48401, A	878	68.8	2.8	139389	17	US-10-236-031B-61	Sequence 61, Appl
806	69.4	2.8	45698	11	US-09-964-429-344	Sequence 344, App	879	68.8	2.8	160552	18	US-10-697-828-11	Sequence 11, Appl
807	69.4	2.8	187844	14	US-10-719-993-6883	Sequence 6883, App	880	68.8	2.8	170245	18	US-10-717-597-322	Sequence 322, App
808	69.4	2.8	196686	13	US-10-087-192-484	Sequence 484, App	881	68.8	2.8	208648	19	US-10-484-577-662	Sequence 682, App
809	69.4	2.8	228139	13	US-10-087-192-232	Sequence 232, App	882	68.8	2.8	208648	19	US-10-484-577-668	Sequence 663, App
810	69	2.8	201	19	US-10-741-600-48310	Sequence 48310, A	883	68.8	2.8	213040	13	US-10-484-577-668	Sequence 668, App
811	69	2.8	617	13	US-10-027-632-259599	Sequence 259599, c	884	68.8	2.8	213040	13	US-10-087-192-856	Sequence 856, App
812	69	2.8	617	17	US-10-027-632-259599	Sequence 259599, c	885	68.8	2.8	227968	18	US-10-723-860-1357	Sequence 1357, Ap
813	68.8	2.8	241	18	US-10-674-124A-7391	Sequence 7391, Ap	886	68.8	2.8	243390	18	US-10-322-281-462	Sequence 462, App
814	68.8	2.8	251	9	US-09-764-847-1205	Sequence 1205, Ap	887	68.8	2.8	325791	11	US-09-768-188A-1	Sequence 1, Appli
815	68.8	2.8	251	14	US-10-092-154-1205	Sequence 1205, Ap	888	68.8	2.8	379652	19	US-10-481-613-71	Sequence 71, Appl
816	68.8	2.8	316	11	US-09-969-034-325	Sequence 325, App	889	68.8	2.8	414295	18	US-10-719-993-6876	Sequence 6876, Ap
817	68.8	2.8	325	14	US-10-060-036-2882	Sequence 2882, Ap	890	68.8	2.8	510510	19	US-10-741-600-17606	Sequence 17606, A
818	68.8	2.8	637	13	US-10-027-632-180187	Sequence 180187, c	891	68.8	2.8	518360	18	US-10-367-094-125	Sequence 125, App
819	68.8	2.8	637	17	US-10-027-632-180187	Sequence 180187, c	892	68.8	2.8	744802	17	US-10-292-798-1369	Sequence 1369, Ap
820	68.8	2.8	672	13	US-10-027-632-157792	Sequence 157792, c	893	68.8	2.8	1790342	18	US-10-719-993-6940	Sequence 6940, Ap
821	68.8	2.8	672	13	US-10-027-632-157792	Sequence 157792, c	894	68.6	2.8	676	17	US-10-027-632-191580	Sequence 191580, c
822	68.8	2.8	719	13	US-10-027-632-26058	Sequence 26058, A	895	68.6	2.8	676	17	US-10-027-632-191580	Sequence 191580, c
823	68.8	2.8	719	13	US-10-027-632-26058	Sequence 26058, A	896	68.4	2.8	461	10	US-09-918-995-14734	Sequence 14734, A
824	68.8	2.8	753	13	US-10-027-632-30463	Sequence 30463, A	897	68.4	2.8	1039	13	US-10-027-632-100652	Sequence 100652, c
825	68.8	2.8	753	17	US-10-027-632-30463	Sequence 30463, A	898	68.4	2.8	1039	17	US-10-027-632-100652	Sequence 100652, c
826	68.8	2.8	1406	19	US-10-491-997-35	Sequence 35, Appl	899	68.4	2.8	1257	13	US-10-027-632-265272	Sequence 265272, c
827	68.8	2.8	2091	17	US-10-104-047-1273	Sequence 1273, Ap	900	68.4	2.8	1257	17	US-10-027-632-265272	Sequence 265272, c
828	68.8	2.8	2091	17	US-10-104-047-1273	Sequence 1273, Ap	901	68.4	2.8	91000	15	US-10-002-491-10	Sequence 10, Appl
829	68.8	2.8	2263	13	US-10-027-632-263694	Sequence 263694, c	902	68.4	2.8	233528	18	US-10-719-993-6856	Sequence 6856, Ap
830	68.8	2.8	2263	13	US-10-027-632-263694	Sequence 263694, c	903	68.2	2.8	345	10	US-09-803-719-1837	Sequence 1837, Ap
831	68.8	2.8	2263	13	US-10-027-632-263694	Sequence 263694, c	904	68.2	2.8	405	18	US-10-357-930-49070	Sequence 49070, A
832	68.8	2.8	2263	17	US-10-027-632-263695	Sequence 263695, c	905	68.2	2.8	415	18	US-10-357-930-49070	Sequence 49070, A
833	68.8	2.8	2875	13	US-10-027-632-112261	Sequence 112261, c	906	68.2	2.8	1027	13	US-10-027-632-121789	Sequence 121789, c
834	68.8	2.8	2875	13	US-10-027-632-112261	Sequence 112261, c	907	68.2	2.8	1027	13	US-10-027-632-121789	Sequence 121789, c
835	68.8	2.8	6902	9	US-09-764-847-1019	Sequence 1019, Ap	908	68.2	2.8	1027	17	US-10-027-632-121789	Sequence 121789, c
836	68.8	2.8	6902	14	US-10-092-154-1019	Sequence 1019, Ap	909	68.2	2.8	1938	17	US-10-027-632-121790	Sequence 121790, c
837	68.8	2.8	7720	9	US-09-954-456-946	Sequence 946, App	910	68.2	2.8	5370	10	US-10-108-2608A-399	Sequence 399, App
838	68.8	2.8	7720	9	US-09-954-456-946	Sequence 946, App	911	68.2	2.8	5370	10	US-09-814-353-19834	Sequence 19834, A
839	68.8	2.8	7720	11	US-09-968-007A-125	Sequence 125, App	912	68.2	2.8	34118	15	US-10-017-161-1071	Sequence 1071, Ap
840	68.8	2.8	7720	11	US-09-968-007A-407	Sequence 407, App	913	68.2	2.8	34118	17	US-10-292-798-909	Sequence 909, App
841	68.8	2.8	7720	11	US-09-968-007A-743	Sequence 743, App	914	68.2	2.8	34875	18	US-10-775-169-316	Sequence 316, App
842	68.8	2.8	7720	16	US-10-094-007B-74	Sequence 74, Appl	915	68.2	2.8	101209	13	US-10-087-192-460	Sequence 460, App
843	68.8	2.8	7720	19	US-10-843-641A-3973	Sequence 3973, Ap	916	68.2	2.8	247682	17	US-10-235-192A-28	Sequence 28, Appl
844	68.8	2.8	7720	19	US-10-843-641A-4616	Sequence 4616, Ap	917	68.2	2.8	1790242	18	US-10-719-993-6940	Sequence 6940, Ap
845	68.8	2.8	7720	19	US-10-843-641A-6595	Sequence 6595, Ap	918	68	2.8	3560	9	US-09-764-869-2411	Sequence 2411, Ap
846	68.8	2.8	7720	19	US-10-843-641A-6877	Sequence 6877, Ap	919	68	2.8	3560	14	US-10-091-504-2411	Sequence 2411, Ap
847	68.8	2.8	7720	19	US-10-843-641A-7213	Sequence 7213, Ap	920	68	2.8	3560	17	US-10-227-577-2411	Sequence 2410, Ap
848	68.8	2.8	7960	9	US-09-764-869-2327	Sequence 2327, Ap	921	68	2.8	3561	9	US-09-764-869-2410	Sequence 2410, Ap
849	68.8	2.8	7960	14	US-10-091-504-2327	Sequence 2327, Ap	922	68	2.8	3561	14	US-10-091-504-2410	Sequence 2410, Ap
850	68.8	2.8	7960	17	US-10-227-577-2327	Sequence 2327, Ap	923	68	2.8	3561	17	US-10-227-577-2410	Sequence 460, App
851	68.8	2.8	9339	9	US-09-764-891-5385	Sequence 5385, Ap	924	68	2.8	103747	18	US-10-450-826-46	Sequence 450, Appl
852	68.8	2.8	17239	9	US-09-764-869-2326	Sequence 2326, Ap	925	67.8	2.8	234	17	US-10-242-535A-19570	Sequence 19570, A
853	68.8	2.8	17239	14	US-10-091-504-2326	Sequence 2326, Ap	926	67.8	2.8	234	17	US-10-085-783A-19570	Sequence 7369, Ap
854	68.8	2.8	18408	17	US-10-227-577-2326	Sequence 2326, Ap	927	67.8	2.8	318	13	US-10-027-632-8562	Sequence 8562, Ap
855	68.8	2.8	18408	17	US-10-227-577-2326	Sequence 2326, Ap	928	67.8	2.8	866	13	US-10-027-632-8562	Sequence 8563, Ap
856	68.8	2.8	21442	19	US-09-764-891-7442	Sequence 7442, Ap	929	67.8	2.8	866	17	US-10-027-632-8562	Sequence 8562, Ap
857	68.8	2.8	21442	19	US-10-741-600-17947	Sequence 17947, A	930	67.8	2.8	866	17	US-10-027-632-8562	Sequence 8563, Ap
858	68.8	2.8	2161	9	US-09-764-847-1020	Sequence 1020, Ap	931	67.8	2.8	1018	13	US-10-027-632-30664	Sequence 30664, A
859	68.8	2.8	2161	14	US-10-092-154-1020	Sequence 1020, Ap	932	67.8	2.8	1018	17	US-10-027-632-30664	Sequence 30664, A
860	68.8	2.8	26047	13	US-10-087-192-598	Sequence 598, App	933	67.8	2.8	4095	17	US-10-158-057-348	Sequence 348, App
861	68.8	2.8	32082	10	US-09-764-891-5679	Sequence 5679, Ap	934	67.8	2.8	16489	9	US-09-764-868-1483	Sequence 1483, Ap
862	68.8	2.8	48436	9	US-09-927-602-38	Sequence 38, Appl	935	67.8	2.8	16489	9	US-09-764-868-1483	Sequence 1483, Ap

C 936	67.8	2.8	25000	11	US-09-968-007A-215	Sequence 215, App	1009	67.2	2.7	560	13	US-10-027-632-50973	Sequence 50973, A
C 937	67.8	2.8	25000	19	US-10-843-641A-6685	Sequence 6685, App	1010	67.2	2.7	560	17	US-10-027-632-50973	Sequence 50973, A
C 938	67.8	2.8	141121	19	US-10-741-600-17651	Sequence 17651, A	1011	67.2	2.7	561	13	US-10-027-632-5034	Sequence 5034, App
C 939	67.6	2.8	36741	9	US-09-761-198-3	Sequence 3, Appl	1012	67.2	2.7	561	17	US-10-027-632-5034	Sequence 5034, App
C 940	67.6	2.8	36741	9	US-09-782-378A-12	Sequence 12, Appl	1013	67.2	2.7	581	13	US-10-027-632-279153	Sequence 279153, A
C 941	67.6	2.8	36741	18	US-10-450-826-60	Sequence 60, Appl	1014	67.2	2.7	581	17	US-10-027-632-279153	Sequence 279153, A
C 942	67.6	2.8	378361	10	US-08-901-326-3	Sequence 3, Appl	1015	67.2	2.7	581	17	US-10-027-632-279153	Sequence 279153, A
C 943	67.6	2.8	378361	18	US-10-483-329-3	Sequence 3, Appl	1016	67.2	2.7	581	17	US-10-027-632-279153	Sequence 279153, A
C 944	67.4	2.7	185	9	US-09-764-887-400	Sequence 40, App	1017	67.2	2.7	588	13	US-10-027-632-77218	Sequence 77218, A
C 945	67.4	2.7	185	9	US-09-764-887-401	Sequence 401, App	1018	67.2	2.7	588	13	US-10-027-632-300376	Sequence 300376, A
C 946	67.4	2.7	185	14	US-10-073-961-400	Sequence 40, App	1019	67.2	2.7	588	17	US-10-027-632-77218	Sequence 77218, A
C 947	67.4	2.7	185	14	US-10-073-961-401	Sequence 401, App	1020	67.2	2.7	588	17	US-10-027-632-300376	Sequence 300376, A
C 948	67.4	2.7	880	13	US-10-027-632-120449	Sequence 120449, App	1021	67.2	2.7	592	13	US-10-027-632-266116	Sequence 266116, A
C 949	67.4	2.7	880	13	US-10-027-632-120449	Sequence 120449, App	1022	67.2	2.7	592	13	US-10-027-632-266116	Sequence 266116, A
C 950	67.4	2.7	2088	13	US-10-027-632-98072	Sequence 98072, A	1023	67.2	2.7	609	13	US-10-027-632-218	Sequence 218, App
C 951	67.4	2.7	2088	17	US-10-027-632-98072	Sequence 98072, A	1024	67.2	2.7	609	13	US-10-027-632-218	Sequence 218, App
C 952	67.4	2.7	2110	13	US-10-027-632-98217	Sequence 98217, A	1025	67.2	2.7	614	13	US-10-027-632-315690	Sequence 315690, A
C 953	67.4	2.7	2110	13	US-10-027-632-98218	Sequence 98218, A	1026	67.2	2.7	614	17	US-10-027-632-315690	Sequence 315690, A
C 954	67.4	2.7	2110	17	US-10-027-632-98218	Sequence 98218, A	1027	67.2	2.7	633	13	US-10-027-632-14901	Sequence 14901, A
C 955	67.4	2.7	2110	17	US-10-027-632-98218	Sequence 98218, A	1028	67.2	2.7	633	13	US-10-027-632-14901	Sequence 14901, A
C 956	67.4	2.7	2884	17	US-10-108-260A-2232	Sequence 2232, App	1029	67.2	2.7	633	13	US-10-027-632-288810	Sequence 288810, A
C 957	67.4	2.7	4382	18	US-10-775-920-305	Sequence 305, App	1030	67.2	2.7	633	13	US-10-027-632-288810	Sequence 288810, A
C 958	67.4	2.7	4654	18	US-10-775-920-303	Sequence 303, App	1031	67.2	2.7	633	17	US-10-027-632-14900	Sequence 14900, A
C 959	67.4	2.7	4654	18	US-10-723-860-326	Sequence 326, App	1032	67.2	2.7	633	17	US-10-027-632-14901	Sequence 14901, A
C 960	67.4	2.7	4698	18	US-10-775-920-302	Sequence 302, App	1033	67.2	2.7	633	17	US-10-027-632-288810	Sequence 288810, A
C 961	67.4	2.7	4704	17	US-10-641-643-1358	Sequence 1358, App	1034	67.2	2.7	633	17	US-10-027-632-288810	Sequence 288810, A
C 962	67.4	2.7	4704	17	US-10-775-920-304	Sequence 304, App	1035	67.2	2.7	633	13	US-10-027-632-182761	Sequence 182761, A
C 963	67.4	2.7	4800	18	US-10-723-860-5038	Sequence 5038, App	1036	67.2	2.7	635	13	US-10-027-632-182761	Sequence 182761, A
C 964	67.4	2.7	55346	18	US-10-719-993-7052	Sequence 7052, App	1037	67.2	2.7	649	13	US-10-027-632-205701	Sequence 205701, A
C 965	67.4	2.7	126001	17	US-10-175-492-13	Sequence 13, Appl	1038	67.2	2.7	649	17	US-10-027-632-205701	Sequence 205701, A
C 966	67.2	2.7	110	9	US-09-764-868-1442	Sequence 1442, App	1039	67.2	2.7	690	13	US-10-027-632-135875	Sequence 135875, A
C 967	67.2	2.7	160	9	US-09-764-860-598	Sequence 598, App	1040	67.2	2.7	690	17	US-10-027-632-135875	Sequence 135875, A
C 968	67.2	2.7	160	14	US-10-074-095-598	Sequence 598, App	1041	67.2	2.7	700	13	US-10-027-632-26932	Sequence 26932, A
C 969	67.2	2.7	160	14	US-10-212-872-598	Sequence 598, App	1042	67.2	2.7	700	13	US-10-027-632-26932	Sequence 26932, A
C 970	67.2	2.7	186	9	US-09-764-887-402	Sequence 402, App	1043	67.2	2.7	700	17	US-10-027-632-26932	Sequence 26932, A
C 971	67.2	2.7	186	14	US-10-073-961-402	Sequence 402, App	1044	67.2	2.7	700	17	US-10-027-632-26932	Sequence 26932, A
C 972	67.2	2.7	201	18	US-10-741-601-14866	Sequence 14866, App	1045	67.2	2.7	731	13	US-10-027-632-160103	Sequence 160103, A
C 973	67.2	2.7	201	18	US-10-741-601-22782	Sequence 22782, A	1046	67.2	2.7	731	17	US-10-027-632-160103	Sequence 160103, A
C 974	67.2	2.7	201	18	US-10-741-601-22783	Sequence 22783, A	1047	67.2	2.7	762	13	US-10-027-632-15259	Sequence 15259, A
C 975	67.2	2.7	201	18	US-10-741-601-22784	Sequence 22784, A	1048	67.2	2.7	762	13	US-10-027-632-15259	Sequence 15259, A
C 976	67.2	2.7	201	18	US-10-741-601-22785	Sequence 22785, A	1049	67.2	2.7	762	17	US-10-027-632-15259	Sequence 15259, A
C 977	67.2	2.7	201	18	US-10-719-993-12520	Sequence 12520, A	1050	67.2	2.7	762	17	US-10-027-632-15259	Sequence 15259, A
C 978	67.2	2.7	201	18	US-10-719-993-32643	Sequence 32643, A	1051	67.2	2.7	763	17	US-10-012-697-1071	Sequence 1071, App
C 979	67.2	2.7	201	18	US-10-719-993-48198	Sequence 48198, A	1052	67.2	2.7	787	13	US-10-027-632-169087	Sequence 169087, A
C 980	67.2	2.7	201	19	US-10-741-600-43524	Sequence 43524, A	1053	67.2	2.7	787	13	US-10-027-632-169088	Sequence 169088, A
C 981	67.2	2.7	201	19	US-10-741-600-47514	Sequence 47514, A	1054	67.2	2.7	787	17	US-10-027-632-169087	Sequence 169087, A
C 982	67.2	2.7	201	19	US-10-741-600-54849	Sequence 54849, A	1055	67.2	2.7	787	17	US-10-027-632-169088	Sequence 169088, A
C 983	67.2	2.7	275	17	US-10-242-355-778	Sequence 778, App	1056	67.2	2.7	865	13	US-10-027-632-9102	Sequence 9102, App
C 984	67.2	2.7	336	10	US-09-764-891-7790	Sequence 7790, App	1057	67.2	2.7	865	13	US-10-027-632-9103	Sequence 9103, App
C 985	67.2	2.7	336	10	US-09-764-891-7791	Sequence 7791, App	1058	67.2	2.7	865	13	US-10-027-632-9104	Sequence 9104, App
C 986	67.2	2.7	388	18	US-10-674-124A-19635	Sequence 19635, A	1059	67.2	2.7	865	17	US-10-027-632-9102	Sequence 9102, App
C 987	67.2	2.7	424	9	US-09-764-860-612	Sequence 612, App	1060	67.2	2.7	865	17	US-10-027-632-9103	Sequence 9103, App
C 988	67.2	2.7	424	9	US-09-764-904-84	Sequence 84, Appl	1061	67.2	2.7	865	17	US-10-027-632-9104	Sequence 9104, App
C 989	67.2	2.7	424	14	US-10-091-948-84	Sequence 84, Appl	1062	67.2	2.7	882	13	US-10-027-632-173690	Sequence 173690, A
C 990	67.2	2.7	424	14	US-10-074-095-612	Sequence 612, App	1063	67.2	2.7	882	13	US-10-027-632-173690	Sequence 173690, A
C 991	67.2	2.7	424	14	US-10-212-872-612	Sequence 612, App	1064	67.2	2.7	943	13	US-10-027-632-34185	Sequence 34185, A
C 992	67.2	2.7	429	18	US-10-674-124A-10130	Sequence 10130, A	1065	67.2	2.7	943	17	US-10-027-632-34185	Sequence 34185, A
C 993	67.2	2.7	429	18	US-10-674-124A-17938	Sequence 17938, A	1066	67.2	2.7	957	13	US-10-027-632-122324	Sequence 122324, A
C 994	67.2	2.7	429	18	US-10-357-930-19317	Sequence 19317, A	1067	67.2	2.7	957	17	US-10-027-632-122324	Sequence 122324, A
C 995	67.2	2.7	446	18	US-10-674-124A-11723	Sequence 11723, A	1068	67.2	2.7	990	13	US-10-027-632-101164	Sequence 101164, A
C 996	67.2	2.7	451	9	US-09-867-701-10468	Sequence 10468, A	1069	67.2	2.7	990	17	US-10-027-632-101164	Sequence 101164, A
C 997	67.2	2.7	463	18	US-10-357-930-50860	Sequence 50860, A	1070	67.2	2.7	1077	13	US-10-027-632-104614	Sequence 104614, A
C 998	67.2	2.7	470	18	US-10-357-930-61740	Sequence 61740, A	1071	67.2	2.7	1077	17	US-10-027-632-104614	Sequence 104614, A
C 999	67.2	2.7	471	18	US-10-674-124A-361	Sequence 361, App	1072	67.2	2.7	1130	9	US-09-764-877-3373	Sequence 3373, App
C 1000	67.2	2.7	473	13	US-10-027-632-282418	Sequence 282418, App	1073	67.2	2.7	1130	17	US-10-242-515-3373	Sequence 3373, App
C 1001	67.2	2.7	473	13	US-10-027-632-282419	Sequence 282419, App	1074	67.2	2.7	1299	13	US-10-027-632-205702	Sequence 205702, A
C 1002	67.2	2.7	473	17	US-10-027-632-282418	Sequence 282418, App	1075	67.2	2.7	1299	17	US-10-027-632-205702	Sequence 205702, A
C 1003	67.2	2.7	473	17	US-10-027-632-282419	Sequence 282419, App	1076	67.2	2.7	1378	13	US-10-027-632-249993	Sequence 249993, A
C 1004	67.2	2.7	488	13	US-10-027-632-45909	Sequence 45909, A	1077	67.2	2.7	1378	17	US-10-027-632-249993	Sequence 249993, A
C 1005	67.2	2.7	488	17	US-10-027-632-45909	Sequence 45909, A	1078	67.2	2.7	1713	10	US-09-764-872-837	Sequence 837, App
C 1006	67.2	2.7	491	10	US-09-814-353-15397	Sequence 15397, A	1079	67.2	2.7	1713	10	US-09-764-872-840	Sequence 840, App
C 1007	67.2	2.7	522	13	US-10-027-632-271411	Sequence 271411, App	1080	67.2	2.7	1817	17	US-10-012-697-1459	GENERAL INFORMATI
C 1008	67.2	2.7	522	17	US-10-027-632-271411	Sequence 271411, App	1081	67.2	2.7	2136	13	US-10-027-632-98762	Sequence 98762, A

c1228	67.2	2.7	90468	17	US-10-085-117-160	Sequence 160, App	c1301	67.2	2.7	299598	18	US-10-322-596-16	Sequence 16, Appl
c1229	67.2	2.7	90556	19	US-10-741-600-17972	Sequence 17972, A	c1302	67.2	2.7	312477	18	US-10-317-883A-12	Sequence 12, Appl
1230	67.2	2.7	93313	19	US-10-741-600-17623	Sequence 17623, A	c1303	67.2	2.7	325348	17	US-10-085-117-358	Sequence 358, App
1231	67.2	2.7	98716	19	US-10-741-600-17754	Sequence 17754, A	1304	67.2	2.7	325791	11	US-09-768-185A-1	Sequence 1, Appl
1232	67.2	2.7	98850	18	US-10-719-993-67798	Sequence 6798, App	1305	67.2	2.7	378361	10	US-09-901-136-3	Sequence 3, Appl
c1233	67.2	2.7	98865	9	US-09-770-689A-3	Sequence 3, Appl	1306	67.2	2.7	378361	18	US-10-483-329-3	Sequence 3, Appl
c1234	67.2	2.7	98865	9	US-10-949-419-3	Sequence 3, Appl	1307	67.2	2.7	389393	18	US-10-417-375-4	Sequence 4, Appl
1235	67.2	2.7	99046	18	US-10-322-281-344	Sequence 344, App	1308	67.2	2.7	389393	18	US-10-417-375-4	Sequence 4, Appl
c1236	67.2	2.7	101193	18	US-10-322-281-468	Sequence 468, App	1309	67.2	2.7	389393	18	US-10-417-375-4	Sequence 4, Appl
1237	67.2	2.7	101270	18	US-10-723-600-631	Sequence 631, App	c1310	67.2	2.7	653458	18	US-10-719-993-6782	Sequence 6782, App
c1238	67.2	2.7	101507	18	US-10-719-993-67772	Sequence 6772, App	c1311	67.2	2.7	653458	18	US-10-461-862-4	Sequence 4, Appl
c1239	67.2	2.7	106707	18	US-10-694-695-8	Sequence 8, Appl	c1312	67.2	2.7	744802	17	US-10-292-798-1369	Sequence 1369, App
c1240	67.2	2.7	106776	18	US-10-417-375-30	Sequence 30, App	c1313	67.2	2.7	744802	17	US-09-795-668-1	Sequence 1, Appl
c1241	67.2	2.7	107036	18	US-10-322-281-756	Sequence 756, App	c1314	67.2	2.7	1503841	9	US-09-795-668-1	Sequence 1, Appl
1242	67.2	2.7	108111	18	US-10-719-993-6843	Sequence 6843, App	c1315	67.2	2.7	1503841	9	US-09-946-807-1	Sequence 1, Appl
c1243	67.2	2.7	110608	18	US-10-775-169-193	Sequence 193, App	1316	67.2	2.7	1980090	18	US-10-719-993-6815	Sequence 6815, App
c1244	67.2	2.7	112486	18	US-10-741-601-5641	Sequence 5641, App	c1317	67.2	2.7	1980090	18	US-10-719-993-6815	Sequence 6815, App
1245	67.2	2.7	112486	19	US-10-741-600-17642	Sequence 17642, A	c1318	67.2	2.7	1980090	19	US-10-741-600-17676	Sequence 17676, A
1246	67.2	2.7	113604	14	US-10-227-195A-1	Sequence 1, Appl	1319	67	2.7	201	19	US-10-741-600-17676	Sequence 17676, A
1247	67.2	2.7	113604	14	US-10-227-195A-2	Sequence 2, Appl	1320	67	2.7	201	19	US-10-741-600-17676	Sequence 17676, A
1248	67.2	2.7	113604	17	US-10-227-152B-1	Sequence 1, Appl	1321	67	2.7	592	13	US-10-027-632-263748	Sequence 263748, A
1249	67.2	2.7	113604	17	US-10-227-152B-2	Sequence 2, Appl	1322	67	2.7	592	17	US-10-027-632-263748	Sequence 263748, A
c1250	67.2	2.7	114793	15	US-10-148-806-3	Sequence 3, Appl	c1323	67	2.7	636	13	US-10-027-632-270043	Sequence 270043, A
c1251	67.2	2.7	115935	18	US-10-775-169-241	Sequence 241, App	1324	67	2.7	636	17	US-10-027-632-270043	Sequence 270043, A
1252	67.2	2.7	122410	19	US-10-741-600-17733	Sequence 17733, A	1325	67	2.7	7219	9	US-09-764-856-107	Sequence 107, App
1253	67.2	2.7	122923	13	US-10-087-192-368	Sequence 288, App	1326	67	2.7	7219	11	US-09-764-856-107	Sequence 107, App
1254	67.2	2.7	125560	19	US-10-741-600-18002	Sequence 18002, A	1327	67	2.7	7219	18	US-10-027-632-263748	Sequence 263748, A
1255	67.2	2.7	127917	18	US-10-775-169-82	Sequence 82, App	c1328	67	2.7	33249	10	US-09-764-891-7364	Sequence 7364, App
1256	67.2	2.7	130001	17	US-10-199-676-23	Sequence 23, App	c1329	67	2.7	33249	18	US-10-719-993-6921	Sequence 6921, App
1257	67.2	2.7	130001	19	US-10-639-300-23	Sequence 23, App	1330	67	2.7	161484	18	US-10-317-401-4	Sequence 4, Appl
c1258	67.2	2.7	133632	13	US-10-087-192-1810	Sequence 1810, App	1331	67	2.7	207433	17	US-10-277-216-5	Sequence 5, Appl
1259	67.2	2.7	136726	17	US-10-085-117-344	Sequence 244, App	1332	67	2.7	207433	17	US-10-277-216-5	Sequence 5, Appl
1260	67.2	2.7	146778	19	US-10-741-600-17710	Sequence 17710, A	c1333	67	2.7	207433	17	US-10-277-216-5	Sequence 5, Appl
c1261	67.2	2.7	147708	18	US-10-450-826-61	Sequence 61, App	1334	66.8	2.7	201	18	US-10-719-993-6782	Sequence 6782, App
c1262	67.2	2.7	152165	18	US-10-719-993-6942	Sequence 6942, App	c1335	66.8	2.7	201	18	US-10-741-601-9877	Sequence 9877, App
c1263	67.2	2.7	152165	19	US-10-741-600-17864	Sequence 17864, A	c1336	66.8	2.7	201	18	US-10-741-601-9877	Sequence 9877, App
c1264	67.2	2.7	152759	18	US-10-322-281-10	Sequence 10, Appl	c1337	66.8	2.7	201	18	US-10-741-601-23411	Sequence 23411, A
1265	67.2	2.7	155937	18	US-10-723-860-2208	Sequence 2208, App	c1338	66.8	2.7	201	18	US-10-719-993-9667	Sequence 9667, App
c1266	67.2	2.7	156416	19	US-10-461-862-12	Sequence 12, App	c1339	66.8	2.7	201	18	US-10-719-993-18650	Sequence 18650, A
1267	67.2	2.7	160361	17	US-10-235-192A-35	Sequence 35, App	c1340	66.8	2.7	201	18	US-10-719-993-21535	Sequence 21535, A
1268	67.2	2.7	160771	18	US-10-450-826-86	Sequence 86, App	1341	66.8	2.7	201	18	US-10-719-993-47397	Sequence 47397, A
1269	67.2	2.7	162025	9	US-09-834-700-13	Sequence 13, App	1342	66.8	2.7	201	18	US-10-719-993-51986	Sequence 51986, A
1270	67.2	2.7	162025	9	US-09-834-700-14	Sequence 14, App	c1343	66.8	2.7	201	18	US-10-719-993-52903	Sequence 52903, A
1271	67.2	2.7	162025	9	US-09-834-700-17	Sequence 17, App	c1344	66.8	2.7	201	19	US-10-741-600-24239	Sequence 24239, A
1272	67.2	2.7	162025	9	US-09-834-700-18	Sequence 18, App	1345	66.8	2.7	201	19	US-10-741-600-31944	Sequence 31944, A
1273	67.2	2.7	162025	16	US-10-272-665-35	Sequence 35, App	c1346	66.8	2.7	201	19	US-10-741-600-38485	Sequence 38485, A
1274	67.2	2.7	162025	16	US-10-272-665-36	Sequence 36, App	c1347	66.8	2.7	201	19	US-10-741-600-41368	Sequence 41368, A
1275	67.2	2.7	162025	16	US-10-273-321-35	Sequence 35, App	c1348	66.8	2.7	201	19	US-10-741-600-50632	Sequence 50632, A
1276	67.2	2.7	162025	16	US-10-273-321-36	Sequence 36, App	1349	66.8	2.7	201	19	US-10-741-600-53362	Sequence 53362, A
1277	67.2	2.7	162025	16	US-10-272-756-35	Sequence 35, App	c1350	66.8	2.7	201	19	US-10-027-632-264728	Sequence 264728, A
1278	67.2	2.7	162025	16	US-10-272-756-36	Sequence 36, App	1351	66.8	2.7	393	17	US-10-027-632-264728	Sequence 264728, A
1279	67.2	2.7	162025	17	US-10-273-328-35	Sequence 35, App	1352	66.8	2.7	470	13	US-10-027-632-277379	Sequence 277379, A
1280	67.2	2.7	162025	17	US-10-273-328-36	Sequence 36, App	1353	66.8	2.7	470	17	US-10-027-632-277379	Sequence 277379, A
1281	67.2	2.7	170834	9	US-09-835-232-7	Sequence 7, App	1354	66.8	2.7	494	13	US-10-027-632-277579	Sequence 277579, A
1282	67.2	2.7	170834	16	US-10-308-485-7	Sequence 7, App	1355	66.8	2.7	494	17	US-10-027-632-277579	Sequence 277579, A
c1283	67.2	2.7	174424	9	US-09-967-768A-314	Sequence 314, App	1356	66.8	2.7	511	17	US-10-027-632-20353	Sequence 20353, A
c1284	67.2	2.7	174424	10	US-09-960-706-969	Sequence 969, App	1357	66.8	2.7	511	17	US-10-027-632-20353	Sequence 20353, A
c1285	67.2	2.7	174424	19	US-10-843-641A-6459	Sequence 6459, App	c1358	66.8	2.7	528	13	US-10-027-632-47412	Sequence 47412, A
c1286	67.2	2.7	174448	13	US-10-087-192-148	Sequence 148, App	c1359	66.8	2.7	528	13	US-10-027-632-47412	Sequence 47412, A
1287	67.2	2.7	175077	13	US-10-087-192-1168	Sequence 1168, App	c1360	66.8	2.7	528	17	US-10-027-632-47413	Sequence 47413, A
c1288	67.2	2.7	175737	18	US-10-723-860-1753	Sequence 1753, App	c1361	66.8	2.7	528	17	US-10-027-632-47413	Sequence 47413, A
c1289	67.2	2.7	181343	18	US-10-723-860-2242	Sequence 2242, App	c1362	66.8	2.7	620	13	US-10-027-632-99407	Sequence 99407, A
1290	67.2	2.7	198522	13	US-10-087-192-244	Sequence 244, App	c1363	66.8	2.7	620	13	US-10-027-632-99407	Sequence 99407, A
c1291	67.2	2.7	202814	18	US-10-719-993-6812	Sequence 6812, App	c1364	66.8	2.7	620	17	US-10-027-632-99407	Sequence 99407, A
c1292	67.2	2.7	202814	18	US-10-087-192-1282	Sequence 1282, App	1365	66.8	2.7	620	17	US-10-027-632-99408	Sequence 99408, A
c1293	67.2	2.7	235033	15	US-10-301-844-1	Sequence 1, Appl	c1366	66.8	2.7	620	17	US-10-027-632-99408	Sequence 99408, A
c1294	67.2	2.7	237326	15	US-10-301-844-2	Sequence 2, Appl	c1367	66.8	2.7	620	17	US-10-027-632-99409	Sequence 99409, A
1295	67.2	2.7	246940	18	US-10-322-281-558	Sequence 558, App	c1368	66.8	2.7	620	13	US-10-027-632-202297	Sequence 202297, A
1296	67.2	2.7	247682	17	US-10-235-192A-28	Sequence 28, App	c1369	66.8	2.7	624	17	US-10-027-632-202297	Sequence 202297, A
c1297	67.2	2.7	250000	16	US-10-225-810-26	Sequence 26, App	c1370	66.8	2.7	747	13	US-10-027-632-144933	Sequence 144933, A
c1298	67.2	2.7	256157	13	US-10-087-192-1204	Sequence 1204, App	c1371	66.8	2.7	747	13	US-10-027-632-144934	Sequence 144934, A
c1299	67.2	2.7	256157	18	US-10-322-281-776	Sequence 776, App	c1372	66.8	2.7	747	13	US-10-027-632-144935	Sequence 144935, A
1300	67.2	2.7	277616	18	US-10-367-094-83	Sequence 83, App	c1373	66.8	2.7	747	17	US-10-027-632-144935	Sequence 144935, A

c1374	66.8	2.7	747	17	US-10-027-632-144934	Sequence 144934,	1447	66.4	2.7	118356	19	US-10-741-600-17643	Sequence 17643, A
c1375	66.8	2.7	747	17	US-10-027-632-144935	Sequence 144935,	1448	66.4	2.7	160552	18	US-10-697-828-11	Sequence 11, Appl
c1376	66.8	2.7	822	13	US-10-027-632-160460	Sequence 160460,	1449	66.4	2.7	196063	18	US-10-322-281-612	Sequence 612, App
c1377	66.8	2.7	822	13	US-10-027-632-160461	Sequence 160461,	1450	66.4	2.7	561515	18	US-10-741-601-5682	Sequence 5682, Ap
c1378	66.8	2.7	822	17	US-10-027-632-160460	Sequence 160460,	1451	66.4	2.7	561515	19	US-10-741-600-17730	Sequence 17730, A
c1379	66.8	2.7	822	17	US-10-027-632-160461	Sequence 160461,	1452	66.2	2.7	146	11	US-09-973-278-843	Sequence 843, App
c1380	66.8	2.7	3820	18	US-10-723-860-5474	Sequence 5474, Ap	1453	66.2	2.7	146	11	US-09-973-278-844	Sequence 844, App
c1381	66.8	2.7	34722	18	US-10-322-281-700	Sequence 700, App	1454	66.2	2.7	146	11	US-09-973-278-846	Sequence 846, App
c1382	66.8	2.7	62555	19	US-10-741-600-17630	Sequence 17630, A	1455	66.2	2.7	315	17	US-10-242-535A-18261	Sequence 18261, A
c1383	66.8	2.7	73764	18	US-10-741-601-5616	Sequence 5616, Ap	1456	66.2	2.7	315	17	US-10-085-783A-18261	Sequence 18261, A
c1384	66.8	2.7	81742	18	US-10-719-993-7045	Sequence 7045, Ap	1457	66.2	2.7	401	9	US-09-795-668-572	Sequence 572, App
c1385	66.8	2.7	98829	14	US-10-017-724-3	Sequence 3, Appli	1458	66.2	2.7	401	9	US-09-795-668-573	Sequence 573, App
c1386	66.8	2.7	117985	18	US-10-719-993-7053	Sequence 7053, Ap	1459	66.2	2.7	401	9	US-09-795-668-572	Sequence 572, App
c1387	66.8	2.7	152165	18	US-10-719-993-6942	Sequence 6942, Ap	1460	66.2	2.7	401	9	US-09-795-686-573	Sequence 573, App
c1388	66.8	2.7	152165	19	US-10-741-600-17864	Sequence 17864, A	1461	66.2	2.7	401	9	US-09-946-807-572	Sequence 572, App
c1389	66.8	2.7	161700	18	US-10-741-601-5623	Sequence 5623, Ap	1462	66.2	2.7	401	9	US-09-946-807-573	Sequence 573, App
c1390	66.8	2.7	161700	18	US-10-741-600-17590	Sequence 17590, A	1463	66.2	2.7	415	18	US-10-674-124A-25156	Sequence 25156, A
c1391	66.8	2.7	169567	18	US-10-719-993-6774	Sequence 6774, Ap	1464	66.2	2.7	426	9	US-09-795-668-1426	Sequence 1426, Ap
c1392	66.8	2.7	176080	17	US-10-235-192A-43	Sequence 43, Appl	1465	66.2	2.7	426	9	US-09-795-686-1426	Sequence 1426, Ap
c1393	66.8	2.7	403035	18	US-10-741-601-5729	Sequence 5729, Ap	1466	66.2	2.7	426	9	US-09-946-807-1426	Sequence 1426, Ap
c1394	66.6	2.7	677	13	US-10-027-632-203836	Sequence 203836,	1467	66.2	2.7	471	10	US-09-918-995-13287	Sequence 13287, A
c1395	66.6	2.7	677	13	US-10-027-632-203836	Sequence 203836,	1468	66.2	2.7	471	10	US-09-918-995-27233	Sequence 27233, A
c1396	66.6	2.7	2089	19	US-10-840-455-6	Sequence 6, Appli	1469	66.2	2.7	543	10	US-09-918-995-27434	Sequence 27434, A
c1397	66.6	2.7	3312	13	US-10-027-632-113132	Sequence 113132,	1470	66.2	2.7	601	9	US-09-818-656A-28	Sequence 28, Appl
c1398	66.6	2.7	3312	17	US-10-027-632-113132	Sequence 113132,	1471	66.2	2.7	601	9	US-09-818-656A-29	Sequence 29, Appl
c1399	66.6	2.7	3347	13	US-10-027-632-114894	Sequence 114894,	1472	66.2	2.7	601	9	US-09-818-656A-30	Sequence 30, Appl
c1400	66.6	2.7	3347	17	US-10-027-632-114894	Sequence 114894,	1473	66.2	2.7	678	13	US-10-027-632-156612	Sequence 156612, A
c1401	66.6	2.7	7260	9	US-09-919-497-24	Sequence 24, Appl	1474	66.2	2.7	778	17	US-10-027-632-156611	Sequence 156611, A
c1402	66.6	2.7	7260	9	US-09-880-107-3739	Sequence 3739, Ap	1475	66.2	2.7	778	17	US-10-027-632-156611	Sequence 156611, A
c1403	66.6	2.7	7260	10	US-09-860-706-1066	Sequence 1066, Ap	1476	66.2	2.7	778	17	US-10-027-632-156612	Sequence 156612, A
c1404	66.6	2.7	7260	10	US-09-873-319-707	Sequence 707, App	1477	66.2	2.7	790	13	US-10-027-632-145713	Sequence 145713, A
c1405	66.6	2.7	7260	14	US-10-136-639-4	Sequence 4, Appli	1478	66.2	2.7	790	13	US-10-027-632-145713	Sequence 145713, A
c1406	66.6	2.7	7260	18	US-10-706-791-1	Sequence 1, Appli	1479	66.2	2.7	2445	13	US-10-027-632-103678	Sequence 103678, A
c1407	66.6	2.7	7260	18	US-10-851-921-1	Sequence 1, Appli	1480	66.2	2.7	2445	13	US-10-027-632-111883	Sequence 111883, A
c1408	66.6	2.7	7476	19	US-10-461-862-67	Sequence 67, Appl	1481	66.2	2.7	2445	17	US-10-027-632-103678	Sequence 103678, A
c1409	66.6	2.7	22021	13	US-10-087-192-1234	Sequence 1234, Ap	1482	66.2	2.7	2445	17	US-10-027-632-111883	Sequence 111883, A
c1410	66.6	2.7	26414	19	US-10-840-455-43	Sequence 43, Appl	1483	66.2	2.7	3206	17	US-10-094-749-924	Sequence 924, App
c1411	66.6	2.7	31116	13	US-10-087-192-1660	Sequence 1660, Ap	1484	66.2	2.7	4870	18	US-10-357-930-25111	Sequence 25111, A
c1412	66.6	2.7	33683	18	US-10-741-601-5739	Sequence 5739, Ap	1485	66.2	2.7	26332	13	US-10-087-192-1558	Sequence 1558, Ap
c1413	66.6	2.7	33683	19	US-10-741-600-17888	Sequence 17888, A	1486	66.2	2.7	32169	10	US-09-764-891-8605	Sequence 8605, Ap
c1414	66.6	2.7	38687	17	US-10-085-117-22	Sequence 22, Appl	1487	66.2	2.7	32189	10	US-09-764-891-8604	Sequence 8604, Ap
c1415	66.6	2.7	51552	9	US-09-733-294A-30	Sequence 30, Appl	1488	66.2	2.7	33362	18	US-10-388-838-36	Sequence 36, Appl
c1416	66.6	2.7	58822	17	US-10-052-482-46	Sequence 46, Appl	1489	66.2	2.7	33578	17	US-10-085-117-238	Sequence 238, App
c1417	66.6	2.7	59748	18	US-10-322-281-296	Sequence 296, App	1490	66.2	2.7	33703	18	US-10-741-601-5707	Sequence 5707, Ap
c1418	66.6	2.7	1030120	19	US-10-741-600-17697	Sequence 17697, A	1491	66.2	2.7	40645	9	US-09-818-656A-3	Sequence 3, Appli
c1419	66.6	2.7	154416	19	US-10-461-862-64	Sequence 64, Appl	1492	66.2	2.7	40645	13	US-10-216-441-3	Sequence 3, Appli
c1420	66.6	2.7	154416	19	US-10-461-862-12	Sequence 12, Appl	1493	66.2	2.7	54701	13	US-10-087-192-945	Sequence 945, App
c1421	66.4	2.7	452	18	US-10-474-495-139	Sequence 139, App	1494	66.2	2.7	59942	18	US-10-741-601-5775	Sequence 5775, Ap
c1422	66.4	2.7	491	10	US-09-918-995-37862	Sequence 37862, A	1495	66.2	2.7	60316	18	US-10-719-993-6833	Sequence 6833, Ap
c1423	66.4	2.7	560	13	US-10-027-632-129126	Sequence 129126,	1496	66.2	2.7	60461	17	US-10-341-434-82	Sequence 82, Appl
c1424	66.4	2.7	560	13	US-10-027-632-129126	Sequence 129126,	1497	66.2	2.7	63588	14	US-10-243-735-3	Sequence 3, Appli
c1425	66.4	2.7	791	13	US-10-027-632-171803	Sequence 171803,	1498	66.2	2.7	63588	18	US-10-730-010-3	Sequence 3, Appli
c1426	66.4	2.7	791	13	US-10-027-632-171804	Sequence 171804,	1499	66.2	2.7	70000	18	US-10-476-991-3	Sequence 2089, Ap
c1427	66.4	2.7	791	13	US-10-027-632-171805	Sequence 171805,	1500	66.2	2.7	93443	18	US-10-723-860-2089	
c1428	66.4	2.7	791	17	US-10-027-632-171803	Sequence 171803,							
c1429	66.4	2.7	791	17	US-10-027-632-171804	Sequence 171804,							
c1430	66.4	2.7	791	13	US-10-027-632-171805	Sequence 171805,							
c1431	66.4	2.7	932	13	US-10-027-632-10502	Sequence 10502, A							
c1432	66.4	2.7	932	13	US-10-027-632-10503	Sequence 10503, A							
c1433	66.4	2.7	932	17	US-10-027-632-10502	Sequence 10502, A							
c1434	66.4	2.7	932	17	US-10-027-632-10503	Sequence 10503, A							
c1435	66.4	2.7	1160	13	US-10-027-632-31127	Sequence 31127, A							
c1436	66.4	2.7	1160	17	US-10-027-632-31127	Sequence 31127, A							
c1437	66.4	2.7	5629	9	US-09-764-847-1162	Sequence 1162, Ap							
c1438	66.4	2.7	5629	14	US-10-092-154-1162	Sequence 1162, Ap							
c1439	66.4	2.7	6265	9	US-09-764-847-1161	Sequence 1161, Ap							
c1440	66.4	2.7	6265	14	US-10-092-154-1161	Sequence 1161, Ap							
c1441	66.4	2.7	9883	13	US-10-016-157A-71	Sequence 71, Appl							
c1442	66.4	2.7	19183	9	US-09-764-877-2799	Sequence 2799, Ap							
c1443	66.4	2.7	19183	17	US-10-242-515-2799	Sequence 2799, Ap							
c1444	66.4	2.7	19969	14	US-10-190-593-3	Sequence 3, Appli							
c1445	66.4	2.7	35236	13	US-10-087-192-370	Sequence 370, App							
c1446	66.4	2.7	46404	13	US-10-087-192-634	Sequence 634, App							

Search completed: May 6, 2005, 02:17:06

Job time : 1412 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 01:33:03 ; Search time 10230 Seconds
(without alignments)
11642.514 Million cell updates/sec

Title: US-09-978-544A-58

Perfect score: 2458

Sequence: 1 gcgcggagccatctgcgc.....acagagcggaactccgtctc 2458

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_rts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2458	100.0	2458	6	CQ767591 Sequence
2	2458	100.0	2458	6	AR252730 Sequence
3	2458	100.0	2458	6	AR528645 Sequence
4	2458	100.0	2458	6	AX358876 Sequence
5	2458	100.0	2458	6	AX362369 Sequence
6	2458	100.0	2458	6	AX403615 Sequence
7	2458	100.0	2458	6	AX454478 Sequence
8	2458	100.0	2458	6	AX464254 Sequence
9	2458	100.0	2458	6	AX490956 Sequence
10	2458	100.0	2458	6	AX538183 Sequence
11	2458	100.0	2458	9	AX326422 Homo sapi
12	2458	100.0	2458	9	AX358340 Homo sapi
13	2450	99.7	2627	9	AX026068 Homo sapi
14	2448.4	99.6	5120	6	CQ802458 Sequence
15	2272	92.4	2298	9	BC009371 Homo sapi
16	1986.4	80.8	2184	6	AR220920 Sequence
17	1441	58.6	179974	2	AC021704 Homo sapi
18	1441	58.6	196972	9	AP000926 Homo sapi
19	1187	48.3	175056	2	AP0002368 Homo sapi

20	1070.6	43.6	3925	10	AF302047
21	1032.4	42.0	1830	10	BC026447
22	1031.2	42.0	1927	6	BD101818
23	1031.2	42.0	1927	10	AB040490
24	919	37.4	1322	10	AY326421
25	885	36.0	1122	10	AY259213
26	652	26.5	2685	6	CQ728740
27	575.2	23.4	1233	6	CQ413475
28	392	15.9	176263	2	AC102389
29	374.6	15.2	229196	2	AC103488
30	359.8	14.6	378	6	CQ704807
31	355	14.4	1119	5	BX935530
32	339.4	13.8	405	6	CQ408352
33	321	13.1	492	6	CQ732408
34	296	12.0	209770	2	AC140409
35	292.6	11.9	1800	5	BC082496
36	221.6	9.0	295	6	CQ395635
37	215.8	8.8	90211	9	CQ401968
38	215.8	8.8	90211	9	AP001970
39	215.8	8.8	172200	2	AC007219
40	203	8.3	175056	2	AP002368
41	203	8.3	179974	2	AC021704
42	190.2	7.7	241	6	CQ676931
43	163.2	6.6	172200	2	AC007219
44	157.8	6.4	1071	6	CQ740724
45	140	5.7	569	11	G90851
46	100	4.1	235459	2	AC094979
47	100	4.1	252623	2	AC094538
48	82.4	3.4	163608	2	AC026081
49	82.4	3.4	166379	9	AC087378
50	82.4	3.4	182598	9	AC103870
51	79.4	3.2	182429	2	AP001557
52	79.4	3.2	219574	9	AP002956
53	76.4	3.1	154090	9	AC025577
54	76.4	3.1	168134	9	AC021058
55	76.4	3.1	186660	2	AC026107
56	76.4	3.1	339940	2	AC139464
57	75.6	3.1	169515	9	AP002777
58	75.6	3.1	189637	2	AC009765
59	74.8	3.0	34379	9	HUMCC1S149
60	74.8	3.0	40289	9	HUMHDAC
61	74.8	3.0	58864	2	HUMHDABCD
62	74.8	3.0	182863	2	AC149626
63	74.8	3.0	180000	2	AC007507
64	74.8	3.0	189223	9	AC016773
65	74.8	3.0	192193	2	AC150018
66	74.6	3.0	156869	2	AP002888
67	74.4	3.0	133814	2	AC027550
68	74.4	3.0	140974	9	AC068533
69	74.4	3.0	145100	2	AC024641
70	74.4	3.0	178388	9	AC092884
71	74.4	3.0	186795	2	AC024737
72	74.4	3.0	190081	2	AC024737
73	74	3.0	162599	9	AL360230
74	74	3.0	195191	9	AC024339
75	73.8	3.0	113996	2	AC026438
76	73.8	3.0	118166	9	AC108111
77	73.8	3.0	126038	2	AC016068
78	73.8	3.0	159513	2	AC148076
79	73.8	3.0	172793	2	AC023659
80	73.8	3.0	202827	9	AC016907
81	73.6	3.0	63601	9	AC080135
82	73.6	3.0	154350	9	AC016948
83	73.4	3.0	119290	2	AC068449
84	73	3.0	59213	2	AC135351
85	73	3.0	177816	9	AC105219
86	72.8	3.0	87349	9	AC025430
87	72.8	3.0	155304	2	AC024713
88	72.8	3.0	162495	9	AC009996
89	72.8	3.0	167687	2	AC023476
90	72.8	3.0	175465	2	AC009821
91	72.8	3.0	185957	2	AP000911
92	72.8	3.0	196928	2	AP000847

93	72.6	3.0	262	9	HUMALN8402	M87913 Human carci	166	70.8	2.9	37000	9	AC004623	9	AC004623 Homo sapi
94	72.6	3.0	67895	9	AL138807	Human DNA	167	70.8	2.9	71819	9	AC007536	9	AC007536 Homo sapi
95	72.6	3.0	132444	9	AC019226	Homo sapi	168	70.8	2.9	122276	9	AC022107	9	AC022107 Homo sapi
96	72.6	3.0	183798	2	AC145523	Papio ham	c 169	70.8	2.9	143673	2	AC087720	2	AC087720 Homo sapi
97	72.6	3.0	219727	2	AC145709	Homo sapi	c 170	70.8	2.9	144768	2	AC010273	2	AC010273 Homo sapi
98	72.4	2.9	33560	2	AP003731	Homo sapi	171	70.8	2.9	156503	2	AC084347	2	AC084347 Homo sapi
99	72.4	2.9	170028	2	AP002342	Homo sapi	172	70.8	2.9	159688	9	AC087311	9	AC087311 Homo sapi
100	72.4	2.9	174548	9	AP002342	Homo sapi	173	70.8	2.9	159789	9	AC105449	9	AC105449 Homo sapi
101	72.4	2.9	199892	2	AC020977	Homo sapi	c 174	70.8	2.9	169920	9	AC139103	9	AC139103 Homo sapi
102	72.2	2.9	3899	9	AF225400S04	Homo sapi	c 175	70.8	2.9	226221	9	AP005976	9	AP005976 Homo sapi
103	72.2	2.9	125377	2	AC118135	Homo sapi	c 176	70.6	2.9	1000	6	CQ631012	6	CQ631012 Sequence
104	72.2	2.9	157749	2	AC135345	Homo sapi	c 177	70.6	2.9	1000	6	AR472075	6	AR472075 Sequence
105	72.2	2.9	159349	9	AC097633	Homo sapi	c 178	70.6	2.9	1000	6	AX305151	6	AX305151 Sequence
106	72.2	2.9	160693	9	AC124043	Homo sapi	c 179	70.6	2.9	107467	9	HS95983	9	HS95983 Homo sapi
107	72.2	2.9	161725	2	AC084000	Homo sapi	c 180	70.6	2.9	124635	9	AP000593	9	AP000593 Homo sapi
108	72.2	2.9	161842	2	AC107931	Homo sapi	c 181	70.6	2.9	134706	9	AC002347	9	AC002347 Homo sapi
109	72.2	2.9	170166	9	AC107982	Homo sapi	c 182	70.6	2.9	221507	9	HS407F11	9	HS407F11 Homo sapi
110	72.2	2.9	171978	9	AC026271	Homo sapi	c 183	70.4	2.9	251	11	BV189945	11	BV189945 sqm16550
111	72.2	2.9	181442	2	AC134875	Homo sapi	184	70.4	2.9	3568	9	HSB802790	9	HSB802790 Homo sapi
112	72.2	2.9	188766	9	AC135329	Homo sapi	185	70.4	2.9	6839	9	HSP2X7123	9	HSP2X7123 Homo sapi
113	72.2	2.9	195397	2	AC135718	Homo sapi	c 186	70.4	2.9	28088	9	AL590099	9	AL590099 Human DNA
114	72.2	2.9	207785	2	AP001091	Homo sapi	c 187	70.4	2.9	35687	9	AC000051	9	AC000051 Homo sapi
115	72	2.9	26552	2	AC132682	Homo sapi	188	70.4	2.9	35758	2	AC127539	2	AC127539 Homo sapi
116	72	2.9	33318	2	AC131089	Homo sapi	c 189	70.4	2.9	36032	2	AC066609	2	AC066609 Homo sapi
117	72	2.9	33901	2	AC127087	Homo sapi	c 190	70.4	2.9	36742	9	D87002	9	D87002 Homo sapien
118	72	2.9	44653	9	HS380F5	Human DNA	191	70.4	2.9	36872	9	BS37334	9	BS37334 Human DNA
119	72	2.9	112401	9	AL606462	Homo sapi	c 192	70.4	2.9	38051	9	HSAC000363	9	HSAC000363 Human cos
120	72	2.9	118504	9	AC094080	Homo sapi	c 193	70.4	2.9	39823	9	AC004785	9	AC004785 Homo sapi
121	72	2.9	138107	9	AC004967	Homo sapi	c 194	70.4	2.9	43603	9	AC107883	9	AC107883 Homo sapi
122	72	2.9	149843	9	AP000892	Homo sapi	c 195	70.4	2.9	49614	9	AF001551	9	AF001551 Homo sapi
123	72	2.9	151796	2	AC096995	Homo sapi	c 196	70.4	2.9	56981	9	HSAP001551	9	HSAP001551 Homo sapi
124	72	2.9	170797	9	AC011379	Homo sapi	c 197	70.4	2.9	60837	9	HS354112	9	HS354112 Human DNA
125	72	2.9	171065	2	AC011216	Homo sapi	c 198	70.4	2.9	62464	9	AL159164	9	AL159164 Human DNA
126	72	2.9	177883	2	AC046159	Homo sapi	c 199	70.4	2.9	65706	2	AC090752	2	AC090752 Homo sapi
127	72	2.9	182587	2	AC131097	Homo sapi	c 200	70.4	2.9	67173	9	AL359962	9	AL359962 Human DNA
128	72	2.9	183881	2	AC087728	Homo sapi	c 201	70.4	2.9	67923	9	AF510423S1	9	AF510423 Homo sapi
129	72	2.9	198888	9	AL158040	Homo sapi	c 202	70.4	2.9	67923	2	AL928684	2	AL928684 Homo sapi
130	72	2.9	279011	9	AL5006467	Homo sapi	c 203	70.4	2.9	67962	2	AL928684	2	AL928684 Homo sapi
131	72	2.9	66959	9	AL5091214	Human DNA	c 204	70.4	2.9	71024	2	AC124002	2	AC124002 Homo sapi
132	71.6	2.9	71456	9	BS000118	Pan trogl	c 205	70.4	2.9	71607	2	AL671114	2	AL671114 Homo sapi
133	71.6	2.9	104378	9	AL139341	Human DNA	c 206	70.4	2.9	73094	2	AL671114	2	AL671114 Homo sapi
134	71.6	2.9	136328	9	AC004126	Human chr	c 207	70.4	2.9	79302	9	AC006958	9	AC006958 Homo sapi
135	71.6	2.9	148736	2	AC051009	Macaca mu	c 208	70.4	2.9	79328	9	AC079121	9	AC079121 Homo sapi
136	71.6	2.9	151321	2	AC012276	Homo sapi	c 209	70.4	2.9	82166	9	AC006237	9	AC006237 Homo sapi
137	71.6	2.9	151367	9	AC025750	Homo sapi	c 210	70.4	2.9	87847	6	CQ870457	6	CQ870457 Sequence
138	71.6	2.9	155874	2	AC004782	Homo sapi	c 211	70.4	2.9	91241	9	AL445428	9	AL445428 Human DNA
139	71.6	2.9	160850	9	AC130184	Macaca mu	c 212	70.4	2.9	91503	9	AL451061	9	AL451061 Human DNA
140	71.6	2.9	161166	2	AC087673	Homo sapi	c 213	70.4	2.9	92909	9	AC073618	9	AC073618 Homo sapi
141	71.6	2.9	177073	2	AP000934	Homo sapi	c 214	70.4	2.9	94882	2	AC002317	2	AC002317 Homo sapi
142	71.6	2.9	195616	2	AC090344	Homo sapi	c 215	70.4	2.9	96206	9	AC013283	9	AC013283 Homo sapi
143	71.6	2.9	197156	2	AC090345	Homo sapi	c 216	70.4	2.9	96596	6	AX695395	6	AX695395 Sequence
144	71.6	2.9	197856	2	AP000777	Homo sapi	c 217	70.4	2.9	97749	9	AC004906	9	AC004906 Homo sapi
145	71.6	2.9	197856	2	AP000777	Homo sapi	c 218	70.4	2.9	104913	9	AC004242	9	AC004242 Homo sapi
146	71.6	2.9	201035	2	AC016744	Homo sapi	c 219	70.4	2.9	110000	2	BS324168 ³	2	BS324168 ³ Continuation (4 of
147	71.6	2.9	201460	9	AP003721	Homo sapi	c 220	70.4	2.9	110000	2	BS324168 ⁴	2	BS324168 ⁴ Continuation (5 of
148	71.4	2.9	198017	9	AC012314	Homo sapi	c 221	70.4	2.9	111373	9	HS715N11	9	HS715N11 Human chrom
149	71.4	2.9	205307	2	AC009968	Homo sapi	c 222	70.4	2.9	111550	2	CR753829	2	CR753829 Human DNA
150	71.2	2.9	166937	9	AC016254	Homo sapi	c 223	70.4	2.9	112130	2	AL135621	2	AL135621 Homo sapi
151	71.2	2.9	174761	9	AL590453	Human DNA	c 224	70.4	2.9	127140	9	AL136137	9	AL136137 Human DNA
152	71.2	2.9	187461	9	AL590453	Human DNA	c 225	70.4	2.9	127384	9	AL157823	9	AL157823 Human DNA
153	71.2	2.9	191115	9	AL590453	Human DNA	c 226	70.4	2.9	129252	9	HSU91327	9	HSU91327 Human chrom
154	71.2	2.9	207471	2	AP001053	Homo sapi	c 227	70.4	2.9	129884	9	AC1355385	9	AC1355385 Homo sapi
155	71	2.9	40629	2	AP006105	Homo sapi	c 228	70.4	2.9	130318	9	AC026979	9	AC026979 Homo sapi
156	71	2.9	88883	9	AC107911	Homo sapi	c 229	70.4	2.9	137390	2	AC113133	2	AC113133 Homo sapi
157	71	2.9	104435	9	AC016292	Homo sapi	c 230	70.4	2.9	141504	2	AC022295	2	AC022295 Homo sapi
158	71	2.9	126259	9	HS371119	Human DNA	c 231	70.4	2.9	143133	2	AC021655	2	AC021655 Homo sapi
159	71	2.9	146515	9	AL157702	Human DNA	c 232	70.4	2.9	143223	9	AL162725	9	AL162725 Human DNA
160	71	2.9	160990	9	AC097461	Homo sapi	c 233	70.4	2.9	146878	9	AC142299	9	AC142299 Pan trogl
161	71	2.9	169828	9	AC008878	Homo sapi	c 234	70.4	2.9	147052	9	AL590640	9	AL590640 Human DNA
162	71	2.9	173126	9	AC015884	Homo sapi	c 235	70.4	2.9	148540	9	HS212P9	9	HS212P9 Homo sapi
163	71	2.9	207651	9	AC148222	Colobus g	c 236	70.4	2.9	149397	6	AX329775	6	AX329775 Sequence
164	71	2.9	231234	2	AC148222	Colobus g	c 237	70.4	2.9	149480	6	AX329776	6	AX329776 Sequence
165	71	2.9	251856	2	AC146256	Pan trogl	c 238	70.4	2.9	149480	6	AX329776	6	AX329776 Sequence

239	70.4	2.9	149480	6	AX336193	AX336193 Sequence	C 312	70.4	2.9	175989	2	AL590962	AL590962 Homo sapi
240	70.4	2.9	149480	9	HU095740	U95740 Human Chrom	313	70.4	2.9	177720	2	AC035680	AC035680 Homo sapi
C 241	70.4	2.9	149490	9	AC130455	AC130455 Homo sapi	C 314	70.4	2.9	177801	9	AC138957	AC138957 Homo sapi
C 242	70.4	2.9	150881	2	AC072036	AC072036 Homo sapi	C 315	70.4	2.9	178067	2	AC024734	AC024734 Homo sapi
C 243	70.4	2.9	150881	2	AC087833	AC087833 Papio anu	C 316	70.4	2.9	178281	2	AC145148	AC145148 Homo sapi
C 244	70.4	2.9	154622	2	AC126336	AC126336 Homo sapi	C 317	70.4	2.9	178714	2	AC129504	AC129504 Homo sapi
C 245	70.4	2.9	155249	9	AC109487	AC109487 Homo sapi	C 318	70.4	2.9	179138	9	CNS07EGV	AL606834 Human chr
246	70.4	2.9	155567	9	AC073492	AC073492 Homo sapi	C 319	70.4	2.9	179188	2	AL590124	AL590124 Homo sapi
247	70.4	2.9	155614	2	AC012620	AC012620 Homo sapi	C 320	70.4	2.9	179676	2	AC015649	AC015649 Homo sapi
248	70.4	2.9	155809	2	AC012369	AC012369 Homo sapi	C 321	70.4	2.9	179966	2	AC023247	AC023247 Homo sapi
249	70.4	2.9	155809	2	AC145106	AC145106 Homo sapi	322	70.4	2.9	180053	2	AP002506	AP002506 Homo sapi
250	70.4	2.9	156281	9	AC146177	AC146177 Pan trogl	323	70.4	2.9	180117	2	AC025256	AC025256 Homo sapi
251	70.4	2.9	156345	2	AC023015	AC023015 Homo sapi	C 324	70.4	2.9	180317	2	AC025590	AC025590 Homo sapi
252	70.4	2.9	157662	9	AL139035	AL139035 Human DNA	C 325	70.4	2.9	180510	9	AC022415	AC022415 Homo sapi
253	70.4	2.9	157792	9	AC069209	AC069209 Homo sapi	326	70.4	2.9	180995	9	AC117500	AC117500 Homo sapi
254	70.4	2.9	157793	9	AC090181	AC090181 Homo sapi	C 327	70.4	2.9	181916	2	AC110927	AC110927 Homo sapi
255	70.4	2.9	157879	9	AC149230	AC149230 Pan trogl	328	70.4	2.9	182703	2	AC073117	AC073117 Homo sapi
256	70.4	2.9	157978	2	AP001444	AP001444 Homo sapi	329	70.4	2.9	183014	9	AC012409	AC012409 Homo sapi
C 257	70.4	2.9	158297	9	AC108779	AC106779 Homo sapi	330	70.4	2.9	183459	9	AC142525	AC142525 Homo sapi
C 258	70.4	2.9	159440	9	AL355392	AL355392 Human DNA	331	70.4	2.9	184467	2	AC073241	AC073241 Homo sapi
C 259	70.4	2.9	159482	2	AL512371	AL512371 Homo sapi	C 332	70.4	2.9	185378	9	AC118754	AC118754 Homo sapi
C 260	70.4	2.9	159516	2	AC048350	AC048350 Homo sapi	C 333	70.4	2.9	185427	2	AC139459	AC139459 Homo sapi
C 261	70.4	2.9	159852	9	AC097476	AC097476 Homo sapi	C 334	70.4	2.9	185919	9	AP001831	AP001831 Homo sapi
262	70.4	2.9	160229	9	AC145900	AC145900 Pan trogl	335	70.4	2.9	186319	2	AC133014	AC133014 Homo sapi
263	70.4	2.9	160234	2	AC150612	AC150612 Callithr	336	70.4	2.9	186481	9	AC145102	AC145102 Homo sapi
C 264	70.4	2.9	161013	9	AC018709	AC018709 Homo sapi	C 337	70.4	2.9	186787	9	AC138959	AC138959 Homo sapi
265	70.4	2.9	161475	9	HS164C20	AL009029 Human DNA	C 338	70.4	2.9	187615	9	AC020724	AC020724 Homo sapi
C 266	70.4	2.9	161841	9	AC135279	AC135279 Homo sapi	339	70.4	2.9	188461	9	AL138836	AL138836 Human DNA
267	70.4	2.9	162337	2	AC023999	AC023999 Homo sapi	C 340	70.4	2.9	188666	9	AC018921	AC018921 Homo sapi
C 268	70.4	2.9	162746	9	AC006050	AC006050 Homo sapi	341	70.4	2.9	189635	9	AP003082	AP003082 Homo sapi
C 269	70.4	2.9	162984	9	AC104333	AC104333 Homo sapi	C 342	70.4	2.9	190414	2	AC146407	AC146407 Pan trogl
C 270	70.4	2.9	163264	2	AC151891	AC151891 Callicebu	C 343	70.4	2.9	190466	2	AC022285	AC022285 Homo sapi
271	70.4	2.9	163795	9	AP000356	AP000356 Homo sapi	344	70.4	2.9	190626	2	AC062036	AC062036 Homo sapi
272	70.4	2.9	163862	2	AC092911	AC092911 Homo sapi	345	70.4	2.9	190683	2	AC147599	AC147599 Homo sapi
C 273	70.4	2.9	164132	9	AC104971	AC104971 Homo sapi	C 346	70.4	2.9	192046	9	AC008083	AC008083 Homo sapi
C 274	70.4	2.9	164175	9	AC119056	AC119056 Papio anu	C 347	70.4	2.9	194006	9	AC074044	AC074044 Homo sapi
275	70.4	2.9	164355	9	AC146132	AC146132 Pan trogl	C 348	70.4	2.9	194399	9	AC146335	AC146335 Homo sapi
276	70.4	2.9	164528	9	AC026191	AC026191 Homo sapi	C 349	70.4	2.9	195779	9	AC146944	AC146944 Homo sapi
277	70.4	2.9	165082	2	AC026559	AC026559 Homo sapi	350	70.4	2.9	197748	2	AC026283	AC026283 Homo sapi
278	70.4	2.9	165138	2	AC068955	AC068955 Homo sapi	351	70.4	2.9	198396	9	AC010355	AC010355 Homo sapi
C 279	70.4	2.9	165178	2	AC025355	AC025355 Homo sapi	C 352	70.4	2.9	199463	2	AC129497	AC129497 Homo sapi
C 280	70.4	2.9	165502	9	BS000051	BS000051 Pan trogl	C 353	70.4	2.9	200655	9	AC091825	AC091825 Homo sapi
281	70.4	2.9	165725	2	AC024027	AC024027 Homo sapi	C 354	70.4	2.9	201279	9	AC090133	AC090133 Homo sapi
C 282	70.4	2.9	165762	2	AC124263	AC124263 Homo sapi	355	70.4	2.9	201456	9	AC026401	AC026401 Homo sapi
283	70.4	2.9	165770	9	AC023396	AC023396 Homo sapi	C 356	70.4	2.9	201466	2	AC147573	AC147573 Homo sapi
C 284	70.4	2.9	166065	2	AC149014	AC149014 Papio anu	C 357	70.4	2.9	204037	2	AC015881	AC015881 Homo sapi
C 285	70.4	2.9	166615	9	AC138928	AC138928 Homo sapi	C 358	70.4	2.9	205040	9	AC015849	AC015849 Homo sapi
286	70.4	2.9	167335	2	AC023527	AC023527 Homo sapi	C 359	70.4	2.9	205317	9	AC093856	AC093856 Homo sapi
287	70.4	2.9	167768	9	AC026224	AC026224 Homo sapi	C 360	70.4	2.9	221286	2	AC138941	AC138941 Homo sapi
288	70.4	2.9	168015	2	AL591434	AL591434 Homo sapi	361	70.4	2.9	221307	2	AL732582	AL732582 Homo sapi
289	70.4	2.9	168070	2	AC126328	AC126328 Homo sapi	C 362	70.4	2.9	222952	2	AC147600	AC147600 Homo sapi
290	70.4	2.9	168247	9	AC005014	AC005014 Homo sapi	C 363	70.4	2.9	229396	2	AC024108	AC024108 Homo sapi
291	70.4	2.9	168544	9	AL513307	AL513307 Human DNA	C 364	70.4	2.9	231800	2	AC147282	AC147282 Pan trogl
C 292	70.4	2.9	169405	9	AC092800	AC092800 Homo sapi	365	70.4	2.9	237235	2	AL499603	AL499603 Homo sapi
293	70.4	2.9	170336	2	AC011244	AC011244 Homo sapi	366	70.2	2.9	53074	9	BS000049	BS000049 Pan trogl
C 294	70.4	2.9	171363	9	AC145129	AC145129 Homo sapi	367	70.2	2.9	62724	9	AC117989	AC117989 Mus muscu
295	70.4	2.9	171631	2	AC069291	AC069291 Homo sapi	368	70.2	2.9	152154	2	AC136369	AC136369 Homo sapi
C 296	70.4	2.9	171721	2	AC015744	AC015744 Homo sapi	369	70.2	2.9	152327	2	AC026295	AC026295 Homo sapi
C 297	70.4	2.9	171788	9	AC073089	AC073089 Homo sapi	C 370	70.2	2.9	152407	2	AC134660	AC134660 Homo sapi
298	70.4	2.9	172061	2	AC027156	AC027156 Homo sapi	C 371	70.2	2.9	152595	2	AC140167	AC140167 Homo sapi
C 299	70.4	2.9	172103	2	AC021871	AC021871 Homo sapi	C 372	70.2	2.9	161667	9	AC005483	AC005483 Homo sapi
300	70.4	2.9	172132	9	AC010149	AC010149 Homo sapi	C 373	70.2	2.9	162066	9	AC018989	AC018989 Homo sapi
C 301	70.4	2.9	172382	2	AC149046	AC149046 Papio anu	374	70.2	2.9	163035	2	AC006405	AC006405 Homo sapi
C 302	70.4	2.9	172902	2	AL358816	AL358816 Homo sapi	375	70.2	2.9	169490	9	AC091910	AC091910 Homo sapi
C 303	70.4	2.9	174071	2	AC139835	AC139835 Homo sapi	376	70.2	2.9	189630	2	AC139788	AC139788 Homo sapi
C 304	70.4	2.9	174498	2	AC147746	AC147746 Homo sapi	C 377	70.2	2.9	171274	2	AC140166	AC140166 Homo sapi
305	70.4	2.9	174677	9	AC063960	AC063960 Homo sapi	378	70.2	2.9	176643	9	AC005324	AC005324 Homo sapi
C 306	70.4	2.9	175250	2	AC069521	AC069521 Homo sapi	379	70.2	2.9	179056	2	AC068936	AC068936 Homo sapi
C 307	70.4	2.9	175606	9	AC011604	AC011604 Homo sapi	380	70.2	2.9	182069	2	AC146134	AC146134 Pan trogl
C 308	70.4	2.9	175667	9	AC009336	AC009336 Homo sapi	381	70.2	2.9	183297	9	AC138804	AC138804 Homo sapi
309	70.4	2.9	175706	9	AL135783	AL135783 Human DNA	C 382	70.2	2.9	187516	2	AC138845	AC138845 Homo sapi
C 310	70.4	2.9	175740	2	AC145033	AC145033 Homo sapi	383	70.2	2.9	189312	2	AC126406	AC126406 Homo sapi
C 311	70.4	2.9	175943	9	AC123777	AC123777 Homo sapi	C 384	70.2	2.9	191594	9	AL160282	AL160282 Human DNA

C 385	70.2	2.9 193255	2	AC138705	AC138705 Homo sapi	C 458	69.6	2.8 141061	9	AC127025	AC127025 Homo sapi
386	70.2	2.9 197470	2	AC026964	AC026964 Homo sapi	459	69.6	2.8 145410	9	AC027455	AC027455 Homo sapi
387	70.2	2.9 205239	2	AC140177	AC140177 Homo sapi	460	69.6	2.8 147823	9	AC074376	AC074376 Homo sapi
388	70.2	2.9 217253	2	AC130343	AC130343 Homo sapi	C 461	69.6	2.8 162325	2	AC143431	AC143431 Macaca mu
C 389	70	2.8 730	6	AX541640	Sequence	462	69.6	2.8 173592	2	AC005073	AC005073 Homo sapi
C 390	70	2.8 3461	6	AX333628	Sequence	C 463	69.6	2.8 176653	2	AP001857	AP001857 Homo sapi
C 391	70	2.8 34641	6	AX334305	Sequence	C 464	69.6	2.8 183380	9	AC093259	AC093259 Homo sapi
C 392	70	2.8 34641	9	HUMRCCL	D00591 Homo sapien	C 465	69.6	2.8 185839	2	AC023278	AC023278 Homo sapi
C 393	70	2.8 44185	9	AP000701	AP000701 Homo sapi	C 466	69.6	2.8 187386	9	AC103702	AC103702 Homo sapi
C 394	70	2.8 44185	9	AC008484	AC008484 Homo sapi	C 467	69.6	2.8 192070	9	AC090616	AC090616 Homo sapi
C 395	70	2.8 59451	9	AC018677	AC018677 Homo sapi	C 468	69.6	2.8 196772	9	AC087392	AC087392 Homo sapi
C 396	70	2.8 103108	9	AC073216	AC073216 Homo sapi	C 469	69.6	2.8 197295	9	AC073585	AC073585 Homo sapi
C 397	70	2.8 113520	9	AC093655	AC093655 Homo sapi	C 470	69.6	2.8 204963	2	AC145617	AC145617 Homo sapi
C 398	70	2.8 119721	2	AC044856	AC044856 Homo sapi	C 471	69.6	2.8 209382	9	AC005071	AC005071 Homo sapi
C 399	70	2.8 134040	2	AL534397	AL534397 Human DNA	C 472	69.6	2.8 215936	9	CNS057CA	AL355076 Human chr
C 400	70	2.8 135820	9	AC026431	AC026431 Homo sapi	473	69.4	2.8 933	6	C0820329	C0820329 Sequence
C 401	70	2.8 143080	9	AC094097	AC094097 Homo sapi	474	69.4	2.8 46501	2	AC145655	AC145655 Homo sapi
C 402	70	2.8 153792	2	AC021763	AC021763 Homo sapi	C 475	69.4	2.8 54475	9	AL136122	AL136122 Human DNA
C 403	70	2.8 158405	9	AC091986	AC091986 Homo sapi	C 476	69.4	2.8 63432	9	BX004859	BX004859 Human DNA
C 404	70	2.8 160760	2	AC119571	AC119571 Pan trogl	C 477	69.4	2.8 63682	9	CR381640	CR381640 Human DNA
C 405	70	2.8 163703	2	AC119571	AC119571 Homo sapi	C 478	69.4	2.8 67326	9	AL129514	AL129514 Homo sapi
C 406	70	2.8 165562	2	AC116004	AC116004 Homo sapi	C 479	69.4	2.8 68430	9	AL360229	AL360229 Human DNA
C 407	70	2.8 170846	9	AC068121	AC068121 Homo sapi	480	69.4	2.8 78750	9	AL360087	AL360087 Homo sapi
C 408	70	2.8 173146	9	AC006370	AC006370 Homo sapi	C 481	69.4	2.8 86684	9	AC010605	AC010605 Homo sapi
C 409	70	2.8 174025	9	AC073288	AC073288 Homo sapi	C 482	69.4	2.8 103857	9	AP000860	AP000860 Homo sapi
C 410	70	2.8 174711	9	AC005696	AC005696 Homo sapi	C 483	69.4	2.8 108906	9	AC022088	AC022088 Homo sapi
C 411	70	2.8 181112	2	AL360012	AL360012 Homo sapi	C 484	69.4	2.8 110737	2	AC011105	AC011105 Homo sapi
C 412	70	2.8 182617	9	AC007731	AC007731 Homo sapi	C 485	69.4	2.8 111344	9	AL139403	AL139403 Human DNA
C 413	70	2.8 186787	2	AP001379	AP001379 Homo sapi	C 486	69.4	2.8 111998	9	AC011509	AC011509 Homo sapi
C 414	70	2.8 187200	2	AC005500	AC005500 Homo sapi	C 487	69.4	2.8 122042	9	AC008924	AC008924 Homo sapi
C 415	70	2.8 192592	9	AL365203	AL365203 Human DNA	488	69.4	2.8 125057	9	AL133419	AL133419 Human DNA
C 416	70	2.8 197973	2	AL590967	AL590967 Homo sapi	489	69.4	2.8 135996	2	AL355273	AL355273 Human DNA
C 417	70	2.8 210378	2	AB063285	AB063285 Homo sapi	490	69.4	2.8 153108	9	AP002993	AP002993 Homo sapi
C 418	70	2.8 250000	9	AP001727	AP001727 Homo sapi	C 491	69.4	2.8 154839	9	AC009501	AC009501 Homo sapi
C 419	69.8	2.8 340000	9	AP001105	AP001105 Homo sapi	C 492	69.4	2.8 157173	9	AC027709	AC027709 Homo sapi
C 420	69.8	2.8 57434	2	AC005808	AC005808 Homo sapi	C 493	69.4	2.8 158276	2	AC024978	AC024978 Homo sapi
C 421	69.8	2.8 65111	2	AC055857	AC055857 Homo sapi	C 494	69.4	2.8 158781	2	AC137675	AC137675 Homo sapi
C 422	69.8	2.8 89820	2	AC007868	AC007868 Genomic S	C 495	69.4	2.8 163004	9	AC122718	AC122718 Homo sapi
C 423	69.8	2.8 105940	2	AC010606	AC010606 Homo sapi	C 496	69.4	2.8 170043	2	AC027015	AC027015 Homo sapi
C 424	69.8	2.8 117846	2	AC073431	AC073431 Homo sapi	497	69.4	2.8 171775	2	AC027015	AC027015 Homo sapi
C 425	69.8	2.8 121822	9	AC105393	AC105393 Homo sapi	C 498	69.4	2.8 172650	2	AC011042	AC011042 Homo sapi
C 426	69.8	2.8 126651	9	AC092815	AC092815 Homo sapi	C 499	69.4	2.8 173651	9	AC023449	AC023449 Homo sapi
C 427	69.8	2.8 128871	9	AL157838	AL157838 Human DNA	C 500	69.4	2.8 175336	9	AC099535	AC099535 Homo sapi
C 428	69.8	2.8 129586	9	AC005086	AC005086 Homo sapi	C 501	69.4	2.8 181720	2	AC022242	AC022242 Homo sapi
C 429	69.8	2.8 145550	2	AP001900	AP001900 Homo sapi	C 502	69.4	2.8 182197	2	AC008821	AC008821 Homo sapi
C 430	69.8	2.8 149838	2	AC023440	AC023440 Homo sapi	C 503	69.4	2.8 184111	9	AC073083	AC073083 Homo sapi
C 431	69.8	2.8 155332	2	AL365439	AL365439 Homo sapi	C 504	69.4	2.8 186010	2	AC146081	AC146081 Pan trogl
C 432	69.8	2.8 156599	2	AC083840	AC083840 Homo sapi	C 505	69.4	2.8 187063	2	HSBA192P3	AL117340 Human DNA
C 433	69.8	2.8 161698	2	AC150198	AC150198 Papio anu	C 506	69.4	2.8 187517	9	CNS01RHM	AL161851 Human chr
C 434	69.8	2.8 164321	2	AP001105	AP001105 Homo sapi	C 507	69.4	2.8 187732	9	AC073655	AC073655 Homo sapi
C 435	69.8	2.8 165000	9	AC137894	AC137894 Homo sapi	C 508	69.4	2.8 188105	9	AC109512	AC109512 Homo sapi
C 436	69.8	2.8 166162	2	AC090404	AC090404 Homo sapi	C 509	69.4	2.8 188105	9	AC073334	AC073334 Homo sapi
C 437	69.8	2.8 171167	9	AC012354	AC012354 Homo sapi	C 510	69.4	2.8 189975	2	AC073334	AC073334 Homo sapi
C 438	69.8	2.8 171665	2	AC084081	AC084081 Homo sapi	C 511	69.4	2.8 191970	2	AC085592	AC085592 Homo sapi
C 439	69.8	2.8 172449	2	AC142165	AC142165 Homo sapi	C 512	69.4	2.8 192670	9	AC087565	AC087565 Homo sapi
C 440	69.8	2.8 174235	9	AC145919	AC145919 Pan trogl	C 513	69.4	2.8 192937	9	AC093420	AC093420 Homo sapi
C 441	69.8	2.8 175416	2	AP006286	AP006286 Homo sapi	514	69.4	2.8 193766	2	AC020715	AC020715 Homo sapi
C 442	69.8	2.8 175570	2	AC149180	AC149180 Papio anu	C 515	69.4	2.8 197992	2	AF225898	AF225898 Homo sapi
C 443	69.8	2.8 178218	2	AC016841	AC016841 Homo sapi	C 516	69.4	2.8 198084	9	AC090594	AC090594 Homo sapi
C 444	69.8	2.8 183937	2	AP001145	AP001145 Homo sapi	C 517	69.4	2.8 201155	9	AC090594	AC090594 Homo sapi
C 445	69.8	2.8 187160	9	AC138230	AC138230 Homo sapi	518	69.4	2.8 202544	9	AC146145	AC146145 Pan trogl
C 446	69.8	2.8 189967	2	AC079553	AC079553 Mus muscu	C 519	69.4	2.8 209347	2	AC107616	AC107616 Homo sapi
C 447	69.8	2.8 190809	9	AL391357	AL391357 Human DNA	C 520	69.4	2.8 325387	2	AY338491	AY338491 Homo sapi
C 448	69.8	2.8 195076	9	AC013337	AC013337 Homo sapi	521	69.2	2.8 84307	2	AC025206	AC025206 Homo sapi
C 449	69.8	2.8 198895	2	AP001337	AP001337 Homo sapi	522	69.2	2.8 91388	9	AC005994	AC005994 Homo sapi
C 450	69.8	2.8 204623	2	AC001338	AC001338 Homo sapi	C 523	69.2	2.8 147233	2	AC087486	AC087486 Homo sapi
C 451	69.8	2.8 209109	9	AC116025	AC116025 Homo sapi	C 524	69.2	2.8 150266	9	AC022408	AC022408 Homo sapi
C 452	69.8	2.8 211291	9	AC107959	AC107959 Homo sapi	525	69.2	2.8 151210	2	AC142890	AC142890 Macaca mu
C 453	69.8	2.8 216129	2	AC022454	AC022454 Homo sapi	526	69.2	2.8 152101	9	AC006987	AC006987 Homo sapi
C 454	69.8	2.8 249021	9	AC015933	AC015933 Homo sapi	527	69.2	2.8 166041	2	AC145137	AC145137 Homo sapi
C 455	69.6	2.8 52586	9	AF258547	AF258547 Homo sapi	528	69.2	2.8 166628	2	AC021753	AC021753 Homo sapi
C 456	69.6	2.8 100976	9	HS1005F21	HS1005F21 Human DNA	529	69.2	2.8 167996	9	AC068981	AC068981 Homo sapi
C 457	69.6	2.8 104726	9	AF258545	AF258545 Homo sapi	530	69.2	2.8 178887	2	AC068981	AC068981 Homo sapi

677	68.8	2.8	90732	9	AL670886	Human DNA
678	68.8	2.8	90780	2	AC093202	Human sapi
679	68.8	2.8	92001	9	AC117476	Human sapi
680	68.8	2.8	93407	9	AC011383	Homo sapi
681	68.8	2.8	93471	9	AL592486	Human DNA
682	68.8	2.8	94024	9	AC007368	Homo sapi
683	68.8	2.8	94170	9	AC068777	Homo sapi
684	68.8	2.8	94667	2	CR759761	Homo sapi
685	68.8	2.8	94718	9	AC026770	Homo sapi
686	68.8	2.8	95271	2	AC015809	Homo sapi
687	68.8	2.8	95663	9	AC010247	Homo sapi
688	68.8	2.8	96376	2	AC007626	Homo sapi
689	68.8	2.8	96588	6	AX695917	Sequence
690	68.8	2.8	97112	9	AL353631	Human DNA
691	68.8	2.8	98300	9	AC062336	Homo sapi
692	68.8	2.8	98404	2	AL355676	Homo sapi
693	68.8	2.8	99109	9	AL805934	Human DNA
694	68.8	2.8	99263	2	CNS01DX9	Human sapi
695	68.8	2.8	99505	9	AP002087	Homo sapi
696	68.8	2.8	99787	9	AL359540	Human DNA
697	68.8	2.8	99867	9	AC009387	Homo sapi
698	68.8	2.8	99930	9	AC068640	Homo sapi
699	68.8	2.8	100000	9	AP000018	Homo sapi
700	68.8	2.8	100000	9	AP000053	Homo sapi
701	68.8	2.8	100000	9	AP000065	Homo sapi
702	68.8	2.8	100000	9	AP000159	Homo sapi
703	68.8	2.8	100000	9	AP000167	Homo sapi
704	68.8	2.8	100000	9	AP000504	Homo sapi
705	68.8	2.8	100234	2	CR759702	Homo sapi
706	68.8	2.8	100562	9	AL355870	Human DNA
707	68.8	2.8	100853	2	AC094086	Homo sapi
708	68.8	2.8	103581	2	AC073615	Homo sapi
709	68.8	2.8	104228	9	AL135917	Human DNA
710	68.8	2.8	104380	2	AL355869	Homo sapi
711	68.8	2.8	104816	9	AC083805	Homo sapi
712	68.8	2.8	105191	9	AL161655	Human sapi
713	68.8	2.8	105587	9	CNS01DU6	Human chr
714	68.8	2.8	105628	2	AC138144	Homo sapi
715	68.8	2.8	106508	9	AC005102	Homo sapi
716	68.8	2.8	106938	6	CQ868668	Sequence
717	68.8	2.8	107627	9	AL513218	Human DNA
718	68.8	2.8	107733	9	AC088472	Homo sapi
719	68.8	2.8	108040	2	AC068150	Homo sapi
720	68.8	2.8	108460	9	HS111C20	Human DNA
721	68.8	2.8	108860	9	AC127525	Homo sapi
722	68.8	2.8	109445	9	AC008946	Homo sapi
723	68.8	2.8	110000	2	AC003656 ⁴	Continuation (5 of
724	68.8	2.8	110000	2	AC003656 ⁶	Continuation (7 of
725	68.8	2.8	110000	2	AC130427 ⁰	Homo sapi
726	68.8	2.8	110000	2	AC140881 ¹	Continuation (2 of
727	68.8	2.8	110000	2	AC141459 ¹	Continuation (2 of
728	68.8	2.8	110000	2	AL590046 ²	Continuation (3 of
729	68.8	2.8	110282	9	AC096563 ⁴	Homo sapi
730	68.8	2.8	110283	9	AF298854	Homo sapi
731	68.8	2.8	110459	9	AC117378	Homo sapi
732	68.8	2.8	110535	9	AC005091	Homo sapi
733	68.8	2.8	110539	9	AL731572	Human DNA
734	68.8	2.8	110804	9	AC004748	Homo sapi
735	68.8	2.8	111051	2	AF322449	Homo sapi
736	68.8	2.8	111554	2	CR753842	Homo sapi
737	68.8	2.8	111731	2	BX323063	Homo sapi
738	68.8	2.8	111908	2	AC108065	Homo sapi
739	68.8	2.8	112058	2	AC055112	Homo sapi
740	68.8	2.8	112417	9	AC060615	Homo sapi
741	68.8	2.8	112661	9	AC004668	Homo sapi
742	68.8	2.8	112707	9	AL359207	Human DNA
743	68.8	2.8	113036	9	AL158160	Human DNA
744	68.8	2.8	113241	9	AC002425	Homo sapi
745	68.8	2.8	113252	9	AC004408	Homo sapi
746	68.8	2.8	113530	9	AC073216	Homo sapi
747	68.8	2.8	113687	9	AC069281	Homo sapi
748	68.8	2.8	113916	9	HUAC003007	Human Chr
749	68.8	2.8	114104	9	AC128712	Human sapi
750	68.8	2.8	114420	9	AL158076	Human sapi
751	68.8	2.8	114477	9	AL591025	Human DNA
752	68.8	2.8	114950	9	AC097652	Homo sapi
753	68.8	2.8	114983	2	AC093209	Homo sapi
754	68.8	2.8	114992	9	AC008772	Homo sapi
755	68.8	2.8	114998	9	AC133681	Homo sapi
756	68.8	2.8	115596	9	AC096948	Homo sapi
757	68.8	2.8	116169	2	AP002080	Homo sapi
758	68.8	2.8	116478	9	AC092287	Homo sapi
759	68.8	2.8	117149	9	AC083984	Homo sapi
760	68.8	2.8	117166	9	AP000436	Homo sapi
761	68.8	2.8	117488	9	AL354981	Human DNA
762	68.8	2.8	117710	9	AC106743	Homo sapi
763	68.8	2.8	118052	9	AC023055	Homo sapi
764	68.8	2.8	118172	9	AC015912	Homo sapi
765	68.8	2.8	118763	9	AC114484	Homo sapi
766	68.8	2.8	118951	9	HS134P22	Human DNA
767	68.8	2.8	118995	9	AC005368	Homo sapi
768	68.8	2.8	119222	9	AC067742	Homo sapi
769	68.8	2.8	119236	9	CNS05TEX	Human chr
770	68.8	2.8	120101	9	AC064872	Homo sapi
771	68.8	2.8	120236	9	AC008523	Homo sapi
772	68.8	2.8	120491	9	AC008859	Homo sapi
773	68.8	2.8	120528	9	AP000812	Homo sapi
774	68.8	2.8	120571	9	CNS01DT3	Human chr
775	68.8	2.8	121103	9	AP006623	Homo sapi
776	68.8	2.8	121478	9	AL772363	Human DNA
777	68.8	2.8	121682	2	AL139127	Homo sapi
778	68.8	2.8	121705	9	AC006452	Homo sapi
779	68.8	2.8	121984	9	AC126309	Homo sapi
780	68.8	2.8	122674	9	AC007021	Homo sapi
781	68.8	2.8	123794	9	AC015917	Homo sapi
782	68.8	2.8	123828	9	AP000353	Homo sapi
783	68.8	2.8	124055	2	AC127600	Homo sapi
784	68.8	2.8	124146	9	AC068706	Homo sapi
785	68.8	2.8	124457	9	AC115115	Homo sapi
786	68.8	2.8	125290	9	AC005048	Homo sapi
787	68.8	2.8	125661	2	AL138773	Human DNA
788	68.8	2.8	126141	2	AL356300	Homo sapi
789	68.8	2.8	126541	9	AC008128	Homo sapi
790	68.8	2.8	126846	9	AL359375	Human DNA
791	68.8	2.8	127145	9	HS1119A7	Human DNA
792	68.8	2.8	127381	9	AL356268	Human DNA
793	68.8	2.8	128151	9	AP001966	Homo sapi
794	68.8	2.8	128230	9	HS313L4	Human DNA s
795	68.8	2.8	128386	9	AL356782	Human DNA
796	68.8	2.8	129231	9	AC092265	Homo sapi
797	68.8	2.8	129541	9	AC004999	Homo sapi
798	68.8	2.8	130526	2	AP000715	Homo sapi
799	68.8	2.8	130618	9	HSU80017	Homo sapi
800	68.8	2.8	131078	9	HSJ1103B4	Human DNA
801	68.8	2.8	131188	9	AL672277	Human DNA
802	68.8	2.8	131682	9	AL590311	Human DNA
803	68.8	2.8	131933	9	AL590311	Human DNA
804	68.8	2.8	132164	9	AC098587	Homo sapi
805	68.8	2.8	132353	9	AC134393	Homo sapi
806	68.8	2.8	132384	9	AC116347	Homo sapi
807	68.8	2.8	132396	9	AL607023	Human DNA
808	68.8	2.8	132551	9	CR354443	Human DNA
809	68.8	2.8	132805	9	HS339A18	Human DNA s
810	68.8	2.8	133541	2	AC027169	Homo sapi
811	68.8	2.8	133544	9	AC100748	Homo sapi
812	68.8	2.8	133786	9	AC091839	Homo sapi
813	68.8	2.8	133973	9	AC131953	Homo sapi
814	68.8	2.8	134036	9	AC007845	Homo sapi
815	68.8	2.8	134161	9	AC104336	Homo sapi
816	68.8	2.8	134957	9	HSU930L11	Human DNA
817	68.8	2.8	134979	9	AL359963	Human DNA
818	68.8	2.8	135331	9	AC008798	Homo sapi
819	68.8	2.8	135404	9	AC084024	Homo sapi
820	68.8	2.8	135932	9	AL441886	Human DNA
821	68.8	2.8	136002	2	AC012343	Homo sapi
822	68.8	2.8	136098	9	AC006970	Homo sapi

823	68.8	2.8	136493	9	AL662899	Human DNA	AL662899	Human DNA	896	68.8	2.8	150256	9	AC120838	Pan trogl
824	68.8	2.8	136755	9	AC002529	Homo sapi	AC002529	Homo sapi	c 897	68.8	2.8	150313	9	AC137672	Homo sapi
825	68.8	2.8	137229	9	AC010877	Homo sapi	AC010877	Homo sapi	c 898	68.8	2.8	150965	9	AC091915	Homo sapi
826	68.8	2.8	137371	9	AC026411	Homo sapi	AC026411	Homo sapi	c 899	68.8	2.8	151111	9	AC002308	Homo sapi
827	68.8	2.8	137808	2	AC008889	Homo sapi	AC008889	Homo sapi	c 900	68.8	2.8	151113	9	AC093858	Homo sapi
828	68.8	2.8	137890	9	AB045364	Homo sapi	AB045364	Homo sapi	c 901	68.8	2.8	151159	2	AC079346	Homo sapi
c 829	68.8	2.8	138144	2	AL928664	Homo sapi	AL928664	Homo sapi	c 902	68.8	2.8	151236	9	HS404K8	Human DNA
c 830	68.8	2.8	138538	9	AC011445	Homo sapi	AC011445	Homo sapi	c 903	68.8	2.8	151284	9	CR626880	Human DNA
831	68.8	2.8	138740	9	AC009113	Homo sapi	AC009113	Homo sapi	c 904	68.8	2.8	151418	2	AC025100	Homo sapi
832	68.8	2.8	138939	9	AC119675	Homo sapi	AC119675	Homo sapi	c 905	68.8	2.8	151504	2	AC104297	Homo sapi
833	68.8	2.8	139111	9	AL158048	Human DNA	AL158048	Human DNA	c 906	68.8	2.8	151736	2	AC024439	Homo sapi
834	68.8	2.8	139118	9	AL133477	Human DNA	AL133477	Human DNA	c 907	68.8	2.8	151820	2	AC140494	Homo sapi
c 835	68.8	2.8	139267	9	AC006435	Homo sapi	AC006435	Homo sapi	c 908	68.8	2.8	151834	9	AC005399	Homo sapi
c 836	68.8	2.8	139389	9	HS6802	Human DNA	HS6802	Human DNA	c 909	68.8	2.8	152224	2	AC007933	Homo sapi
c 837	68.8	2.8	139486	2	L49235	Homo sapien	L49235	Homo sapien	c 910	68.8	2.8	152311	2	AC011571	Homo sapi
c 838	68.8	2.8	139665	2	AP000865	Homo sapi	AP000865	Homo sapi	c 911	68.8	2.8	152336	2	AC009594	Homo sapi
c 839	68.8	2.8	139722	9	AC093770	Homo sapi	AC093770	Homo sapi	c 912	68.8	2.8	152474	2	AC138873	Homo sapi
c 840	68.8	2.8	139934	9	HUB384D8	Homo sapi	HUB384D8	Homo sapi	c 913	68.8	2.8	152502	2	AC012583	Homo sapi
c 841	68.8	2.8	140020	2	AC046162	Homo sapi	AC046162	Homo sapi	c 914	68.8	2.8	152502	2	AC012583	Homo sapi
842	68.8	2.8	140292	9	CNS01DU8	Human chr	AL133223	Human chr	c 915	68.8	2.8	152709	2	AC114799	Homo sapi
c 843	68.8	2.8	140486	2	AC021624	Homo sapi	AC021624	Homo sapi	c 916	68.8	2.8	153026	9	AL391280	Human DNA
c 844	68.8	2.8	140552	2	AC133562	Homo sapi	AC133562	Homo sapi	c 917	68.8	2.8	153728	9	AP003355	Homo sapi
c 845	68.8	2.8	140609	9	AP003550	Homo sapi	AP003550	Homo sapi	c 918	68.8	2.8	153788	2	AC027472	Homo sapi
c 846	68.8	2.8	140919	9	AC110747	Homo sapi	AC110747	Homo sapi	c 919	68.8	2.8	154381	2	AC009096	Homo sapi
c 847	68.8	2.8	141220	2	AC024238	Homo sapi	AC024238	Homo sapi	c 920	68.8	2.8	154606	9	AC097358	Homo sapi
848	68.8	2.8	141252	9	AC146263	Pan trogl	AC146263	Pan trogl	c 921	68.8	2.8	154677	2	AC138931	Homo sapi
849	68.8	2.8	141704	9	AC007993	Homo sapi	AC007993	Homo sapi	c 922	68.8	2.8	155022	9	AC002395	Homo sapi
850	68.8	2.8	141779	9	AC002377	Human PAC	AC002377	Human PAC	c 923	68.8	2.8	155304	9	AC055845	Homo sapi
c 851	68.8	2.8	142067	9	BX323860	Human DNA	BX323860	Human DNA	c 924	68.8	2.8	155306	2	AC010272	Homo sapi
c 852	68.8	2.8	142118	9	AC104081	Homo sapi	AC104081	Homo sapi	c 925	68.8	2.8	155306	2	AC008373	Homo sapi
c 853	68.8	2.8	142123	9	AC004690	Homo sapi	AC004690	Homo sapi	c 926	68.8	2.8	155498	2	AC015478	Homo sapi
c 854	68.8	2.8	142790	9	AL445685	Human DNA	AL445685	Human DNA	c 927	68.8	2.8	155569	2	AC026862	Homo sapi
c 855	68.8	2.8	142807	2	HS4J02553	Homo sapi	AL7002553	Homo sapi	c 928	68.8	2.8	155892	2	AP002513	Homo sapi
c 856	68.8	2.8	142871	9	AC020629	Homo sapi	AC020629	Homo sapi	c 929	68.8	2.8	155937	2	AC016341	Homo sapi
c 857	68.8	2.8	143146	9	AC079855	Homo sapi	AC079855	Homo sapi	c 930	68.8	2.8	155974	9	AC022119	Homo sapi
c 858	68.8	2.8	143229	2	AL61620	Homo sapi	AL61620	Homo sapi	c 931	68.8	2.8	156168	9	AC124917	Homo sapi
c 859	68.8	2.8	143376	9	AC012331	Homo sapi	AC012331	Homo sapi	c 932	68.8	2.8	156279	2	AC027707	Homo sapi
c 860	68.8	2.8	143563	9	HS55C23	Human DNA	AL032821	Human DNA	c 933	68.8	2.8	156471	2	AC145874	Pan trogl
861	68.8	2.8	143689	2	AC018374	Homo sapi	AC018374	Homo sapi	c 934	68.8	2.8	156471	2	AC013568	Homo sapi
862	68.8	2.8	143744	9	AC124283	Homo sapi	AC124283	Homo sapi	c 935	68.8	2.8	156690	2	AC027163	Homo sapi
863	68.8	2.8	144000	9	AC123764	Homo sapi	AC123764	Homo sapi	c 936	68.8	2.8	156989	2	AC059176	Homo sapi
864	68.8	2.8	144333	9	AC105036	Homo sapi	AC105036	Homo sapi	c 937	68.8	2.8	157067	2	AC073580	Homo sapi
c 865	68.8	2.8	144703	9	AP003112	Homo sapi	AP003112	Homo sapi	c 938	68.8	2.8	157162	9	AL360224	Human DNA
c 866	68.8	2.8	145100	2	AC024641	Homo sapi	AC024641	Homo sapi	c 939	68.8	2.8	157216	9	AC087491	Homo sapi
-867	68.8	2.8	145481	9	AL356862	Human DNA	AL356862	Human DNA	c 940	68.8	2.8	157358	9	AC009163	Homo sapi
868	68.8	2.8	145540	9	AP001052	Homo sapi	AP001052	Homo sapi	c 941	68.8	2.8	157631	2	AC142079	Homo sapi
c 869	68.8	2.8	145797	2	AC116938	Pan trogl	AC116938	Pan trogl	c 942	68.8	2.8	157912	9	AL133387	Human DNA
c 870	68.8	2.8	145947	9	AL353588	Human DNA	AL353588	Human DNA	c 943	68.8	2.8	157927	9	AP006278	Homo sapi
871	68.8	2.8	146050	2	AC040943	Homo sapi	AC040943	Homo sapi	c 944	68.8	2.8	158162	2	AC143351	Homo sapi
872	68.8	2.8	146096	2	AP001009	Homo sapi	AP001009	Homo sapi	c 945	68.8	2.8	158560	9	AC098969	Homo sapi
c 873	68.8	2.8	146652	2	AL445304	Homo sapi	AL445304	Homo sapi	c 946	68.8	2.8	158702	9	AC104472	Homo sapi
c 874	68.8	2.8	146699	9	BS000226	Pan trogl	BS000226	Pan trogl	c 947	68.8	2.8	158766	2	AC015851	Homo sapi
c 875	68.8	2.8	146746	9	HS50222	Human DNA	BS44484	Human DNA	c 948	68.8	2.8	159344	9	HS422G23	Human DNA
876	68.8	2.8	147102	9	AC002476	Human PAC	AC002476	Human PAC	c 949	68.8	2.8	159449	9	AC074008	Homo sapi
c 877	68.8	2.8	147292	2	AC023010	Homo sapi	AC023010	Homo sapi	c 950	68.8	2.8	159479	2	AC074352	Homo sapi
c 878	68.8	2.8	147354	2	AC145081	Homo sapi	AC145081	Homo sapi	c 951	68.8	2.8	159530	2	AC133922	Homo sapi
c 879	68.8	2.8	147545	9	AC126614	Homo sapi	AC126614	Homo sapi	c 952	68.8	2.8	159539	9	AL512625	Human DNA
880	68.8	2.8	147849	2	AC139366	Homo sapi	AC139366	Homo sapi	c 953	68.8	2.8	159620	9	AC087069	Homo sapi
c 881	68.8	2.8	148064	9	AC022861	Homo sapi	AC022861	Homo sapi	c 954	68.8	2.8	159705	2	AC092928	Homo sapi
c 882	68.8	2.8	148831	2	AC068526	Homo sapi	AC068526	Homo sapi	c 955	68.8	2.8	159752	9	AC006480	Homo sapi
c 883	68.8	2.8	148841	9	AC011462	Homo sapi	AC011462	Homo sapi	c 956	68.8	2.8	159797	9	AC104697	Homo sapi
c 884	68.8	2.8	149002	2	AL445484	Homo sapi	AL445484	Homo sapi	c 957	68.8	2.8	159840	2	AP000869	Homo sapi
c 885	68.8	2.8	149202	2	AC073467	Homo sapi	AC073467	Homo sapi	c 958	68.8	2.8	159926	9	AC007653	Homo sapi
886	68.8	2.8	149265	2	AC021562	Homo sapi	AC021562	Homo sapi	c 959	68.8	2.8	159974	9	AL139008	Human DNA
887	68.8	2.8	149433	9	AL135901	Human DNA	AL135901	Human DNA	c 960	68.8	2.8	160069	2	AC023329	Homo sapi
888	68.8	2.8	149437	2	AC027218	Homo sapi	AC027218	Homo sapi	c 961	68.8	2.8	160182	2	AC026994	Homo sapi
889	68.8	2.8	149559	9	AL139327	Human DNA	AL139327	Human DNA	c 962	68.8	2.8	160222	9	AC068287	Homo sapi
890	68.8	2.8	149594	2	AC021747	Homo sapi	AC021747	Homo sapi	c 963	68.8	2.8	160225	2	AC037438	Homo sapi
c 891	68.8	2.8	149679	2	AC080115	Homo sapi	AC080115	Homo sapi	c 964	68.8	2.8	160354	9	AC145952	Pan trogl
c 892	68.8	2.8	149884	9	AC016736	Homo sapi	AC016736	Homo sapi	c 965	68.8	2.8	160484	9	AC106858	Homo sapi
c 893	68.8	2.8	149920	9	AC093754	Homo sapi	AC093754	Homo sapi	c 966	68.8	2.8	160597	9	AL590666	Human DNA
c 894	68.8	2.8	149988	9	AL591602	Human DNA	AL591602	Human DNA	c 967	68.8	2.8	160755	2	AC138899	Homo sapi
c 895	68.8	2.8	150172	9	AC006285	Homo sapi	AC006285	Homo sapi	c 968	68.8	2.8	161010	2	AC146128	Pan trogl

C 969	68.8	2.8	161079	2	AC036148	AC036148 Homo sapi	C1042	68.8	2.8	167563	9	AC069280	AC069280 Homo sapi
C 970	68.8	2.8	161090	9	AC117415	AC117415 Homo sapi	C1043	68.8	2.8	167646	9	BX664718	BX664718 Human DNA
C 971	68.8	2.8	161147	9	AL354822	AL354822 Human DNA	1044	68.8	2.8	167787	9	AC010624	AC010624 Homo sapi
C 972	68.8	2.8	161264	9	AC007011	AC007011 Homo sapi	1045	68.8	2.8	167862	9	AC011966	AC011966 Homo sapi
C 973	68.8	2.8	161366	9	AC090939	AC090939 Homo sapi	1046	68.8	2.8	167981	2	AC079909	AC079909 Homo sapi
C 974	68.8	2.8	161406	9	AP002376	AP002376 Homo sapi	1047	68.8	2.8	168197	2	AC140520	AC140520 Homo sapi
C 975	68.8	2.8	161447	9	AC023202	AC023202 Homo sapi	C1048	68.8	2.8	168242	9	AC140830	AC140830 Homo sapi
C 976	68.8	2.8	161498	9	AC113376	AC113376 Homo sapi	1049	68.8	2.8	168243	9	AC008526	AC008526 Homo sapi
C 977	68.8	2.8	161502	9	AC138392	AC138392 Homo sapi	1050	68.8	2.8	168268	9	AC009124	AC009124 Homo sapi
C 978	68.8	2.8	161815	9	AC079199	AC079199 Homo sapi	1051	68.8	2.8	168324	9	AL133391	AL133391 Human DNA
C 979	68.8	2.8	161920	9	AP001053	AP001053 Homo sapi	1052	68.8	2.8	168430	2	AC145037	AC145037 Homo sapi
C 980	68.8	2.8	162010	2	AC010824	AC010824 Homo sapi	1053	68.8	2.8	168430	9	AC0933110	AC0933110 Homo sapi
C 981	68.8	2.8	162166	9	AL355298	AL355298 Human DNA	C1054	68.8	2.8	168585	9	AC040933	AC040933 Homo sapi
C 982	68.8	2.8	162237	9	AL133549	AL133549 Human DNA	1055	68.8	2.8	168702	9	AC079018	AC079018 Homo sapi
C 983	68.8	2.8	162538	2	BX649414	BX649414 Homo sapi	1056	68.8	2.8	168753	9	AC006120	AC006120 Homo sapi
C 984	68.8	2.8	162554	9	AC079354	AC079354 Homo sapi	C1057	68.8	2.8	168802	2	AC148538	AC148538 Pan trogl
C 985	68.8	2.8	162615	9	AC021683	AC021683 Homo sapi	1058	68.8	2.8	168814	9	AC010237	AC010237 Homo sapi
C 986	68.8	2.8	162659	2	AC138875	AC138875 Homo sapi	1059	68.8	2.8	168862	9	AC090532	AC090532 Homo sapi
C 987	68.8	2.8	162691	2	AC013523	AC013523 Homo sapi	1060	68.8	2.8	168907	9	AF205406	AF205406 Homo sapi
C 988	68.8	2.8	162792	2	AP001856	AP001856 Homo sapi	1061	68.8	2.8	168956	9	AC090286	AC090286 Homo sapi
C 989	68.8	2.8	162817	2	AC150233	AC150233 Papio anu	1062	68.8	2.8	168991	2	AC090411	AC090411 Homo sapi
C 990	68.8	2.8	163038	2	AC135542	AC135542 Pan trogl	1063	68.8	2.8	169137	9	AC010217	AC010217 Homo sapi
C 991	68.8	2.8	163197	2	AC091392	AC091392 Pan trogl	C1064	68.8	2.8	169166	9	AC027687	AC027687 Homo sapi
C 992	68.8	2.8	163218	9	AC005837	AC005837 Homo sapi	1065	68.8	2.8	169181	2	AC023303	AC023303 Homo sapi
C 993	68.8	2.8	163253	9	HSBB14084	AL121877 Human DNA	1066	68.8	2.8	169223	2	AL353675	AL353675 Homo sapi
C 994	68.8	2.8	163437	9	AC092606	AC092606 Homo sapi	1067	68.8	2.8	169405	9	AC092800	AC092800 Homo sapi
C 995	68.8	2.8	163455	2	AC009427	AC009427 Homo sapi	C1068	68.8	2.8	169675	9	AC060766	AC060766 Homo sapi
C 996	68.8	2.8	163494	9	AC079865	AC079865 Homo sapi	1069	68.8	2.8	169869	2	AC005867	AC005867 Homo sapi
C 997	68.8	2.8	163496	9	AC092567	AC092567 Homo sapi	C1070	68.8	2.8	169997	2	AC008440	AC008440 Homo sapi
C 998	68.8	2.8	163496	9	AC092567	AC092567 Homo sapi	1071	68.8	2.8	170000	2	AC004524	AC004524 Homo sapi
C 999	68.8	2.8	163597	9	AC016888	AC016888 Homo sapi	1072	68.8	2.8	170039	2	AL318814	AL318814 Homo sapi
C1000	68.8	2.8	163612	9	AC112183	AC112183 Homo sapi	1073	68.8	2.8	170245	9	HS109F14	AL355094 Human chr
C1001	68.8	2.8	163632	9	AL513185	AL513185 Human DNA	C1074	68.8	2.8	170273	9	CNS05TCD	AC020626 Homo sapi
C1002	68.8	2.8	163681	9	AL136992	AL136992 Human DNA	1075	68.8	2.8	170346	9	AC020626	AC020626 Homo sapi
C1003	68.8	2.8	163682	9	HSDJ71117	AL132713 Human DNA	1076	68.8	2.8	170458	9	AC146100	AC146100 Pan trogl
C1004	68.8	2.8	163837	9	BX664615	BX664615 Human DNA	1077	68.8	2.8	170513	9	AC106788	AC106788 Homo sapi
C1005	68.8	2.8	163846	9	AC068552	AC068552 Homo sapi	C1078	68.8	2.8	170758	9	AC004965	AC004965 Homo sapi
C1006	68.8	2.8	163871	9	HS1158E12	AC011584 Human DNA	1079	68.8	2.8	170776	2	AC138929	AC138929 Homo sapi
C1007	68.8	2.8	164055	9	AC011387	AC011387 Homo sapi	1080	68.8	2.8	170783	2	AC024943	AC024943 Homo sapi
C1008	68.8	2.8	164072	9	AC104109	AC104109 Homo sapi	1081	68.8	2.8	170790	9	AC025609	AC025609 Homo sapi
C1009	68.8	2.8	164118	2	AC021384	AC021384 Homo sapi	1082	68.8	2.8	170970	9	AL354707	AL354707 Human DNA
C1010	68.8	2.8	164286	9	AC020899	AC020899 Homo sapi	C1083	68.8	2.8	171003	2	AC133556	AC133556 Homo sapi
C1011	68.8	2.8	164508	2	AC104130	AC104130 Homo sapi	C1084	68.8	2.8	171206	2	AC026573	AC026573 Homo sapi
C1012	68.8	2.8	164611	9	AC068675	AC068675 Homo sapi	1085	68.8	2.8	171255	9	AC007912	AC007912 Homo sapi
C1013	68.8	2.8	164682	9	AC006199	AC006199 Homo sapi	1086	68.8	2.8	171381	9	AL162730	AL162730 Human DNA
C1014	68.8	2.8	164831	2	AC145155	AC145155 Homo sapi	1087	68.8	2.8	171423	2	AC025664	AC025664 Homo sapi
C1015	68.8	2.8	164851	9	AL161448	AL161448 Human DNA	C1088	68.8	2.8	171528	2	AC025196	AC025196 Homo sapi
C1016	68.8	2.8	164872	9	AC035260	AC035260 Homo sapi	C1089	68.8	2.8	171773	2	AC025230	AC025230 Homo sapi
C1017	68.8	2.8	164946	9	AP000553	AP000553 Homo sapi	C1090	68.8	2.8	171853	9	AP000880	AP000880 Homo sapi
C1018	68.8	2.8	164950	2	AC105191	AC105191 Homo sapi	C1091	68.8	2.8	171902	2	AP000846	AP000846 Homo sapi
C1019	68.8	2.8	165025	2	AC055871	AC055871 Homo sapi	1092	68.8	2.8	171934	9	AC092050	AC092050 Homo sapi
C1020	68.8	2.8	165080	2	AC117493	AC117493 Homo sapi	1093	68.8	2.8	171939	9	AC021855	AC021855 Homo sapi
C1021	68.8	2.8	165197	9	HSAC002070	AC002070 Human BAC	1094	68.8	2.8	171987	9	AC100757	AC100757 Homo sapi
C1022	68.8	2.8	165471	2	AC015713	AC015713 Homo sapi	C1095	68.8	2.8	172010	9	AC083876	AC083876 Homo sapi
C1023	68.8	2.8	165604	2	AC026008	AC026008 Homo sapi	C1096	68.8	2.8	172024	2	AC140907	AC140907 Homo sapi
C1024	68.8	2.8	165608	9	AC004492	AC004492 Homo sapi	1097	68.8	2.8	172094	2	AC018477	AC018477 Homo sapi
C1025	68.8	2.8	165654	2	AC027747	AC027747 Homo sapi	C1098	68.8	2.8	172091	2	AC139275	AC139275 Homo sapi
C1026	68.8	2.8	165682	2	AC140892	AC140892 Homo sapi	C1099	68.8	2.8	172110	9	AC012044	AC012044 Homo sapi
C1027	68.8	2.8	165699	2	AP001802	AP001802 Homo sapi	C1100	68.8	2.8	172169	2	AC124275	AC124275 Homo sapi
C1028	68.8	2.8	165718	2	AC127508	AC127508 Homo sapi	1101	68.8	2.8	172182	2	AC021986	AC021986 Homo sapi
C1029	68.8	2.8	165862	2	AC136995	AC136995 Homo sapi	1102	68.8	2.8	172206	9	AC092119	AC092119 Homo sapi
C1030	68.8	2.8	165870	9	AC138919	AC138919 Homo sapi	1103	68.8	2.8	172319	9	AC078819	AC078819 Homo sapi
C1031	68.8	2.8	165902	9	AC106763	AC106763 Homo sapi	1104	68.8	2.8	172509	2	AC024716	AC024716 Homo sapi
C1032	68.8	2.8	165909	2	AC079152	AC079152 Homo sapi	1105	68.8	2.8	172611	9	AC019129	AC019129 Homo sapi
C1033	68.8	2.8	166138	9	AC084756	AC084756 Homo sapi	C1106	68.8	2.8	172718	9	AC096649	AC096649 Homo sapi
C1034	68.8	2.8	166299	9	AC092602	AC092602 Homo sapi	1107	68.8	2.8	172823	2	AC018740	AC018740 Homo sapi
C1035	68.8	2.8	166606	2	AC020685	AC020685 Homo sapi	C1108	68.8	2.8	172903	9	AL157882	AL157882 Human DNA
C1036	68.8	2.8	166827	9	CR788307	CR788307 Human DNA	C1109	68.8	2.8	172969	9	AC090574	AC090574 Homo sapi
C1037	68.8	2.8	166935	2	AL359391	AL359391 Homo sapi	C1110	68.8	2.8	173137	2	AC107017	AC107017 Homo sapi
C1038	68.8	2.8	166905	2	AC025729	AC025729 Homo sapi	1111	68.8	2.8	173275	2	AC145031	AC145031 Homo sapi
C1039	68.8	2.8	167152	9	AC092939	AC092939 Homo sapi	1112	68.8	2.8	173275	9	AC092375	AC092375 Homo sapi
C1040	68.8	2.8	167195	9	AC009044	AC009044 Homo sapi	1113	68.8	2.8	173597	2	AC025749	AC025749 Homo sapi
C1041	68.8	2.8	167412	2	AL356352	AL356352 Homo sapi	C1114	68.8	2.8	173608	9	AC107993	AC107993 Homo sapi

c1115	68.8	2.8	173645	2	AC010770	AC010770 Homo sapi	1188	68.8	2.8	180787	9	AC099333	AC099333 Homo sapi
c1116	68.8	2.8	173977	2	AC141242	AC141242 Homo sapi	1189	68.8	2.8	181001	9	AC106782	AC106782 Homo sapi
c1117	68.8	2.8	174010	2	AC023814	AC023814 Homo sapi	1190	68.8	2.8	181016	9	AC068273	AC068273 Homo sapi
c1118	68.8	2.8	174613	2	AC012522	AC012522 Homo sapi	c1191	68.8	2.8	181230	9	AC149856	AC149856 Homo sapi
c1119	68.8	2.8	174758	2	AC149552	AC149552 Homo sapi	c1192	68.8	2.8	181329	9	AC092365	AC092365 Homo sapi
c1120	68.8	2.8	174799	2	AC143548	AC143548 Homo sapi	c1193	68.8	2.8	181395	9	AC083800	AC083800 Homo sapi
c1121	68.8	2.8	175014	2	AC080112	AC080112 Homo sapi	c1194	68.8	2.8	181400	9	AC084251	AC084251 Homo sapi
c1122	68.8	2.8	175073	2	AC105936	AC105936 Homo sapi	c1195	68.8	2.8	181505	2	AC025415	AC025415 Homo sapi
c1123	68.8	2.8	175136	9	AC104984	AC104984 Homo sapi	c1196	68.8	2.8	181561	9	AC015911	AC015911 Homo sapi
c1124	68.8	2.8	175320	9	AC009283	AC009283 Homo sapi	c1197	68.8	2.8	181585	9	AL1139350	AL1139350 Human DNA
c1125	68.8	2.8	175559	2	AC145101	AC145101 Homo sapi	c1198	68.8	2.8	181971	9	AC016182	AC016182 Homo sapi
c1126	68.8	2.8	175581	9	AP001525	AP001525 Homo sapi	c1199	68.8	2.8	182012	9	AL359846	AL359846 Human DNA
c1127	68.8	2.8	175740	2	AC145033	AC145033 Homo sapi	1200	68.8	2.8	182078	2	AC1359845	AC1359845 Homo sapi
c1128	68.8	2.8	175789	2	AP000425	AP000425 Homo sapi	c1201	68.8	2.8	182101	9	AC007599	AC007599 Homo sapi
c1129	68.8	2.8	175945	2	AC022147	AC022147 Homo sapi	1202	68.8	2.8	182199	2	AC021805	AC021805 Homo sapi
c1130	68.8	2.8	175990	2	AC139267	AC139267 Homo sapi	1203	68.8	2.8	182209	9	AL357060	AL357060 Human DNA
c1131	68.8	2.8	175999	2	AC021154	AC021154 Homo sapi	1204	68.8	2.8	182245	2	AC149842	AC149842 Homo sapi
c1132	68.8	2.8	176120	2	AC137519	AC137519 Homo sapi	1205	68.8	2.8	182261	2	AC087053	AC087053 Homo sapi
c1133	68.8	2.8	176121	9	AC131011	AC131011 Homo sapi	c1206	68.8	2.8	182288	9	AC018839	AC018839 Homo sapi
c1134	68.8	2.8	176157	2	AC013776	AC013776 Homo sapi	1207	68.8	2.8	182320	9	AC013394	AC013394 Homo sapi
c1135	68.8	2.8	176277	2	AC025941	AC025941 Homo sapi	1208	68.8	2.8	182340	2	AC024417	AC024417 Homo sapi
c1136	68.8	2.8	176393	9	AC051654	AC051654 Homo sapi	c1209	68.8	2.8	182406	2	AC139805	AC139805 Homo sapi
c1137	68.8	2.8	176653	2	AP001857	AP001857 Homo sapi	1210	68.8	2.8	182416	2	AC023044	AC023044 Homo sapi
c1138	68.8	2.8	176691	9	AC008479	AC008479 Homo sapi	c1211	68.8	2.8	182826	9	AC148688	AC148688 Macaca mu
c1139	68.8	2.8	176692	9	AC106882	AC106882 Homo sapi	c1212	68.8	2.8	182902	9	AC092405	AC092405 Homo sapi
c1140	68.8	2.8	176845	9	AC040163	AC040163 Homo sapi	c1213	68.8	2.8	182972	2	AC023550	AC023550 Homo sapi
c1141	68.8	2.8	176967	2	AC022742	AC022742 Homo sapi	c1214	68.8	2.8	183009	2	CNS01DTG	AL132718 Human chr
c1142	68.8	2.8	177355	9	AC023310	AC023310 Homo sapi	1215	68.8	2.8	183084	2	AC025936	AC025936 Homo sapi
c1143	68.8	2.8	177607	9	AC090642	AC090642 Homo sapi	1216	68.8	2.8	183314	2	AC024197	AC024197 Homo sapi
c1144	68.8	2.8	177637	9	AC146037	AC146037 Pan trogl	1217	68.8	2.8	183317	9	AC107214	AC107214 Homo sapi
c1145	68.8	2.8	177726	9	AC148671	AC148671 Macaca mu	1218	68.8	2.8	183534	2	AC139504	AC139504 Homo sapi
c1146	68.8	2.8	177951	2	AC074383	AC074383 Homo sapi	c1219	68.8	2.8	183684	2	AL162715	AL162715 Homo sapi
c1147	68.8	2.8	178066	9	AC087641	AC087641 Homo sapi	c1220	68.8	2.8	183687	9	AC064864	AC064864 Homo sapi
c1148	68.8	2.8	178127	2	AC079076	AC079076 Homo sapi	1221	68.8	2.8	183689	2	AC146129	AC146129 Pan trogl
c1149	68.8	2.8	178142	9	AC013546	AC013546 Homo sapi	1222	68.8	2.8	183946	2	AC009164	AC009164 Homo sapi
c1150	68.8	2.8	178216	2	AC051662	AC051662 Homo sapi	c1223	68.8	2.8	184135	2	AC145283	AC145283 Homo sapi
c1151	68.8	2.8	178229	2	AC010611	AC010611 Homo sapi	c1224	68.8	2.8	184139	9	AC022966	AC022966 Homo sapi
c1152	68.8	2.8	178315	9	AC122688	AC122688 Homo sapi	c1225	68.8	2.8	184231	2	AC023651	AC023651 Homo sapi
c1153	68.8	2.8	178344	2	AC067846	AC067846 Homo sapi	1226	68.8	2.8	184329	2	AP001896	AP001896 Homo sapi
c1154	68.8	2.8	178404	2	AC090321	AC090321 Homo sapi	1227	68.8	2.8	184539	2	AC027192	AC027192 Homo sapi
c1155	68.8	2.8	178418	2	AC013243	AC013243 Homo sapi	c1228	68.8	2.8	184663	9	DJ201G24	AF129756 Homo sapi
c1156	68.8	2.8	178444	2	AC133284	AC133284 Homo sapi	1229	68.8	2.8	184802	9	AP001160	AP001160 Homo sapi
c1157	68.8	2.8	178453	9	AC072044	AC072044 Homo sapi	1230	68.8	2.8	185000	2	AC007799	AC007799 Homo sapi
c1158	68.8	2.8	178513	2	AC013364	AC013364 Homo sapi	c1231	68.8	2.8	185117	2	AC140147	AC140147 Homo sapi
c1159	68.8	2.8	178531	9	AL445985	AL445985 Human DNA	1232	68.8	2.8	185315	9	AC087368	AC087368 Homo sapi
c1160	68.8	2.8	178778	9	AC132936	AC132936 Homo sapi	c1233	68.8	2.8	185447	9	AL450992	AL450992 Human DNA
c1161	68.8	2.8	179056	9	AC068936	AC068936 Homo sapi	c1234	68.8	2.8	185591	2	AC016878	AC016878 Homo sapi
c1162	68.8	2.8	179070	9	AC114486	AC114486 Homo sapi	1235	68.8	2.8	185872	9	AC091144	AC091144 Homo sapi
c1163	68.8	2.8	179144	9	AC026746	AC026746 Homo sapi	c1236	68.8	2.8	185887	2	AC133553	AC133553 Homo sapi
c1164	68.8	2.8	179150	2	AC017077	AC017077 Homo sapi	1237	68.8	2.8	186092	9	AC006582	AC006582 Pan trogl
c1165	68.8	2.8	179177	9	AC090719	AC090719 Homo sapi	1238	68.8	2.8	186161	2	AC151887	AC151887 Saimiri s
c1166	68.8	2.8	179254	2	AC134306	AC134306 Homo sapi	c1239	68.8	2.8	186428	9	AC016355	AC016355 Homo sapi
c1167	68.8	2.8	179308	9	AC114402	AC114402 Homo sapi	c1240	68.8	2.8	186473	2	AC051660	AC051660 Homo sapi
c1168	68.8	2.8	179339	9	AP000870	AP000870 Homo sapi	c1241	68.8	2.8	186533	9	AC024606	AC024606 Homo sapi
c1169	68.8	2.8	179462	2	AC021102	AC021102 Homo sapi	1242	68.8	2.8	186580	9	AC069503	AC069503 Homo sapi
c1170	68.8	2.8	179641	2	AC098591	AC098591 Homo sapi	1243	68.8	2.8	186591	6	AX706984	AX706984 Sequence
c1171	68.8	2.8	179664	2	AC025249	AC025249 Homo sapi	1244	68.8	2.8	186592	6	AX707914	AX707914 Sequence
c1172	68.8	2.8	179680	9	AP003775	AP003775 Homo sapi	1245	68.8	2.8	186722	2	AC139491	AC139491 Homo sapi
c1173	68.8	2.8	179759	2	AC132868	AC132868 Homo sapi	c1246	68.8	2.8	186769	2	AC090591	AC090591 Homo sapi
c1174	68.8	2.8	179883	2	AC007721	AC007721 Homo sapi	c1247	68.8	2.8	187129	2	AC017065	AC017065 Homo sapi
c1175	68.8	2.8	179969	9	AC016643	AC016643 Homo sapi	c1248	68.8	2.8	187229	9	AC027672	AC027672 Homo sapi
c1176	68.8	2.8	180014	9	AC139778	AC139778 Homo sapi	c1249	68.8	2.8	187374	2	AC090912	AC090912 Homo sapi
c1177	68.8	2.8	180269	9	AC016025	AC016025 Homo sapi	1250	68.8	2.8	187540	2	AC009760	AC009760 Homo sapi
c1178	68.8	2.8	180365	9	AC046143	AC046143 Homo sapi	c1251	68.8	2.8	187587	9	AC016026	AC016026 Homo sapi
c1179	68.8	2.8	180372	2	CNS01RGJ	AL158058 Human chr	1252	68.8	2.8	187662	2	AC113616	AC113616 Homo sapi
c1180	68.8	2.8	180400	2	AC133568	AC133568 Homo sapi	c1253	68.8	2.8	187741	2	AC087681	AC087681 Homo sapi
c1181	68.8	2.8	180561	2	AC150737	AC150737 Homo sapi	c1254	68.8	2.8	187770	9	AC090787	AC090787 Homo sapi
c1182	68.8	2.8	180562	9	AC018697	AC018697 Homo sapi	1255	68.8	2.8	187836	2	AC023634	AC023634 Homo sapi
c1183	68.8	2.8	180624	2	AC103716	AC103716 Homo sapi	c1256	68.8	2.8	187934	9	AP003068	AP003068 Homo sapi
c1184	68.8	2.8	180633	2	AC080056	AC080056 Homo sapi	c1257	68.8	2.8	188000	2	AC007895	AC007895 Homo sapi
c1185	68.8	2.8	180680	9	AL137141	AL137141 Human DNA	1258	68.8	2.8	188162	2	CNS05TDR	AL357092 Human chr
c1186	68.8	2.8	180708	9	AC136687	AC136687 Homo sapi	1259	68.8	2.8	188167	9	AC068550	AC068550 Homo sapi
c1187	68.8	2.8	180713	9	AC149286	AC149286 Pan trogl	1260	68.8	2.8	188643	9	AC142329	AC142329 Pan trogl

c1261	68.8	2.8	188679	2	AC023121	1334	68.8	2.8	197999	2	AC134688	AC134688 Homo sapi
1262	68.8	2.8	188787	2	AC090215	c1335	68.8	2.8	198008	2	AC142197	AC142197 Homo sapi
1263	68.8	2.8	188896	9	AL136221	c1336	68.8	2.8	198222	2	AC092429	AC092429 Homo sapi
1264	68.8	2.8	188980	2	AC090087	c1337	68.8	2.8	198410	2	AP000831	AP000831 Homo sapi
1265	68.8	2.8	189099	9	AP003973	1338	68.8	2.8	198440	9	AC018499	AC018499 Homo sapi
1266	68.8	2.8	189156	9	AL138756	1339	68.8	2.8	198459	9	AC018502	AC018502 Homo sapi
1267	68.8	2.8	189326	9	AC018462	c1340	68.8	2.8	198611	2	AC139800	AC139800 Homo sapi
1268	68.8	2.8	189396	2	AL161418	c1341	68.8	2.8	198684	2	AC148309	AC148309 Pan trogl
1269	68.8	2.8	189436	2	AL691432	c1342	68.8	2.8	198942	9	AC008517	AC008517 Homo sapi
1270	68.8	2.8	189495	9	AC099845	c1343	68.8	2.8	198949	9	AC010287	AC010287 Homo sapi
1271	68.8	2.8	189559	9	AC099845	c1344	68.8	2.8	198949	9	AC010351	AC010351 Homo sapi
1272	68.8	2.8	189639	2	AP002475	1345	68.8	2.8	198254	2	AC064808	AC064808 Homo sapi
1273	68.8	2.8	189819	2	AC069321	1346	68.8	2.8	199268	2	AC099523	AC099523 Homo sapi
1274	68.8	2.8	189828	2	AP000763	c1347	68.8	2.8	199287	2	AC068659	AC068659 Homo sapi
1275	68.8	2.8	189920	2	AC138067	c1348	68.8	2.8	199321	9	AP000941	AP000941 Homo sapi
1276	68.8	2.8	189971	2	AL450342	c1349	68.8	2.8	199601	9	AL389915	AL389915 Human DNA
1277	68.8	2.8	190015	9	AL450342	c1350	68.8	2.8	199776	9	AC011499	AC011499 Homo sapi
1278	68.8	2.8	190155	9	AC105184	c1351	68.8	2.8	199875	9	AC138891	AC138891 Homo sapi
1279	68.8	2.8	190162	9	AC099244	1352	68.8	2.8	199882	2	AC134407	AC134407 Homo sapi
1280	68.8	2.8	190210	2	AC023218	c1353	68.8	2.8	200000	2	AC149081	AC149081 Pan trogl
1281	68.8	2.8	190310	2	AC023225	c1354	68.8	2.8	200123	2	AC007517	AC007517 Homo sapi
1282	68.8	2.8	190558	2	AP001403	1355	68.8	2.8	200191	9	AL390027	AL390027 Human DNA
1283	68.8	2.8	190710	2	AC140893	c1356	68.8	2.8	200274	9	AC115088	AC115088 Homo sapi
1284	68.8	2.8	190711	9	AF254983	1357	68.8	2.8	200415	2	AC139287	AC139287 Homo sapi
1285	68.8	2.8	190779	9	AC025106	c1358	68.8	2.8	200430	9	AC005632	AC005632 Homo sapi
1286	68.8	2.8	190871	9	AC044797	1359	68.8	2.8	200594	9	AC011500	AC011500 Homo sapi
1287	68.8	2.8	190915	2	AC142199	c1360	68.8	2.8	200638	9	AL356253	AL356253 Human DNA
1288	68.8	2.8	190940	2	AC119062	c1361	68.8	2.8	201300	2	AC138833	AC138833 Homo sapi
1289	68.8	2.8	191103	9	AC122133	1362	68.8	2.8	201306	2	AC087390	AC087390 Homo sapi
1290	68.8	2.8	191170	2	AC146696	c1363	68.8	2.8	201390	9	AC018979	AC018979 Homo sapi
1291	68.8	2.8	191197	2	AP001779	1364	68.8	2.8	201519	9	AC099689	AC099689 Homo sapi
1292	68.8	2.8	191280	9	AC087389	c1365	68.8	2.8	201535	9	AC007248	AC007248 Homo sapi
1293	68.8	2.8	191433	9	AC069152	c1366	68.8	2.8	201572	9	AC007298	AC007298 Homo sapi
1294	68.8	2.8	191540	9	AC144780	1367	68.8	2.8	201934	9	AL645504	AL645504 Human DNA
1295	68.8	2.8	191540	9	AC010984	c1368	68.8	2.8	201986	9	AC136948	AC136948 Homo sapi
1296	68.8	2.8	191911	9	AC098965	c1369	68.8	2.8	202041	2	AC007427	AC007427 Homo sapi
1297	68.8	2.8	191911	9	AP000943	c1370	68.8	2.8	202041	2	AC090232	AC090232 Homo sapi
1298	68.8	2.8	193047	9	AC138705	c1371	68.8	2.8	202847	9	AC097328	AC097328 Homo sapi
1299	68.8	2.8	193265	2	AC138705	1372	68.8	2.8	203216	2	AC079440	AC079440 Homo sapi
1300	68.8	2.8	193273	2	AC012054	c1373	68.8	2.8	204230	9	AC019071	AC019071 Homo sapi
1301	68.8	2.8	193279	9	AC009466	c1374	68.8	2.8	204367	2	AC150724	AC150724 Callithri
1302	68.8	2.8	193519	9	AC023123	1375	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1303	68.8	2.8	193519	9	AC109446	c1376	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1304	68.8	2.8	193665	9	AC105314	1377	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1305	68.8	2.8	193772	2	AC106833	c1378	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1306	68.8	2.8	193774	2	AC139457	1379	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1307	68.8	2.8	193989	9	AC015743	1380	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1308	68.8	2.8	194067	2	AC146067	c1381	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1309	68.8	2.8	194122	2	AC138778	1382	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1310	68.8	2.8	194143	2	AC022222	c1383	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1311	68.8	2.8	194157	2	AC144368	c1384	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1312	68.8	2.8	194191	2	AC097332	c1385	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1313	68.8	2.8	194219	2	AC023054	1386	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1314	68.8	2.8	194296	9	AL354864	1387	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1315	68.8	2.8	194372	2	AC139782	1388	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1316	68.8	2.8	194372	2	AC139782	1389	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1317	68.8	2.8	195067	9	AC019184	c1390	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1318	68.8	2.8	195076	9	AL391357	1391	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1319	68.8	2.8	195122	9	AC124276	1392	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1320	68.8	2.8	195330	9	AC026347	1393	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1321	68.8	2.8	195588	9	AC020765	c1394	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1322	68.8	2.8	195646	9	AC093709	c1395	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1323	68.8	2.8	195808	2	AC142442	1396	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1324	68.8	2.8	195880	9	AC074117	1397	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1325	68.8	2.8	196512	9	AC020911	c1398	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1326	68.8	2.8	196716	2	AC026750	c1399	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1327	68.8	2.8	196849	2	AC010640	1400	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1328	68.8	2.8	196849	2	AC142542	c1401	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1329	68.8	2.8	196975	2	AC083848	c1402	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1330	68.8	2.8	196975	2	AC083848	c1403	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1331	68.8	2.8	197156	2	AC090345	c1404	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1332	68.8	2.8	197156	2	AP002954	c1405	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl
1333	68.8	2.8	197308	9	AC016724	c1406	68.8	2.8	204641	2	AC145342	AC145342 Pan trogl

QY 301 CAACCTGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAA 360
DB 301 CAACCTGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAA 360
QY 361 GGGAAACCAAAAGTGGTGATCACTTCTCCAGTCGTCATGCTTACAAATAACTTGACTGAG 420
DB 361 GGGAAACCAAAAGTGGTGATCACTTCTCCAGTCGTCATGCTTACAAATAACTTGACTGAG 420
QY 421 GAACAGAGGGCGAGTGGCTTTTGGCTTCCAAATTTCTGGCAGGAGATGCTCTTGGCAG 480
DB 421 GAACAGAGGGCGAGTGGCTTTTGGCTTCCAAATTTCTGGCAGGAGATGCTCTTGGCAG 480
QY 481 ATTGAACCTCTGAAGCCAGTGATGAGGCGGCTACACCTGTAAAGTTAAGAAATTCAGGG 540
DB 481 ATTGAACCTCTGAAGCCAGTGATGAGGCGGCTACACCTGTAAAGTTAAGAAATTCAGGG 540
QY 541 CGCTACCTGTGGAGCCATGTCACTCTTAAAGTCTTAAAGTCTTAGTAGACCATCCAAAGCCAAAGTGT 600
DB 541 CGCTACCTGTGGAGCCATGTCACTCTTAAAGTCTTAAAGTCTTAGTAGACCATCCAAAGCCAAAGTGT 600
QY 601 GAGTTGGAAGGAGAGCTGACAGAAAGAGTGACCTGACTTTGCGAGTGTAGTCACTCTCT 660
DB 601 GAGTTGGAAGGAGAGCTGACAGAAAGAGTGACCTGACTTTGCGAGTGTAGTCACTCTCT 660
QY 661 GGCACAGAGCCCATTTGTATTACTGTCAGCGAATCCGAGAGAAAGAGGAGGAGATGAA 720
DB 661 GGCACAGAGCCCATTTGTATTACTGTCAGCGAATCCGAGAGAAAGAGGAGGAGATGAA 720
QY 721 CGTCTGCTCCCAAATCTAGGATTTGACTACAAACACCTCGACGAGTTCCTGTCAGAAAT 780
DB 721 CGTCTGCTCCCAAATCTAGGATTTGACTACAAACACCTCGACGAGTTCCTGTCAGAAAT 780
QY 781 CTTTACCATGTCTACTCTGAGCTGACAGAGTGACAGGACCAAGCTGGGAAGGAA 840
DB 781 CTTTACCATGTCTACTCTGAGCTGACAGAGTGACAGGACCAAGCTGGGAAGGAA 840
QY 841 AGCTGTGTGGTCGAGTAAGTGTACAGTATGTACAAAGCATCGGCATGGTTGACAGGAC 900
DB 841 AGCTGTGTGGTCGAGTAAGTGTACAGTATGTACAAAGCATCGGCATGGTTGACAGGAC 900
QY 901 GTGACAGGCATAGTGGCTGGAGCCCTGTGATTTTCTTCTTGGTGTGGCTGCTTAATCCGA 960
DB 901 GTGACAGGCATAGTGGCTGGAGCCCTGTGATTTTCTTCTTGGTGTGGCTGCTTAATCCGA 960
QY 961 AGGAAGACAAGTAAGTATGGAAGACAGAGACCTTAATGAAATTCGAGAAAGATGCT 1020
DB 961 AGGAAGACAAGTAAGTATGGAAGACAGAGACCTTAATGAAATTCGAGAAAGATGCT 1020
QY 1021 GAAGCTCCAAAAGCCGCTTGTGAAACCCAGCTCTCTCTCAGGCTCTCGAGCTCA 1080
DB 1021 GAAGCTCCAAAAGCCGCTTGTGAAACCCAGCTCTCTCTCAGGCTCTCGAGCTCA 1080
QY 1081 CGCTCTGGTTCTTCTCACTCGCTCCACAGCAATAGTGTCTCAGCAGCCAGCGGACA 1140
DB 1081 CGCTCTGGTTCTTCTCACTCGCTCCACAGCAATAGTGTCTCAGCAGCCAGCGGACA 1140
QY 1141 CTGTCACTGACGACGACCCAGCGCTGGCCACCAGGCATACAGGCTAGTGGGG 1200
DB 1141 CTGTCACTGACGACGACCCAGCGCTGGCCACCAGGCATACAGGCTAGTGGGG 1200
QY 1201 CCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCACCATGTAAATCTGACCAAGCAGAA 1260
DB 1201 CCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCACCATGTAAATCTGACCAAGCAGAA 1260
QY 1261 ACCACACCCAGCATGATCCCGAGCCAGACGAGGCTTCCAAACGCTCTGAATTAACATG 1320
DB 1261 ACCACACCCAGCATGATCCCGAGCCAGACGAGGCTTCCAAACGCTCTGAATTAACATG 1320
QY 1321 GACTTGACTCCCAACGCTTTCTTAGGAGTCAGGGTCTTTTGACTCTTCTGCTCAATTTGAGC 1380
DB 1321 GACTTGACTCCCAACGCTTTCTTAGGAGTCAGGGTCTTTTGACTCTTCTGCTCAATTTGAGC 1380
QY 1381 TCAAGTCAACAGCCACACAAACAGATGAGAGGTCTATCTAAGTAGCAGTGGCAATTCGACG 1440

DB 1381 TCAAGTCAACAGCCACACAAACAGATGAGAGGTCTATCTAAGTAGCAGTGGCAATTCGACG 1440
QY 1441 GAAACAGATTTCAGATGAGCATTTTCTTATACAAATACCAAAACAGCAAAAGGATGTAAAGCT 1500
DB 1441 GAAACAGATTTCAGATGAGCATTTTCTTATACAAATACCAAAACAGCAAAAGGATGTAAAGCT 1500
QY 1501 GATTTCATCTGTAAAAAGGCATCTTATTGTGCTTTTAGACAGAGTAAAGGAAAGCAGGAG 1560
DB 1501 GATTTCATCTGTAAAAAGGCATCTTATTGTGCTTTTAGACAGAGTAAAGGAAAGCAGGAG 1560
QY 1561 TCCAAATCTATTGTGTGACCCAGGACCTGTGTGAGAAAGTTCGGGAAAGGTGAGGTGAAT 1620
DB 1561 TCCAAATCTATTGTGTGACCCAGGACCTGTGTGAGAAAGTTCGGGAAAGGTGAGGTGAAT 1620
QY 1621 ATACCTAAACCTTTTAAATGTGGGATATTGTATCAGTGTCTTTGATTCACAAATTTTCAAG 1680
DB 1621 ATACCTAAACCTTTTAAATGTGGGATATTGTATCAGTGTCTTTGATTCACAAATTTTCAAG 1680
QY 1681 AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTATTGGAATTTTA 1740
DB 1681 AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTATTGGAATTTTA 1740
QY 1741 GTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG 1800
DB 1741 GTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG 1800
QY 1801 AGCTTAACCACTTCTAAGAAACTCCAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC 1860
DB 1801 AGCTTAACCACTTCTAAGAAACTCCAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC 1860
QY 1861 TTTCAATTTGTCATAAGGTTTGGATTTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA 1920
DB 1861 TTTCAATTTGTCATAAGGTTTGGATTTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA 1920
QY 1921 GAAGGTGATGAGTTTCTCCACTCTATCTACTATCTACTATTCTGATTTGAGCCCAAAA 1980
DB 1921 GAAGGTGATGAGTTTCTCCACTCTATCTACTATCTACTATTCTGATTTGAGCCCAAAA 1980
QY 1981 TAACTATGAAGAGAGACAAAAATTTGTGACAAAGGATTTGTGAAGAGCTTTCCATCTTCAT 2040
DB 1981 TAACTATGAAGAGAGACAAAAATTTGTGACAAAGGATTTGTGAAGAGCTTTCCATCTTCAT 2040
QY 2041 GATGTTATGAGGATTTGTGACAAACATTAATATGAGCAATTTGTGAGATTTCC 2100
DB 2041 GATGTTATGAGGATTTGTGACAAACATTAATATGAGCAATTTGTGAGATTTCC 2100
QY 2101 CCTCAATCAGATGCTCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACA 2160
DB 2101 CCTCAATCAGATGCTCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACA 2160
QY 2161 ACATGTCATTTATCAAGCTCTTGAAGAAATTTCTTAGAGAAAGGGATCTAGGAAT 2220
DB 2161 ACATGTCATTTATCAAGCTCTTGAAGAAATTTCTTAGAGAAAGGGATCTAGGAAT 2220
QY 2221 GCTGAAAGATTACCAACATACCATTAAGTCTCTTTCTGAGAAAAATGTGAAACCG 2280
DB 2221 GCTGAAAGATTACCAACATACCATTAAGTCTCTTTCTGAGAAAAATGTGAAACCG 2280
QY 2281 AATTCGAAGACTGGGTGGACTAGAAAGGAGATTTAGATCAAGTTTCTTAAATGTCAA 2340
DB 2281 AATTCGAAGACTGGGTGGACTAGAAAGGAGATTTAGATCAAGTTTCTTAAATGTCAA 2340
QY 2341 GGAAGGTAGCCGGCATGGTCCAGGACCTGTAGGAAATTCAGCAGGTGGAGGTTGCA 2400
DB 2341 GGAAGGTAGCCGGCATGGTCCAGGACCTGTAGGAAATTCAGCAGGTGGAGGTTGCA 2400
QY 2401 GTGAGCCGAGATTTATGCCATTTGCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCC 2458
DB 2401 GTGAGCCGAGATTTATGCCATTTGCACTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCC 2458

[illegible]

Db	1801	AGCTAACCACTTCTTAGAAAACTCCAAAAAAGGAAACATGTGTCTTCTTCTATCTTGACTTTAACTC	1860			
Qy	1861	TTCTATTTGTGCATGAAGGTTTGGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA	1920			
Db	1861	TTCTATTTGTGCATGAAGGTTTGGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA	1920			
Qy	1921	GAAGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCAGTATTTCTATTTGATGGAGTTC	1980			
Db	1921	GAAGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCAGTATTTCTATTTGATGGAGTTC	1980			
Qy	1981	TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTTCCATCTTTTCAT	2040			
Db	1981	TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTTCCATCTTTTCAT	2040			
Qy	2041	GATGTTATGAGGATTGTTGACAAACATTAGAAATATATAATGAGCAATTTGTGGATTTTCC	2100			
Db	2041	GATGTTATGAGGATTGTTGACAAACATTAGAAATATATAATGAGCAATTTGTGGATTTTCC	2100			
Qy	2101	CCTCAAAATCAGATGCTCTAAGGACCTTCTGCTAGATATTTCTGGAAGGAGAGAAAAATACA	2160			
Db	2101	CCTCAAAATCAGATGCTCTAAGGACCTTCTGCTAGATATTTCTGGAAGGAGAGAAAAATACA	2160			
Qy	2161	ACATGTCATTTATCAACGTCCTTAGAAAGAAATCTTCTAGAGAAAAAGGATCTTAGGAAT	2220			
Db	2161	ACATGTCATTTATCAACGTCCTTAGAAAGAAATCTTCTAGAGAAAAAGGATCTTAGGAAT	2220			
Qy	2221	GCTGAAAGATTACCCAAACATACCAATATAGTCTCTTTCTGAGAAAAATGTGAAACCAG	2280			
Db	2221	GCTGAAAGATTACCCAAACATACCAATATAGTCTCTTTCTGAGAAAAATGTGAAACCAG	2280			
Qy	2281	AATTGCAAGACTGGGTGACTAGAAAGGAGATTAGATCAGTTTCTTCTTAATATGTCAA	2340			
Db	2281	AATTGCAAGACTGGGTGACTAGAAAGGAGATTAGATCAGTTTCTTCTTAATATGTCAA	2340			
Qy	2341	GGAAGGTAGCCGGCATGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGTTGCA	2400			
Db	2341	GGAAGGTAGCCGGCATGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGTTGCA	2400			
Qy	2401	GTGAGCCGAGATTATGCAATTGCACTCAGCCTGGGTGACAGAGCGGGACTCCGCTCTC	2458			
Db	2401	GTGAGCCGAGATTATGCAATTGCACTCAGCCTGGGTGACAGAGCGGGACTCCGCTCTC	2458			
RESULT 3						
AR528645						
LOCUS	AR528645	2458 bp	DNA			
DEFINITION	Sequence 387 from patent US 6725730.					
ACCESSION	AR528645					
VERSION	AR528645.1 GI:53916723					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 2458)					
AUTHORS	Bollinger,C.L. Jr.					
TITLE	Crane test weight assembly and method					
JOURNAL	Patent: US 6725730-A 387 27-APR-2004;					
FEATURES	Location/Qualifiers					
source	1..2458					
	/organism="unknown"					
	/mol_type="genomic DNA"					
ORIGIN						
Query Match 100.0%; Score 2458; DB 6; Length 2458;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 2458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	GGCCCGGAGCCCATCTGCCCCAGCGGGACAGCGGGCGGGCGCGGCTCCGCCCGGGCAC	60			
Db	1	GGCCCGGAGCCCATCTGCCCCAGCGGGACAGCGGGCGGGCGGGCTCCGCCCGGGCAC	60			
Qy	61	ATGGGCTGACGCCACCTTCGCGCGCACCCCGAGGGCGCGGCCCGACGTTCGCCGAGGTCGGT	120			

QY 1201 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAAATCTGACCAAAAGCAGAA 1260
DB 1201 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAAATCTGACCAAAAGCAGAA 1260
QY 1261 ACCACACCCAGCATGATCCCAAGCCAGACGAGAGCTTCCAAACGGTCTGAAATTAACAATG 1320
DB 1261 ACCACACCCAGCATGATCCCAAGCCAGACGAGAGCTTCCAAACGGTCTGAAATTAACAATG 1320
QY 1321 GACTTGACTCCACAGCTTTCTTAGGAGTCAAGGCTCTTTGGACTCTTCTCGTCAATGGAGC 1380
DB 1321 GACTTGACTCCACAGCTTTCTTAGGAGTCAAGGCTCTTTGGACTCTTCTCGTCAATGGAGC 1380
QY 1381 TCAAGTCAACGACCAACAACCCAGATGAGAGTCAATCTAAAGTACGAGTCAATGGACG 1440
DB 1381 TCAAGTCAACGACCAACAACCCAGATGAGAGTCAATCTAAAGTACGAGTCAATGGACG 1440
QY 1441 GAAACAGATTCAGATGAGATTTTCCCTTATACAAACCAAGCAAGGATGTAAGCT 1500
DB 1441 GAAACAGATTCAGATGAGATTTTCCCTTATACAAACCAAGCAAGGATGTAAGCT 1500
QY 1501 GATTTCATCTGTAAGAGGATCTTATTGTGCTTTAGACCAAGTAAGGAAAGCAGAG 1560
DB 1501 GATTTCATCTGTAAGAGGATCTTATTGTGCTTTAGACCAAGTAAGGAAAGCAGAG 1560
QY 1561 TCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAAGGTGAGTGAAT 1620
DB 1561 TCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAAGGTGAGTGAAT 1620
QY 1621 ATACCTAAACCTTTTAATGTGGGATTTTGTATCAGTGCCTTTGATTCACAAATTTTCAAG 1680
DB 1621 ATACCTAAACCTTTTAATGTGGGATTTTGTATCAGTGCCTTTGATTCACAAATTTTCAAG 1680
QY 1681 AGGAAATGGGATGCTGTTGTAATTTTCTATGCAATTTCTGCAAACTTATTGGATTATTA 1740
DB 1681 AGGAAATGGGATGCTGTTGTAATTTTCTATGCAATTTCTGCAAACTTATTGGATTATTA 1740
QY 1741 GTTATTTCAGACAGTCAACGAGAACCCACAGCCTTATTACACTGTCTACCATGCTTAAC 1800
DB 1741 GTTATTTCAGACAGTCAACGAGAACCCACAGCCTTATTACACTGTCTACCATGCTTAAC 1800
QY 1801 AGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTAATCTGACTTAAC 1860
DB 1801 AGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTAATCTGACTTAAC 1860
QY 1861 TTCAATTTGTCATAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA 1920
DB 1861 TTCAATTTGTCATAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA 1920
QY 1921 GAAGAGTGAATGAGTTTCTCCACTCTATACATAATCTCACTATTGTTGATTGAGCCCAAAA 1980
DB 1921 GAAGAGTGAATGAGTTTCTCCACTCTATACATAATCTCACTATTGTTGATTGAGCCCAAAA 1980
QY 1981 TAACTATGAAGAGGAGACAAAATTTGTGACAAAGGATTTGTAAGAGCTTTCATCTTCAT 2040
DB 1981 TAACTATGAAGAGGAGACAAAATTTGTGACAAAGGATTTGTAAGAGCTTTCATCTTCAT 2040
QY 2041 GATGTTATGAGGATTTGTTGACAAACATTAGAAATATATAATGAGCAATTTGGAATTTCC 2100
DB 2041 GATGTTATGAGGATTTGTTGACAAACATTAGAAATATATAATGAGCAATTTGGAATTTCC 2100
QY 2101 CCTCAAAATCAGATGCTCTAAGGAGCTTTCTGCTAGATATTCTTGGAAAGGAGAAATACA 2160
DB 2101 CCTCAAAATCAGATGCTCTAAGGAGCTTTCTGCTAGATATTCTTGGAAAGGAGAAATACA 2160
QY 2161 ACATGTCAATTTATCAACGCTCTTAGAAAGATTTCTTCTAGAGAAAAGGGATCTAGGAAT 2220
DB 2161 ACATGTCAATTTATCAACGCTCTTAGAAAGATTTCTTCTAGAGAAAAGGGATCTAGGAAT 2220
QY 2221 GCTGAAAGATTTACCAACATACCAATATAGTCTCTTCTTCTGAGAAAATCTGAAACGAG 2280
DB 2221 GCTGAAAGATTTACCAACATACCAATATAGTCTCTTCTTCTGAGAAAATCTGAAACGAG 2280

QY 2281 AATTGCAAGACTGGGTGAGCTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA 2340
DB 2281 AATTGCAAGACTGGGTGAGCTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA 2340
QY 2341 GGAAAGGTAGCCGGGCATGCTGCCAGGACCTGTAGGAAAATCCACAGGTGGAGTTGCA 2400
DB 2341 GGAAAGGTAGCCGGGCATGCTGCCAGGACCTGTAGGAAAATCCACAGGTGGAGTTGCA 2400
QY 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGGCTGGGTGACAGAGCGGACTCCGTCTC 2458
DB 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGGCTGGGTGACAGAGCGGACTCCGTCTC 2458

RESULT 4
AX358876
LOCUS AX358876 2458 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 129 from Patent WO0193983.
ACCESSION AX358876
VERSION AX358876.1 GI:18675339
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0193983-A 129 13-DEC-2001;
Genentech Inc. (US)
FEATURES
source 1. 2458
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 2458; DB 6; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCCGGGAGCCCATCTGCCCGGAGGACAGCGGCGCGGGCCCGGCTCCGCCCGGCAC 60
DB 1 GCGCCGGGAGCCCATCTGCCCGGAGGACAGCGGCGCGGGCCCGGCTCCGCCCGGCAC 60
QY 61 ATGCTGAGGCCACTCGCGGCGACCCCGAGGCGCGGCGCCAGCTCGCCGAGGTCCGT 120
DB 61 ATGCTGAGGCCACTCGCGGCGACCCCGAGGCGCGGCGCCAGCTCGCCGAGGTCCGT 120
QY 121 CGGAGGCGCGCGCGCGCGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
DB 121 CGGAGGCGCGCGCGCGCGCGGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
QY 181 GGGATCGGGATGTCCT 240
DB 181 GGGATCGGGATGTCCT 240
QY 241 GGGACTCAGCTGAGATCAAGAGAGTGGCAGAGAAAGGTCACTTTGCCCTGCCACCAT 300
DB 241 GGGACTCAGCTGAGATCAAGAGAGTGGCAGAGAAAGGTCACTTTGCCCTGCCACCAT 300
QY 301 CAACCTGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAA 360
DB 301 CAACCTGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAA 360
QY 361 GGGAAACCAAAAAGTGGTGATCACTTACTCCAGTCTCATGTCTACAATAAATTGACTGAG 420
DB 361 GGGAAACCAAAAAGTGGTGATCACTTACTCCAGTCTCATGTCTACAATAAATTGACTGAG 420
QY 421 GAACAGAGGCGGAGTGGCTTTGCTTCCAAATTTCTTGGCAGGAGATGCCTCTCTTGAG 480
DB 421 GAACAGAGGCGGAGTGGCTTTGCTTCCAAATTTCTTGGCAGGAGATGCCTCTCTTGAG 480

Db 421 GAA CAG AAG GCG CGA GTG GCG CTT TGG CTT CCA A TTT C TGT G CAG GAG ATG CCT C CTT G CAG 480
Qy 481 ATT GAA CCT CTG AAG CCG CAG TGA TGG GCG GGT TAC ACC TGT AAG GTT AAG AAT T CAG GG 540
Db 481 ATT GAA CCT CTG AAG CCG CAG TGA TGG GCG GGT TAC ACC TGT AAG GTT AAG AAT T CAG GG 540
Qy 541 CGT TAC GTG GAG CCG ATG C ATC TTT AAA AGT CTT A GTG AGA C ATC CAA G CCG CAA GTG 600
Db 541 CGT TAC GTG GAG CCG ATG C ATC TTT AAA AGT CTT A GTG AGA C ATC CAA G CCG CAA GTG 600
Qy 601 GAG TTG AAG GAG AGT G A CAA AAG AAG TGA C C TGT G A C TTT T G CAG TGT G A G T C A T C T C T 660
Db 601 GAG TTG AAG GAG AGT G A CAA AAG AAG TGA C C TGT G A C TTT T G CAG TGT G A G T C A T C T C T 660
Qy 661 GGC A CAG A G C C A T T G T G T A T T A C T G C A G C A G A A T C C G A G A A A G A G G A G G A T G A A 720
Db 661 GGC A CAG A G C C A T T G T G T A T T A C T G C A G C A G A A T C C G A G A A A G A G G A G G A T G A A 720
Qy 721 CGT C T G C C T C C A A A T C T A G A T T G A C T A C A C C C T G G A C G A G T T C T G C C A G A A T 780
Db 721 CGT C T G C C T C C A A A T C T A G A T T G A C T A C A C C C T G G A C G A G T T C T G C C A G A A T 780
Qy 781 CTT A C C A T G T C T A C T C T G A C T G T A C C A G T G C A C A G C A G C A A C G A A G C T G G A A G A A 840
Db 781 CTT A C C A T G T C T A C T C T G A C T G T A C C A G T G C A C A G C A G C A A C G A A G C T G G A A G A A 840
Qy 841 A G C T G T G T G C G A G T A A C T G T A C A G T A T G T A C A A G C A T C G G A T G G T T G C A G A G C A 900
Db 841 A G C T G T G T G C G A G T A A C T G T A C A G T A T G T A C A A G C A T C G G A T G G T T G C A G A G C A 900
Qy 901 G T G A C A G G A T A G T G G C T G G A G C C T G A T T T C T T G T G T G C T C T A A T C C G A 960
Db 901 G T G A C A G G A T A G T G G C T G G A G C C T G A T T T C T T G T G T G C T C T A A T C C G A 960
Qy 961 A G S A A G A C A A A A A G A T A T G A G A A G A A G A G A C C T A A T G A A A T T C G A A A G A T G C T 1020
Db 961 A G S A A G A C A A A A A G A T A T G A G A A G A A G A G A C C T A A T G A A A T T C G A A A G A T G C T 1020
Qy 1021 G A A G C T C C A A A A G C C G T C T T G T A A A C C C A G C T C T T C T C A G G C T C T C G A G C T C A 1080
Db 1021 G A A G C T C C A A A A G C C G T C T T G T A A A C C C A G C T C T T C T C A G G C T C T C G A G C T C A 1080
Qy 1081 C G C T C T G G T T C T C C A C T C G C T C C A G A A A T A G T G C C T C A C G C A G C C A G C G A C A 1140
Db 1081 C G C T C T G G T T C T C C A C T C G C T C C A G A A A T A G T G C C T C A C G C A G C C A G C G A C A 1140
Qy 1141 C T G T C A A C T G A C G C A G C A C C C A G C C A G C G G C T G G C C A C C A G C G A T A C A G C C T A G T G G G 1200
Db 1141 C T G T C A A C T G A C G C A G C A C C C A G C C A G C G G C T G G C C A C C A G C G A T A C A G C C T A G T G G G 1200
Qy 1201 C C A G A G T G A G A G T T C T G A C C A A A A A G T C C A C C A T G T A A T C T G A C C A A A G C A G A A 1260
Db 1201 C C A G A G T G A G A G T T C T G A C C A A A A A G T C C A C C A T G T A A T C T G A C C A A A G C A G A A 1260
Qy 1261 A C C A C A C C C A G A T A T C C C A C C A G C A G A G C A G C C T C C A A C G G T C T G A A T T A C A A T G 1320
Db 1261 A C C A C A C C C A G A T A T C C C A C C A G C A G A G C A G C C T C C A A C G G T C T G A A T T A C A A T G 1320
Qy 1321 G A C T T G A C T C C C A C G C T T C C T A G A G T C A G G T C T T T G A C T C T T C T G C A T T G G A G C 1380
Db 1321 G A C T T G A C T C C C A C G C T T C C T A G A G T C A G G T C T T T G A C T C T T C T G C A T T G G A G C 1380
Qy 1381 T C A A G T C A C C A G C A C A C C A G A T G A G A G T C A T C T A A G T A G C A G T G A G C A T T G C A C G 1440
Db 1381 T C A A G T C A C C A G C A C A C C A G A T G A G A G T C A T C T A A G T A G C A G T G A G C A T T G C A C G 1440
Qy 1441 G A A C A G A T T C A G A T G A C A T T T C C T T A C A T A C A A T A C A A C A A G A A A G G A T G T A A G C T 1500
Db 1441 G A A C A G A T T C A G A T G A C A T T T C C T T A C A T A C A A T A C A A C A A G A A A G G A T G T A A G C T 1500
Qy 1501 G A T T C A T C T G T A A A A A G C A T C T T A T T G C C T T T A C C A G A T A A G G A A A G C A G G A G 1560
Db 1501 G A T T C A T C T G T A A A A A G C A T C T T A T T G C C T T T A C C A G A T A A G G A A A G C A G G A G 1560

Qy 1561 T C C A A A T C T A T T T G T G A C C A G A C C T G T G T G A G A A G T T G G G A A A G G T G A G G T G A A T 1620
Db 1561 T C C A A A T C T A T T T G T G A C C A G A C C T G T G T G A G A A G T T G G G A A A G G T G A G G T G A A T 1620
Qy 1621 A T A C C T A A A A C T T T T A A T G T G G A T A T T T G T A T C A G T C T T T G A T T C A C A A T T T T C A A G 1680
Db 1621 A T A C C T A A A A C T T T T A A T G T G G A T A T T T G T A T C A G T C T T T G A T T C A C A A T T T T C A A G 1680
Qy 1681 A G G A A A T G G G A T G C T G T T T G T A A A T T T C T A T G C A T T T C T G C A A A C T T A T T G G A T T A T T A 1740
Db 1681 A G G A A A T G G G A T G C T G T T T G T A A A T T T C T A T G C A T T T C T G C A A A C T T A T T G G A T T A T T A 1740
Qy 1741 G T T A T T C A G A C A G T C A A G C A G A C C C A C A G C C T T A T A C C T G T C T A C C A T G T A C T G 1800
Db 1741 G T T A T T C A G A C A G T C A A G C A G A C C C A C A G C C T T A T A C C T G T C T A C C A T G T A C T G 1800
Qy 1801 A G C T A A C C A C T T C T A A A A A C T C C A A A A A A G A A A C A T G T C T T C T A T T T G A C C C A A A 1860
Db 1801 A G C T A A C C A C T T C T A A A A A C T C C A A A A A A G A A A C A T G T C T T C T A T T T G A C C C A A A 1860
Qy 1861 T T C A T T T G C A T A A G G T T T G G A T A T T A A T T C A A G G G A G T T G A A A T A G T G G A G A T G A 1920
Db 1861 T T C A T T T G C A T A A G G T T T G G A T A T T A A T T C A A G G G A G T T G A A A T A G T G G A G A T G A 1920
Qy 1921 G A A G A G T G A A T G A G T T T C C C A C T C T A T A C T A A T C T A C T A T T T G T A T T G A T T G A G C C C A A A 1980
Db 1921 G A A G A G T G A A T G A G T T T C C C A C T C T A T A C T A A T C T A C T A T T T G T A T T G A T T G A G C C C A A A 1980
Qy 1981 T A A C T A T G A A G A G A C A A A A A T T C T G A C A A A G G A T T C T G A A G A G C T T T T C C A T C T T C A T 2040
Db 1981 T A A C T A T G A A G A G A C A A A A A T T C T G A C A A A G G A T T C T G A A A G G A T T T G A A G A G C T T T C C A T C T T C A T 2040
Qy 2041 G A T G T T A T G A G G A T T G T G A C A A A C A T T A G A A A T A T A T A A T G G A G A C A A T T G T G G A T T T C C 2100
Db 2041 G A T G T T A T G A G G A T T G T G A C A A A C A T T A G A A A T A T A T A A T G G A G A C A A T T G T G G A T T T C C 2100
Qy 2101 C C T C A A A T C A G A T G C C T C T A A G A C T T C C T G C T A G A T A T T C T G A A G A G A A A A T A C A 2160
Db 2101 C C T C A A A T C A G A T G C C T C T A A G A C T T C C T G C T A G A T A T T C T G A A G A G A A A A T A C A 2160
Qy 2161 A C A T G C A T T T A T C A A C G T C C T T A G A A A G A A T T C T C T A G A A A A A A G G A T C T A G A A T 2220
Db 2161 A C A T G C A T T T A T C A A C G T C C T T A G A A A G A A T T C T C T A G A A A A A A G G A T C T A G A A T 2220
Qy 2221 G C T G A A A G A T T A C C A A C A T A C C A T T A G T C T C T T T C T G A G A A A A T G T G A A A C C A G 2280
Db 2221 G C T G A A A G A T T A C C A A C A T A C C A T T A G T C T C T T T C T G A G A A A A T G T G A A A C C A G 2280
Qy 2281 A A T T G C A A G A C T G G G T G A C T A G A A A G G A G A T T A G A T C A G T T T T C T C T T A A T A T G T C A A 2340
Db 2281 A A T T G C A A G A C T G G G T G A C T A G A A A G G A G A T T A G A T C A G T T T T C T C T T A A T A T G T C A A 2340
Qy 2341 G G A A G G T A G C C G G C A T G G T C C A G G C A C C T G T A G G A A A A T C C A G A G G T G G A G G T T G C A 2400
Db 2341 G G A A G G T A G C C G G C A T G G T C C A G G C A C C T G T A G G A A A A T C C A G A G G T G G A G G T T G C A 2400
Qy 2401 G T G A G C C A G A T T A T G C C A T T G C A C C A G C C G T G G T G A C A G A G G G A C T C C G T C T C 2458
Db 2401 G T G A G C C A G A T T A T G C C A T T G C A C C A G C C T G G T G A C A G A G G G A C T C C G T C T C 2458

RESULT 5

AX362369
LOCUS
DEFINITION
Sequence 129 from Patent WO0208288.
AX362369
ACCESSION
AX362369.1 GI:18694642
VERSION
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM

AX362369 2458 bp DNA linear PAT 15-FEB-2002

Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[illegible]

1141 CTGTCAACTGACGACGACCCAGCCAGGCTGGCCACCAGGCATACAGCCTAGTGGG 1200
Db
1141 CTGTCAACTGACGACGACCCAGCCAGGCTGGCCACCAGGCATACAGCCTAGTGGG 1200
Qy
1201 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAACTGACCAAGCAGAA 1260
Db
1201 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAACTGACCAAGCAGAA 1260
Qy
1261 ACCACACCAGCATGATCCCGACCGACGACGAGCCTTCCAAACGGTCTGAATTTCAATG 1320
Db
1261 ACCACACCAGCATGATCCCGACCGACGACGAGCCTTCCAAACGGTCTGAATTTCAATG 1320
Qy
1321 GACTTGACTCCACCGCTTCTTAGAGTCCAGGCTCTTGGACTCTCTCGTCAATGGAGC 1380
Db
1321 GACTTGACTCCACCGCTTCTTAGAGTCCAGGCTCTTGGACTCTCTCGTCAATGGAGC 1380
Qy
1381 TCAAGTCAACGACCCACACCAACAGATGAGAGTCACTAAAGTAGCAGTGGCATTTGCACG 1440
Db
1381 TCAAGTCAACGACCCACACCAACAGATGAGAGTCACTAAAGTAGCAGTGGCATTTGCACG 1440
Qy
1441 GAACAGATTCAGATGAGCATTTTCTTATACAAATACCAACCAAGCAAGGATGTAAGCT 1500
Db
1441 GAACAGATTCAGATGAGCATTTTCTTATACAAATACCAACCAAGCAAGGATGTAAGCT 1500
Qy
1501 GATTCATCTGTAAAGGATCTTATCTGCTTTAGACAGATTAAGCAAGCAGGAG 1560
Db
1501 GATTCATCTGTAAAGGATCTTATCTGCTTTAGACAGATTAAGCAAGCAGGAG 1560
Qy
1561 TCCAAATCTATTGTTGACCAAGGCTGTTGGTGAGAGGTTGGGCAAGGTCAGTGAAT 1620
Db
1561 TCCAAATCTATTGTTGACCAAGGCTGTTGGTGAGAGGTTGGGCAAGGTCAGTGAAT 1620
Qy
1621 ATACCTAAACCTTTTAATGTTGGATATTGTTGATCAGTCTTTGATTCACAAATTTCAAG 1680
Db
1621 ATACCTAAACCTTTTAATGTTGGATATTGTTGATCAGTCTTTGATTCACAAATTTCAAG 1680
Qy
1681 AGGAATGGAGTCTGTTGTAATTTCTATGCAATTTCTGCAAACTTATGGATATTA 1740
Db
1681 AGGAATGGAGTCTGTTGTAATTTCTATGCAATTTCTGCAAACTTATGGATATTA 1740
Qy
1741 GTTATTGACAGAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACCATGACTG 1800
Db
1741 GTTATTGACAGAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACCATGACTG 1800
Qy
1801 AGCTAACCACTTCTAAGAACTCCAAAAGAAACATGTGTCTTCTATTCTGACTTAAC 1860
Db
1801 AGCTAACCACTTCTAAGAACTCCAAAAGAAACATGTGTCTTCTATTCTGACTTAAC 1860
Qy
1861 TTCAATTTGATAGGTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGAGATGGA 1920
Db
1861 TTCAATTTGATAGGTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGAGATGGA 1920
Qy
1921 GAAGAGTGAATGAGTTCTCCCACTTACTATCTCACTATTGTTGTTGAGGCCAAAA 1980
Db
1921 GAAGAGTGAATGAGTTCTCCCACTTACTATCTCACTATTGTTGTTGAGGCCAAAA 1980
Qy
1981 TAACCTATGAAGAGGACAAAAATTTGTGACAAAGGATTTGAAAGACTTTCCATCTTCAT 2040
Db
1981 TAACCTATGAAGAGGACAAAAATTTGTGACAAAGGATTTGTGAAAGACTTTCCATCTTCAT 2040
Qy
2041 GATGTTATGAGGATTTGTGACAAATTTAGAAATATTAATAGGAGCAATTTGGATTTCC 2100
Db
2041 GATGTTATGAGGATTTGTGACAAATTTAGAAATATTAATAGGAGCAATTTGGATTTCC 2100
Qy
2101 CCTCAATCAGATGCTCTTAGGACTTTCTGCTAGATATTCTGGAAGGAGAAATACA 2160
Db
2101 CCTCAATCAGATGCTCTTAGGACTTTCTGCTAGATATTCTGGAAGGAGAAATACA 2160
Qy
2161 ACATGCTATTTATCAACGCTCTTAGAAAGATTTCTTCTAGAGAAAAAGGATCTAGGAAT 2220
Db
2161 ACATGCTATTTATCAACGCTCTTAGAAAGATTTCTTCTAGAGAAAAAGGATCTAGGAAT 2220
Qy
2221 GCTGAAGATTACCAACATACCATTAATAGTCTCTTTCTGAGAAAAATGTGAACACAG 2280

Db 2221 GCTGAAGATTACCAACATACCATTAATAGTCTCTTTCTGAGAAAAATGTGAACACAG 2280
Qy 2281 AATTGCAAGACTGGGTGGAGTAGAAAGGAGATTAGATCAGTTTTCTCTTAATATGTCAA 2340
Db 2281 AATTGCAAGACTGGGTGGAGTAGAAAGGAGATTAGATCAGTTTTCTCTTAATATGTCAA 2340
Qy 2341 GGAAGGTAGCCGGGATCGTGGCAGGCACCTGTAGAAAAATCCAGAGGTGAGGTTGCA 2400
Db 2341 GGAAGGTAGCCGGGATCGTGGCAGGCACCTGTAGAAAAATCCAGAGGTGAGGTTGCA 2400
Qy 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGCTGGTGACAGAGCGGACTCCGCTC 2458
Db 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGCTGGTGACAGAGCGGACTCCGCTC 2458
RESULT 7
AX454478 2458 bp DNA linear PAT 06-JUL-2002
LOCUS
DEFINITION Sequence 63 from Patent WO0208284.
ACCESSION AX454478
VERSION AX454478.1 GI:21713863
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K. P., Ferrara, N., Gerber, H., Gerritsen, M. E., Goddard, A.,
Godowski, P. J., Gurney, A. L., Hillan, K. J., Marsters, S. A., Pan, J.,
Paoni, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 63 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);
Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
I. (US)
FEATURES
source
1. 2458
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 2458; DB 6; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGCGGGAGCCCATCTGCCCCAGGGGCGACGGGGCGGGCTCCGCCCGGCAC 60
Db 1 GCGCGGGAGCCCATCTGCCCCAGGGGCGACGGGGCGGGCTCCGCCCGGCAC 60
Qy 61 ATGCTGTCAGCACCTCGCGGCGACCCCGAGCGCGCGCCAGCTCCGCCGAGTCCGT 120
Db 61 ATGCTGTCAGCACCTCGCGGCGACCCCGAGCGCGCGCCAGCTCCGCCGAGTCCGT 120
Qy 121 CGGAGGCGCGCGCGCCCGGAGCAAGCAGCACTAGCGGGGAAGCGCGCGTCCG 180
Db 121 CGGAGGCGCGCGCGCCCGGAGCAAGCAGCACTAGCGGGGAAGCGCGCGTCCG 180
Qy 181 GGGATCGGGATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 181 GGGATCGGGATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Qy 241 GGGACTCACACTGAGATCAAGAGAGTGCAGAGGAAAGTCACTTTGCCCTGCCACCAT 300
Db 241 GGGACTCACACTGAGATCAAGAGAGTGCAGAGGAAAGTCACTTTGCCCTGCCACCAT 300

QY	301	CAACTGGGGCTTCAGAAAAGACACCTCTGGATATTGTAATGGCTGCTCACCGAATAATGAA	360	Db	1381	TCAAGTCCACGCCACACACACAGTGAAGAGGTCATCTAAGTAGCAGTGAACATTCACG	1440
Db	301	CAACTGGGGCTTCAGAAAAGACACCTCTGGATATTGTAATGGCTGCTCACCGAATAATGAA	360	QY	1441	GAAACAGATTTCAGATGAGCATTTTCCTTTATACATACCAACACAGCAAAAGGATGTAAAGCT	1500
QY	361	GGGAACCAAAAGTGGTATCACCTTACTCCAGTCGTCATGCTTACAAATTAACCTGACTGAG	420	Db	1441	GAAACAGATTTCAGATGAGCATTTTCCTTTATACATACCAACACAGCAAAAGGATGTAAAGCT	1500
Db	361	GGGAACCAAAAGTGGTATCACCTTACTCCAGTCGTCATGCTTACAAATTAACCTGACTGAG	420	QY	1501	GATTTCATCTGTAAAGAGCATCTTATTGTGCTTTAGACCAAGAGTAAGGAAAGCAGGAG	1560
QY	421	GAAACAGAGGCGAGTGGCTTTGCTTCCAAATTTCTGCGAGGAGATGCTCTCTTGCAG	480	Db	1501	GATTTCATCTGTAAAGAGCATCTTATTGTGCTTTAGACCAAGAGTAAGGAAAGCAGGAG	1560
Db	421	GAAACAGAGGCGAGTGGCTTTGCTTCCAAATTTCTGCGAGGAGATGCTCTCTTGCAG	480	QY	1561	TCCAAATCTATTGTTGACCAAGGAGCTTGTGAGGAGTGGGGAAGGTGAGGTCAAT	1620
QY	481	ATTGAACCTCTGAGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	540	Db	1561	TCCAAATCTATTGTTGACCAAGGAGCTTGTGAGGAGTGGGGAAGGTGAGGTCAAT	1620
Db	481	ATTGAACCTCTGAGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	540	QY	1621	ATACCTAAACCTTTTAAATGTGGGATATTTTGTATGATGCTTTTGTATGATGCTTTTCAAG	1680
QY	541	CGCTACGTTGGAGCCATGTCATCTTAAAGTCTTGTAGAGACCATCAAGCCCAAGTGT	600	Db	1621	ATACCTAAACCTTTTAAATGTGGGATATTTTGTATGATGCTTTTGTATGATGCTTTTCAAG	1680
Db	541	CGCTACGTTGGAGCCATGTCATCTTAAAGTCTTGTAGAGACCATCAAGCCCAAGTGT	600	QY	1681	AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTTATTTGGATTATTA	1740
QY	601	GAGTTGGAGAGAGCTGACAGAGGAGTACCTGACTTTTGCAGTGTGAGTCAATCTCT	660	Db	1681	AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTTATTTGGATTATTA	1740
Db	601	GAGTTGGAGAGAGCTGACAGAGGAGTACCTGACTTTTGCAGTGTGAGTCAATCTCT	660	QY	1741	GTTATTCAGACAGTCAAGCAGAACCCACAGCCCTTATTAACCTGTCTACACCATGACTG	1800
QY	661	GGCAGAGAGCCATTTGTATTAATCTGGCAGGAAATCCGAGAGAAAGAGGAGAGATGAA	720	Db	1741	GTTATTCAGACAGTCAAGCAGAACCCACAGCCCTTATTAACCTGTCTACACCATGACTG	1800
Db	661	GGCAGAGAGCCATTTGTATTAATCTGGCAGGAAATCCGAGAGAAAGAGGAGAGATGAA	720	QY	1801	AGCTAACCACTTCTAAGAACTCCAAAGAAAGAAACATGTGTCTTCTATTTGACTTAAC	1860
QY	721	CGTCTGCTCCCAATCTAGGATTTGACTACCAACCCCTGACGAGTCTGCTGAGAAAT	780	Db	1801	AGCTAACCACTTCTAAGAACTCCAAAGAAAGAAACATGTGTCTTCTATTTGACTTAAC	1860
Db	721	CGTCTGCTCCCAATCTAGGATTTGACTACCAACCCCTGACGAGTCTGCTGAGAAAT	780	QY	1861	TTCATTTGTCATTAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGA	1920
QY	781	CTTACCAATGCTTACTCTGAGTGTACAGTGTACAGGAGCAACGAAAGCTGGAGGAA	840	Db	1861	TTCATTTGTCATTAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGA	1920
Db	781	CTTACCAATGCTTACTCTGAGTGTACAGTGTACAGGAGCAACGAAAGCTGGAGGAA	840	QY	1921	GAAGTGTGAATGAGTTTCTCCCACTCTATACCTATTAATCTCACTATTTGTTATTTGAGCCCAAAA	1980
QY	841	AGCTGTGTGGAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	900	Db	1921	GAAGTGTGAATGAGTTTCTCCCACTCTATACCTATTAATCTCACTATTTGTTATTTGAGCCCAAAA	1980
Db	841	AGCTGTGTGGAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	900	QY	1981	TAACTATGAAGAGAGCAAAATTTTGTGCAAAAGGATTTGAGAGCTTTTCCATCTTTCAT	2040
QY	901	GTGACAGGATAGTGGTGGAGCCCTGCTGATTTTCTTCTGTTGGTGGTGGTGGTGGTGGT	960	Db	1981	TAACTATGAAGAGAGCAAAATTTTGTGCAAAAGGATTTGAGAGCTTTTCCATCTTTCAT	2040
Db	901	GTGACAGGATAGTGGTGGAGCCCTGCTGATTTTCTTCTGTTGGTGGTGGTGGTGGTGGT	960	QY	2041	GATGTTATGAGGATTTGTTGACAAACATTAGAAATATATAATGAGCAATTTGTGGATTTCC	2100
QY	961	AGGAAAGCAAAAGATATGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1020	Db	2041	GATGTTATGAGGATTTGTTGACAAACATTAGAAATATATAATGAGCAATTTGTGGATTTCC	2100
Db	961	AGGAAAGCAAAAGATATGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1020	QY	2101	CCTCAAATCAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACA	2160
QY	1021	GAGGCTCCAAAGCCGCTTGTGAAACCCAGCTCTCTTCTTCTCAGGCTCTCGAGCTCA	1080	Db	2101	CCTCAAATCAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACA	2160
Db	1021	GAGGCTCCAAAGCCGCTTGTGAAACCCAGCTCTCTTCTTCTCAGGCTCTCGAGCTCA	1080	QY	2161	ACATGTCATTTTATCAAGCTCTTGAAGAAATTTCTTAGAGAAAAGGATCTAGGAAT	2220
QY	1081	CGCTCTGGTCTTCTTCTCAGCTCGCTTCAACAGCAAAATGATGCTCAAGCAGCAGGACA	1140	Db	2161	ACATGTCATTTTATCAAGCTCTTGAAGAAATTTCTTAGAGAAAAGGATCTAGGAAT	2220
Db	1081	CGCTCTGGTCTTCTTCTCAGCTCGCTTCAACAGCAAAATGATGCTCAAGCAGCAGGACA	1140	QY	2221	GCTGAAAGATTTACCCCAACATACCATTAATAGTCTCTTCTTCTGAGAAAATGTGAACCCAG	2280
QY	1141	CTGTCAACTGACGAGCAGCCAGCCAGGCTGCGCAACCCAGGATATAGTGGTGGTGGG	1200	Db	2221	GCTGAAAGATTTACCCCAACATACCATTAATAGTCTCTTCTTCTGAGAAAATGTGAACCCAG	2280
Db	1141	CTGTCAACTGACGAGCAGCCAGCCAGGCTGCGCAACCCAGGATATAGTGGTGGTGGG	1200	QY	2281	AATTGCAAGATCTGGTGGGAGTGAAGGAGGAGATTAAGTCAAGTCTTCTTAAATGTCAA	2340
QY	1201	CCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCAAATGATCTGACCAAGCAGAA	1260	Db	2281	AATTGCAAGATCTGGTGGGAGTGAAGGAGGAGATTAAGTCAAGTCTTCTTAAATGTCAA	2340
Db	1201	CCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCAAATGATCTGACCAAGCAGAA	1260	QY	2341	GGAAAGTACCGGGGATGCTGCGAGGCACTTGTAGGAAAATCCAGCAGGTGGAGTTGCA	2400
QY	1261	ACCACCCAGATGATCCCGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1320	Db	2341	GGAAAGTACCGGGGATGCTGCGAGGCACTTGTAGGAAAATCCAGCAGGTGGAGTTGCA	2400
Db	1261	ACCACCCAGATGATCCCGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1320	QY	2401	GTGAGCCGAGATTAATGCAATTTGCACTCCAGCCTGGTGCACAGAGCGGAGCTCCGCTC	2458
QY	1321	GACTTGAATCCCAAGCTTTTCTAGGAGTCAAGGCTTTTGGACTCTTCTCTGCTCAATGGAGC	1380	Db	2401	GTGAGCCGAGATTAATGCAATTTGCACTCCAGCCTGGTGCACAGAGCGGAGCTCCGCTC	2458
Db	1321	GACTTGAATCCCAAGCTTTTCTAGGAGTCAAGGCTTTTGGACTCTTCTCTGCTCAATGGAGC	1380	QY			
QY	1381	TCAAGTCAACAGCCACACACAGATGAGAGGTCATCTAAGTAGCAGTGAACATTTGCACG	1440	Db			

AX464254
LOCUS AX464254 2458 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 387 from Patent WO0140466.
ACCESSION AX464254
VERSION AX464254.1 GI:21899143
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 387 07-JUN-2001;
Genentech Inc. (US)
FEATURES
source location/Qualifiers
1..2458
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 2458; DB 6; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCCGGAGGCCATCTGCCCCCAGGGGCA CGGGGCGGGGCGGGCTCCGCGCCGGCAC 60
Db 1 GGGCCGGAGGCCATCTGCCCCCAGGGGCA CGGGGCGGGGCGGGCTCCGCGCCGGCAC 60
QY 61 ATGGCTGAGCACCTCGCGGCACCCCGAGCGCGCGCCAGCTCGCCGAGTCCGT 120
Db 61 ATGGCTGAGCACCTCGCGGCACCCCGAGCGCGCGCCAGCTCGCCGAGTCCGT 120
QY 121 CGGAGCGCCGGCGCGCCCGAGGCAAGAGCAACTGAGCGGGGAAGCGCCGCTCCG 180
Db 121 CGGAGCGCCGGCGCGCCCGAGGCAAGAGCAACTGAGCGGGGAAGCGCCGCTCCG 180
QY 181 GGGATCGGGATGTCCT 240
Db 181 GGGATCGGGATGTCCT 240
QY 241 GGGATCAGCTGAGTCAAGAGTGGCAGAGGAAAGGTCACTTTCCTTCCCTGCCACCAT 300
Db 241 GGGATCAGCTGAGTCAAGAGTGGCAGAGGAAAGGTCACTTTCCTTCCCTGCCACCAT 300
QY 301 CAACCTGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCAACCGATAATGAA 360
Db 301 CAACCTGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCAACCGATAATGAA 360
QY 361 GGGAAACAAAAGTGGTGATCACTTACCTCCAGTCTCATGTCTACAATACTTGACTGAG 420
Db 361 GGGAAACAAAAGTGGTGATCACTTACCTCCAGTCTCATGTCTACAATACTTGACTGAG 420
QY 421 GAAAGAGGGCGGAGTGGCTTTCCTTCCAAATTCCTGGCAGGAGATGCCTCTTCGAG 480
Db 421 GAAAGAGGGCGGAGTGGCTTTCCTTCCAAATTCCTGGCAGGAGATGCCTCTTCGAG 480
QY 481 ATTGAACCTCTGAAGCCAGTGAAGCGCGGTACACTCTGAAGTTTAAAGATTCAGGG 540
Db 481 ATTGAACCTCTGAAGCCAGTGAAGCGCGGTACACTCTGAAGTTTAAAGATTCAGGG 540
QY 541 CGCTACGTGTGGAGCCATGTCTATCTTAAAGTCTTTAGTGAGACCATCCAAGCCCAAGTGT 600
Db 541 CGCTACGTGTGGAGCCATGTCTATCTTAAAGTCTTTAGTGAGACCATCCAAGCCCAAGTGT 600
QY 601 GAGTTGGAAGGAGAGCTGACAGAGGAAGTGAACCTGACTTTGCGAGTGTGAGTCACTCCT 660
Db 601 GAGTTGGAAGGAGAGCTGACAGAGGAAGTGAACCTGACTTTGCGAGTGTGAGTCACTCCT 660

QY 661 GGCACAGAGCCCATTTGTGTATTACTGGCAGCGAAATCCGAGAGAAAAGAGGAGAGATGAA 720
Db 661 GGCACAGAGCCCATTTGTGTATTACTGGCAGCGAAATCCGAGAGAAAAGAGGAGAGATGAA 720
QY 721 CGTCTGCCCTCCCAATCTAGGATTGACTACACCAACCCCTGGACGAGTTCTGCTGCAGAA 780
Db 721 CGTCTGCCCTCCCAATCTAGGATTGACTACACCAACCCCTGGACGAGTTCTGCTGCAGAA 780
QY 781 CTTACCATGTCCTACTCTGGGACTGTACACGAGGCAACGAAAGCTGGGAAGAA 840
Db 781 CTTACCATGTCCTACTCTGGGACTGTACACGAGGCAACGAAAGCTGGGAAGAA 840
QY 841 AGCTGTGTGGTGGAGTAATCTGTACAGTATGTACAAAGATCGGCAATGGTTGCGAGGCA 900
Db 841 AGCTGTGTGGTGGAGTAATCTGTACAGTATGTACAAAGATCGGCAATGGTTGCGAGGCA 900
QY 901 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTTGGTGGCTGCTAATCCGA 960
Db 901 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTTGGTGGCTGCTAATCCGA 960
QY 961 AGGAAAGACAAAGAAAGATATGAGGAAGAGAGAGACCTAATGAAATTCGAGAAATGCT 1020
Db 961 AGGAAAGACAAAGAAAGATATGAGGAAGAGAGAGACCTAATGAAATTCGAGAAATGCT 1020
QY 1021 GAAAGTCCAAAGCCCGTCTTGTGAAACCCAGCTCCTCTCTCAGGCTCTCGGAGTCA 1080
Db 1021 GAAAGTCCAAAGCCCGTCTTGTGAAACCCAGCTCCTCTCTCAGGCTCTCGGAGTCA 1080
QY 1081 CGCTCTGGTTCTTCTCCAGCTCCACAGCAATAGTGCTCACGAGCCAGCGGACA 1140
Db 1081 CGCTCTGGTTCTTCTCCAGCTCCACAGCAATAGTGCTCACGAGCCAGCGGACA 1140
QY 1141 CTGTCAACTGACGAGCACCCAGCGGCTGGCCACCCAGGCAATACAGCTAGTGGGG 1200
Db 1141 CTGTCAACTGACGAGCACCCAGCGGCTGGCCACCCAGGCAATACAGCTAGTGGGG 1200
QY 1201 CCAGAGGTGAGAGTCTGAAACCAAGAAAGTCCACCATTAATCTGACCAAGACAGAA 1260
Db 1201 CCAGAGGTGAGAGTCTGAAACCAAGAAAGTCCACCATTAATCTGACCAAGACAGAA 1260
QY 1261 ACCACCCAGCATGATCCCGAGGAGAGAGGCTTCCAAACGGTCTGAATTAACAATG 1320
Db 1261 ACCACCCAGCATGATCCCGAGGAGAGAGGCTTCCAAACGGTCTGAATTAACAATG 1320
QY 1321 GACTTGACTCCACGCTTCTTAGAGTACAGGCTCTTTGGACTCTTCTCGTCAATGGAGC 1380
Db 1321 GACTTGACTCCACGCTTCTTAGAGTACAGGCTCTTTGGACTCTTCTCGTCAATGGAGC 1380
QY 1381 TCAAGTCAACGACCAACCAAGATGAGAGGTCACTTAAGTAGCAGTGAGCATTTGCACG 1440
Db 1381 TCAAGTCAACGACCAACCAAGATGAGAGGTCACTTAAGTAGCAGTGAGCATTTGCACG 1440
QY 1441 GAAAGATTCAGATGAGCATTTTCTTATACAAATCCAAACCAAGCAAGAGTGTAAAGT 1500
Db 1441 GAAAGATTCAGATGAGCATTTTCTTATACAAATCCAAACCAAGCAAGAGTGTAAAGT 1500
QY 1501 GATTTCATCTGTAAGAGGATCTTATTGTGCTTTTAGACAGAGTAAGGGAAAGCAGAG 1560
Db 1501 GATTTCATCTGTAAGAGGATCTTATTGTGCTTTTAGACAGAGTAAGGGAAAGCAGAG 1560
QY 1561 TCCAAATCTATTGTGTGACAGGACCTGTGTGTGAGAGGTTGGGGAAAGGTGAGTGAAT 1620
Db 1561 TCCAAATCTATTGTGTGACAGGACCTGTGTGTGAGAGGTTGGGGAAAGGTGAGTGAAT 1620
QY 1621 ATACCTAAACCTTTTAATGTGGGATATTTGTATCAGTGCTTTGATTCACAAATTTCAAG 1680
Db 1621 ATACCTAAACCTTTTAATGTGGGATATTTGTATCAGTGCTTTGATTCACAAATTTCAAG 1680
QY 1681 AGGAAATGGGATGCTGTTGTAAATTTTCTATGATTTCTCAAACTTATTTGGATTATTA 1740
Db 1681 AGGAAATGGGATGCTGTTGTAAATTTTCTATGATTTCTCAAACTTATTTGGATTATTA 1740

QY	1741	GTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG	1800
Db	1741	GTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG	1800
QY	1801	AGCTAACACCTCTTAAGAACTCCAAAGAAAGGAAACATGTCTTCTATTCTGACTTAAC	1860
Db	1801	AGCTAACACCTCTTAAGAACTCCAAAGAAAGGAAACATGTCTTCTATTCTGACTTAAC	1860
QY	1861	TTCTATTGTCTAAGAGTTTGATATTATTTCAAGGGAGTTGAAATAGTGGGAGATGGA	1920
Db	1861	TTCTATTGTCTAAGAGTTTGATATTATTTCAAGGGAGTTGAAATAGTGGGAGATGGA	1920
QY	1921	GAAGAGTCAATGAGTTTCTCCACTCTATCTACTATCTCACTATTGTGATGAGCCCAAAA	1980
Db	1921	GAAGAGTCAATGAGTTTCTCCACTCTATCTACTATCTCACTATTGTGATGAGCCCAAAA	1980
QY	1981	TAACTATGAAGAGGACAAAAATTTGTGACAAAGATTTGAGAGCTTTCCATCTTCAT	2040
Db	1981	TAACTATGAAGAGGACAAAAATTTGTGACAAAGATTTGAGAGCTTTCCATCTTCAT	2040
QY	2041	GATGTTATGAGGATTTGTGACAAACATTAGAAATATATATAATGGAGCAATTTCCATTTCC	2100
Db	2041	GATGTTATGAGGATTTGTGACAAACATTAGAAATATATATAATGGAGCAATTTCCATTTCC	2100
QY	2101	CCTCAAAATCAGATGCTCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAAATACA	2160
Db	2101	CCTCAAAATCAGATGCTCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAAATACA	2160
QY	2161	ACATGTCATTTATCAAGCTCTTAGAAGAAATCTTCTAGAGAAAGGGATCTAGGAAT	2220
Db	2161	ACATGTCATTTATCAAGCTCTTAGAAGAAATCTTCTAGAGAAAGGGATCTAGGAAT	2220
QY	2221	GCTGAAGATTTACCAACATACCATATATAGTCTCTTTCTTGAGAAATGTGAACACAG	2280
Db	2221	GCTGAAGATTTACCAACATACCATATATAGTCTCTTTCTTGAGAAATGTGAACACAG	2280
QY	2281	AATTGCAAGACTGGTGGACTAGAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA	2340
Db	2281	AATTGCAAGACTGGTGGACTAGAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA	2340
QY	2341	GGAGGTAGCCGGGATGCTGAGCAAGGAGGAGATTTAGATCAGTTTCTCTTAATATGTCAA	2400
Db	2341	GGAGGTAGCCGGGATGCTGAGCAAGGAGGAGATTTAGATCAGTTTCTCTTAATATGTCAA	2400
QY	2401	GTGAGCCGAGATTATGCACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCC	2458
Db	2401	GTGAGCCGAGATTATGCACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCC	2458
RESULT 9			
LOCUS	AX490956	2458 bp	DNA linear PAT 16-AUG-2002
DEFINITION	Sequence 63 from Patent WO0200690.		
ACCESSION	AX490956		
VERSION	AX490956.1 GI:22323815		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Baker, K.P., Ferrara, N., Gerber, H., Gieritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stepan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.		
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 0200690-A 63 03-JAN-2002;		
FEATURES	Genentech, Inc. (US)		
source	Location/Qualifiers		
	1..2458		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		

/db_xref="taxon:9606"			
ORIGIN	Query Match	100.0%;	Score 2458; DB 6; Length 2458;
	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 2458; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	CGCGCGGAGCCCATCTGCCCCCAGGGGCGACGGGGCGCGGGCGGCTCCCGCCGGCAC	60
Db	1	CGCGCGGAGCCCATCTGCCCCCAGGGGCGACGGGGCGCGGGCGGCTCCCGCCGGCAC	60
QY	61	ATGGCTGAGCCCACTCGCGGCACCCCGAGGCGCGCGCCGAGCTCGCCGAGGTCCT	120
Db	61	ATGGCTGAGCCCACTCGCGGCACCCCGAGGCGCGCGCCGAGCTCGCCGAGGTCCT	120
QY	121	CGGAGGCGCGCGCGCGCGCGGCAAGCAGCAACTGAGCGGGGAAGCGCCGCTCCG	180
Db	121	CGGAGGCGCGCGCGCGCGCGGCAAGCAGCAACTGAGCGGGGAAGCGCCGCTCCG	180
QY	181	GGGATCGGGATGTCCT	240
Db	181	GGGATCGGGATGTCCT	240
QY	241	GGGACTCACACTGAGATCAAGAGAGTGGCAGAGGAAAGGTCACTTTGCCCTGCCACCAT	300
Db	241	GGGACTCACACTGAGATCAAGAGAGTGGCAGAGGAAAGGTCACTTTGCCCTGCCACCAT	300
QY	301	CAACTGGGGCTTCCAGAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAA	360
Db	301	CAACTGGGGCTTCCAGAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAA	360
QY	361	GGGAAACAAAGAGTGTGATCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	420
Db	361	GGGAAACAAAGAGTGTGATCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	420
QY	421	GGGAAACAAAGAGTGTGATCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	480
Db	421	GGGAAACAAAGAGTGTGATCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	480
QY	481	ATTGAACTCTGAAGCCAGTGTGATGAGGCGCGGTACACCTGTAAGGTAAAGATTCAAGG	540
Db	481	ATTGAACTCTGAAGCCAGTGTGATGAGGCGCGGTACACCTGTAAGGTAAAGATTCAAGG	540
QY	541	CGCTACCTGTGGAGCCCATGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGT	600
Db	541	CGCTACCTGTGGAGCCCATGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGT	600
QY	601	GAGTTGGAAGGAGAGCTGACAGAGGAGTGAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	660
Db	601	GAGTTGGAAGGAGAGCTGACAGAGGAGTGAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	660
QY	661	GGCAGAGGCGCCATTTGTTATCTGCGAGCGAATCCGAGAGAAAGAGGAGGAGATGAA	720
Db	661	GGCAGAGGCGCCATTTGTTATCTGCGAGCGAATCCGAGAGAAAGAGGAGGAGATGAA	720
QY	721	CGTCTGCTCCCAATCTTAGGATTGACTACCAACCCCTGGACGAGTTCCTGCTCAGAT	780
Db	721	CGTCTGCTCCCAATCTTAGGATTGACTACCAACCCCTGGACGAGTTCCTGCTCAGAT	780
QY	781	CTTACCATGTCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	840
Db	781	CTTACCATGTCTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	840
QY	841	AGCTGTGTGGTGGAGTAACTGTACAGTATGTACAAAGCATCGGATGTTGCGAGGACA	900
Db	841	AGCTGTGTGGTGGAGTAACTGTACAGTATGTACAAAGCATCGGATGTTGCGAGGACA	900
QY	901	GTGACAGGCAATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	960
Db	901	GTGACAGGCAATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	960
QY	961	AGGAAAGACAAAGAAAGATATGAGGAAGAGAGACCTTAATGAAATTCGAGAGATGCT	1020
Db	961	AGGAAAGACAAAGAAAGATATGAGGAAGAGAGACCTTAATGAAATTCGAGAGATGCT	1020

Db 961 AGGAAGACAAAGAAAGATATGAGGAAGAGAGACCTAATGAATTCGAGAGATGCT 1020
Qy 1021 GAAGTCTCAAAAGCCGCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCTCGAGCTCA 1080
Db 1021 GAAGTCTCAAAAGCCGCTTGTGAAACCCAGCTCCTCTTCTCAGGCTCTCGAGCTCA 1080
Qy 1081 CGCTCTGGTCTTCTCCTCACTCGCTCCAGAGAAATAGTGCCTCAGCGAGCCAGCGGACA 1140
Db 1081 CGCTCTGGTCTTCTCCTCACTCGCTCCAGAGAAATAGTGCCTCAGCGAGCCAGCGGACA 1140
Qy 1141 CTGTCAACTGAGCGCAGCACCAGCCAGCGCTGGCCAGCCAGGCATACAGCCTAGTGGGG 1200
Db 1141 CTGTCAACTGAGCGCAGCACCAGCCAGCGCTGGCCAGCCAGGCATACAGCCTAGTGGGG 1200
Qy 1201 CCAGAGGTGAGAGGTTCTGAAACAAAGAAAGTCCACCATGCTAAATCTGACCAAGCAGAA 1260
Db 1201 CCAGAGGTGAGAGGTTCTGAAACAAAGAAAGTCCACCATGCTAAATCTGACCAAGCAGAA 1260
Qy 1261 ACCACACCAGCATGATCCCGAGCCAGAGCAGAGCGCTTCCAAACGGTCTGAATTAATG 1320
Db 1261 ACCACACCAGCATGATCCCGAGCCAGAGCAGAGCGCTTCCAAACGGTCTGAATTAATG 1320
Qy 1321 GACTTGACTCCACGCTTCTTAGAGTCAGGTCAGGTCCTTCTCGTCAATGGAGC 1380
Db 1321 GACTTGACTCCACGCTTCTTAGAGTCAGGTCAGGTCCTTCTCGTCAATGGAGC 1380
Qy 1381 TCAAGTCAACGCCACACACAGATGAGAGTCACTAAAGTAGCAGTGAGCATTTGCAG 1440
Db 1381 TCAAGTCAACGCCACACACAGATGAGAGTCACTAAAGTAGCAGTGAGCATTTGCAG 1440
Qy 1441 GNAAGATTGAGATGAGCATTTTCTTATACAAATACCAAGCAAGCAAGGATGTAAGCT 1500
Db 1441 GNAAGATTGAGATGAGCATTTTCTTATACAAATACCAAGCAAGCAAGGATGTAAGCT 1500
Qy 1501 GATTCACTGTAAAGGATCTTATTTGCTTTAGACACAGTAAGCGGAAGCAGAG 1560
Db 1501 GATTCACTGTAAAGGATCTTATTTGCTTTAGACACAGTAAGCGGAAGCAGAG 1560
Qy 1561 TCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAAGGTGAGGTGAAT 1620
Db 1561 TCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAAGGTGAGGTGAAT 1620
Qy 1621 ATACCTAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTCACATTTTCAAG 1680
Db 1621 ATACCTAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTCACATTTTCAAG 1680
Qy 1681 AGGAATCGGATGCTGTTGTAAATTTTCTATGCAATTTCTGCAACTTATTGGATTATTA 1740
Db 1681 AGGAATCGGATGCTGTTGTAAATTTTCTATGCAATTTCTGCAACTTATTGGATTATTA 1740
Qy 1741 GTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGACTG 1800
Db 1741 GTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGACTG 1800
Qy 1801 AGCTAACCATCTTAAGAAACTTCCAAAAGAAAGAAACATGTGTCTTCTATTCTGACTTAAC 1860
Db 1801 AGCTAACCATCTTAAGAAACTTCCAAAAGAAAGAAACATGTGTCTTCTATTCTGACTTAAC 1860
Qy 1861 TTCAATTTGCTAAGGTTTGGATATTAATTTCAAGGGAGTTGAATAGTGGAGATGGA 1920
Db 1861 TTCAATTTGCTAAGGTTTGGATATTAATTTCAAGGGAGTTGAATAGTGGAGATGGA 1920
Qy 1921 GAAGAGTGAATGAGTTTCTCCACCTCTATCTAATCTCACTATTGTTGATGAGCCAAAA 1980
Db 1921 GAAGAGTGAATGAGTTTCTCCACCTCTATCTAATCTCACTATTGTTGATGAGCCAAAA 1980
Qy 1981 TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTTGTGAAGAGCTTTCCATCTTCAT 2040
Db 1981 TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTTGTGAAGAGCTTTCCATCTTCAT 2040
Qy 2041 GATGTTATGAGGATTTGTGACAAACATTAAGAAATATTAATGGAGCAATTTGGATTTC 2100
Db 2041 GATGTTATGAGGATTTGTGACAAACATTAAGAAATATTAATGGAGCAATTTGGATTTC 2100

Qy 2101 CCTCAAAATCAGATGCTCTTAAGGACTTTTCTCTCTAGATATTTCTGGAAGGAGAAAAATACA 2160
Db 2101 CCTCAAAATCAGATGCTCTTAAGGACTTTTCTCTCTAGATATTTCTGGAAGGAGAAAAATACA 2160
Qy 2161 ACATGCTCAATTTATCAACGCTCTTACAAAGAAATTTCTTAGAGAAAAGGATCTAGGAAT 2220
Db 2161 ACATGCTCAATTTATCAACGCTCTTACAAAGAAATTTCTTAGAGAAAAGGATCTAGGAAT 2220
Qy 2221 GCTGAAAGATTACCCAAACATACATTATAGTCTCTTTCTTCTGAGAAAAATGTGAACACAG 2280
Db 2221 GCTGAAAGATTACCCAAACATACATTATAGTCTCTTTCTTCTGAGAAAAATGTGAACACAG 2280
Qy 2281 AATTGCAAGACTGCGGTGAGCTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA 2340
Db 2281 AATTGCAAGACTGCGGTGAGCTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA 2340
Qy 2341 GGAAGGTAGCCGGCATGGTCCAGGCACCTGTAGGAAATCCAGAGGTGAGGTTGCA 2400
Db 2341 GGAAGGTAGCCGGCATGGTCCAGGCACCTGTAGGAAATCCAGAGGTGAGGTTGCA 2400
Qy 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGGGGACTCCGTCTC 2458
Db 2401 GTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGGGGACTCCGTCTC 2458

RESULT 10

AX538183
LOCUS AX538183 2458 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 58 from Patent EPI241183.
ACCESSION AX538183
VERSION AX538183.1 GI:25270330
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1
AUTHORS Wood, W.I., Goddard, A., Gurney, A., Yuan, J., Baker, K.P. and Chen, J.
TITLE Human hcar-like protein and nucleic acids encoding it
JOURNAL Patent: EP 1241183-A 58 18-SEP-2002;
Genentech, Inc. (US)

FEATURES

source
1..2458
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2458; DB 6; Length 2458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGCGGAGGCCCATCTGCCCCCAGGGGCACGGGGCGGGGGCGGGTCCCGCCCGGCAC 60
Db 1 GCGCGGAGGCCCATCTGCCCCCAGGGGCACGGGGCGGGGGCGGGTCCCGCCCGGCAC 60
Qy 61 ATGGCTGACGACCATCTGGCGGCACCCCGAGCGCGCGCCAGCTCGCGCGAGGTCCGT 120
Db 61 ATGGCTGACGACCATCTGGCGGCACCCCGAGCGCGCGCCAGCTCGCGCGAGGTCCGT 120
Qy 121 CGGAGGCGCCCGCGCCCGCGGAGCAAGACGACAACTAGCGGGGAAGCGCCCGGTCCG 180
Db 121 CGGAGGCGCCCGCGCCCGCGGAGCAAGACGACAACTAGCGGGGAAGCGCCCGGTCCG 180
Qy 181 GGGATCGGGATGTCCCT 240
Db 181 GGGATCGGGATGTCCCT 240
Qy 241 GGGACTCACACTGAGATCAAGAGATGCGACAGGAAAGGTACCTTCCCTGCCACCAT 300
Db 241 GGGACTCACACTGAGATCAAGAGATGCGACAGGAAAGGTACCTTCCCTGCCACCAT 300

301 CAACCTGGGGCTTCCAGAAAAAGACACTCTCGGATATTGAATGGCTGCTCACCGAATATGAA 360 QY
301 CAACCTGGGGCTTCCAGAAAAAGACACTCTCGGATATTGAATGGCTGCTCACCGAATATGAA 360 Db
361 GGGAAACAAAAGTGGTGATCACTTACTCAGTCGTCTACCTCTACAAATAACTTGACTGAG 420 QY
361 GGGAAACAAAAGTGGTGATCACTTACTCAGTCGTCTACCTCTACAAATAACTTGACTGAG 420 Db
421 GAAACAGAGGSCCGAGTGGCTTGGCTTCCAAATTTCTCGCAGGAGATGCTCTCTTGCAG 480 QY
421 GAAACAGAGGSCCGAGTGGCTTGGCTTCCAAATTTCTCGCAGGAGATGCTCTCTTGCAG 480 Db
481 ATTGAACCTCTGAAGCCCGAGTGAGGGCCGGTACACCTGTGAAGTTAAGAATTCAGGG 540 QY
481 ATTGAACCTCTGAAGCCCGAGTGATGAGGGCCGGTACACCTGTGAAGTTAAGAATTCAGGG 540 Db
541 CGCTACGTGTGGAGCCATGTCATCTTAAAGTCTTAGTGAGACCATCCAGGCCCAAGTGT 600 QY
541 CGCTACGTGTGGAGCCATGTCATCTTAAAGTCTTAGTGAGACCATCCAGGCCCAAGTGT 600 Db
601 GAGTTGGAAGGAGAGCTGACAGAAAGGAAGTGAACCTGACTTTGCGAGTGTGAGTCACTCT 660 QY
601 GAGTTGGAAGGAGAGCTGACAGAAAGGAAGTGAACCTGACTTTGCGAGTGTGAGTCACTCT 660 Db
661 GSCACAGAGCCCATTTGTGTATTACTGGCAGCGAATCCGAGAGAAGAGGGAGAGATGAA 720 QY
661 GSCACAGAGCCCATTTGTGTATTACTGGCAGCGAATCCGAGAGAAGAGGGAGAGATGAA 720 Db
721 CGTCTGCTCCCAATCTAGGATGACTACAAACCACTCGACAGTTCCTGCTCAGAA 780 QY
721 CGTCTGCTCCCAATCTAGGATGACTACAAACCACTCGACAGTTCCTGCTCAGAA 780 Db
781 CTTACCATGCTCTACTCTGAGCTGACAGTGCAAGAGGAGAGAGCTGGGAGGAA 840 QY
781 CTTACCATGCTCTACTCTGAGCTGACAGTGCAAGAGGAGAGAGCTGGGAGGAA 840 Db
841 AGCTGTGTGGTGGAGTAACTGTACAGTATGACAAAGCATCGGCATGCTGGTGGCTTAATCCGA 900 QY
841 AGCTGTGTGGTGGAGTAACTGTACAGTATGACAAAGCATCGGCATGCTGGTGGCTTAATCCGA 900 Db
901 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTGGTGGCTGCTTAATCCGA 960 QY
901 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTCTGGTGGCTGCTTAATCCGA 960 Db
961 AGGAAAGACAAAGAAAGATATGAGGAAGAGAGACCTTAATGAATTCGAGAAATGCT 1020 QY
961 AGGAAAGACAAAGAAAGATATGAGGAAGAGAGACCTTAATGAATTCGAGAAATGCT 1020 Db
1021 GAAGCTCCAAAGCCGCTTTGTGAAACCCAGCTCTCTCTCTCGAGCTCTCGAGCTCA 1080 QY
1021 GAAGCTCCAAAGCCGCTTTGTGAAACCCAGCTCTCTCTCTCGAGCTCTCGAGCTCA 1080 Db
1081 CGCTCTGGTCTTCTCTCACTCGCTCCAGCAAAATAGTGCCTCAGGCCTCTCGAGCTCA 1140 QY
1081 CGCTCTGGTCTTCTCTCACTCGCTCCAGCAAAATAGTGCCTCAGGCCTCTCGAGCTCA 1140 Db
1141 CTGTCAACTGACGACAGCCACCCAGCGGCTGSCCAACCCAGGCATACAGCTTAGTGGGG 1200 QY
1141 CTGTCAACTGACGACAGCCACCCAGCGGCTGSCCAACCCAGGCATACAGCTTAGTGGGG 1200 Db
1201 CCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCACATGCTAATCTGACCAAGAGAGAA 1260 QY
1201 CCAGAGGTGAGAGGTTCTGAAACCAAGAAAGTCCACATGCTAATCTGACCAAGAGAGAA 1260 Db
1261 ACCACACCCAGCATGATCCCGACGACGAGCAGGCTTCCAAAGCTGCTGAAATTAATG 1320 QY
1261 ACCACACCCAGCATGATCCCGACGACGAGCAGGCTTCCAAAGCTGCTGAAATTAATG 1320 Db
1321 GACTTGACTCCACGCTTCTCTAGAGTCAAGGCTTTTGGACTTCTCTGCTCAATGAGC 1380 QY
1321 GACTTGACTCCACGCTTCTCTAGAGTCAAGGCTTTTGGACTTCTCTGCTCAATGAGC 1380 Db
1381 TCAAGTCAACGACCAACACACAGATGAGGCTCATCTAGTAGCAGTGGAGCTTGCACG 1440 QY

RESULT 11

1381 TCAAGTCAACGACCAACACACAGATGAGGCTCATCTAAGTAGCAGTGAGCATTTGCACG 1440 Db
1441 GAAACAGATTCAAGTAGCATTTTCTTATACAAATACCAACCAAGCAAAAGGATGTAAAGCT 1500 QY
1441 GAAACAGATTCAAGTAGCATTTTCTTATACAAATACCAACCAAGCAAAAGGATGTAAAGCT 1500 Db
1501 GATTTCATCTGTAAAAAGGCATCTTATTGTGCTTTTGAACAGAGTAAGGGAAAGCAGAG 1560 QY
1501 GATTTCATCTGTAAAAAGGCATCTTATTGTGCTTTTGAACAGAGTAAGGGAAAGCAGAG 1560 Db
1561 TCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAAGGTGAGTGAAT 1620 QY
1561 TCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAAGGTGAGTGAAT 1620 Db
1621 ATACCTTAAACCTTTTAAATGTGGGATATTGTTGATCAGTCTTTGATTCACAAATTTCAAG 1680 QY
1621 ATACCTTAAACCTTTTAAATGTGGGATATTGTTGATCAGTCTTTGATTCACAAATTTCAAG 1680 Db
1681 AGGAAATGGGATGCTGTTTGTAAAATTTCTATGCAATTTCTGCAAACTTATTGGATTATTA 1740 QY
1681 AGGAAATGGGATGCTGTTTGTAAAATTTCTATGCAATTTCTGCAAACTTATTGGATTATTA 1740 Db
1741 GTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG 1800 QY
1741 GTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG 1800 Db
1801 AGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGCTCTTCTTATCTGACTTAAC 1860 QY
1801 AGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGCTCTTCTTATCTGACTTAAC 1860 Db
1861 TTCAATTTGTCATAAGGTTGGGATTAATAATTCAGGGGAGTTGAAATAGTGGGAGATGGA 1920 QY
1861 TTCAATTTGTCATAAGGTTGGGATTAATAATTCAGGGGAGTTGAAATAGTGGGAGATGGA 1920 Db
1921 GAAGAGTGAATGAGTTTCTCCACTCTATATACTCTCACTATTTGTATTTGAGGCCCAAAA 1980 QY
1921 GAAGAGTGAATGAGTTTCTCCACTCTATATACTCTCACTATTTGTATTTGAGGCCCAAAA 1980 Db
1981 TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCAT 2040 QY
1981 TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCAT 2040 Db
2041 GATGTTATGAGGATTTGTCACAAACATTAGAAATATATATGAGCAATTTGGATTTCC 2100 QY
2041 GATGTTATGAGGATTTGTCACAAACATTAGAAATATATATGAGCAATTTGGATTTCC 2100 Db
2101 CCTCAAAATCAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACA 2160 QY
2101 CCTCAAAATCAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACA 2160 Db
2161 ACATGTCATTTATCAACGTCCTTAGAAGAAATTTCTTAGAAGAAAGGATCTAGGAAT 2220 QY
2161 ACATGTCATTTATCAACGTCCTTAGAAGAAATTTCTTAGAAGAAAGGATCTAGGAAT 2220 Db
2221 GCTGAAAGATTACCAACATACCATTAAGTCTCTCTCTCTGAGAAAAATGTGAACACAG 2280 QY
2221 GCTGAAAGATTACCAACATACCATTAAGTCTCTCTCTCTGAGAAAAATGTGAACACAG 2280 Db
2281 AATTGCAAGACTGGGTGAGCTAGAAAAGGAGATTAGATCAGTTTCTTAAATATGTCAA 2340 QY
2281 AATTGCAAGACTGGGTGAGCTAGAAAAGGAGATTAGATCAGTTTCTTAAATATGTCAA 2340 Db
2341 GGAAGGTAGCGGGCATGTGCGAGGACCTGTAGAAAAATCCAGCAGGTGGAGTTGCA 2400 QY
2341 GGAAGGTAGCGGGCATGTGCGAGGACCTGTAGAAAAATCCAGCAGGTGGAGTTGCA 2400 Db
2401 GTGAGCCGAGATTATGCCAATTTGCACTCCAGCCTGGGTGACAGAGCGGACTCCGCTC 2458 QY
2401 GTGAGCCGAGATTATGCCAATTTGCACTCCAGCCTGGGTGACAGAGCGGACTCCGCTC 2458 Db

AY326422	AY326422	2458 bp	mRNA	linear	PRI 01-DEC-2003
LOCUS	Homo sapiens adipocyte adhesion molecule mRNA, complete cds.				
DEFINITION	AY326422				
ACCESSION	AY326422.1	GI:32816051			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2458)				
AUTHORS	EGUCHI, J., WADA, J., HIDA, K. and ZHANG, H.				
TITLE	Molecular cloning of adipocyte adhesion molecule (ACAM)				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2458)				
AUTHORS	EGUCHI, J., WADA, J., HIDA, K. and ZHANG, H.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-JUN-2003) Department of Medicine and Clinical Science, Okayama University Graduate School of Medicine and Dentistry, 2-5-1 Shikata-cho, Okayama 700-8558, Japan				
FEATURES	Location/Qualifiers				
source	1..2458				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	190..1311				
	/note="ACAM"				
	/codon_start=1				
	/product="adipocyte adhesion molecule"				
	/protein_id="AAP88386.1"				
	/db_xref="GI:32816052"				
	/translation="MSLLLLLLVSYVYVTLGTHTEIKRVABEKVLPCHQLGLPEK				
	DTLDEWLLTNEGKQVITYVSSRVNLTPEQKRVAFASNFAGDASLQIEPLK				
	PSDEGRYTCVKNSGRVYVSHVILKLVLPKPKCELEGTESDLTLQCESGTE				
	PIVYVQRIRKEGSDRLPPKSRIDYVHNPGRVLLQNTMSYGLYQCTAGNEAKES				
	CVVRVTVQVQISGVAGAVTGIAGALLILFLVLLLRKDKERYEERPEPNEIRED				
	AEAPKRLVKSSESSSRSSRSSTRANSASRQRTLSTUDNAPQPLATQAYS				
	LVPVPRGSEPKVHNLTKAETTPSMIPQSRAFQTV"				
ORIGIN					
Query Match	100.0%; Score 2458; DB 9; Length 2458;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 2458; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 GGGCCGGAGGCCATCTGCCCCAGGGGCAAGGGGCGGGGCGGGCTCCCGCCGGCAC	60			
Db	1 GGGCCGGAGGCCATCTGCCCCAGGGGCAAGGGGCGGGGCGGGCTCCCGCCGGCAC	60			
Qy	61 ATGGCTGAGCCACCTCGCGGCGACCCCGAGGCGCGGCGCCAGCTCGCGGAGTCCGT	120			
Db	61 ATGGCTGAGCCACCTCGCGGCGACCCCGAGGCGCGGCGCCAGCTCGCGGAGTCCGT	120			
Qy	121 CGGAGGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180			
Db	121 CGGAGGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	180			
Qy	181 GGGATCGGGATGTCCT	240			
Db	181 GGGATCGGGATGTCCT	240			
Qy	241 GGGATCACTGAGATCAAGAGATGGGAGGAAAGGTCACTTTGGCCCTGCCACCAT	300			
Db	241 GGGATCACTGAGATCAAGAGATGGGAGGAAAGGTCACTTTGGCCCTGCCACCAT	300			
Qy	301 CAACCTGGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTCTCACCAGTAATGAA	360			
Db	301 CAACCTGGGGCTTCCAGAAAAGACACTCTGGATATTGAATGGCTCTCACCAGTAATGAA	360			
Qy	361 GGGAAACCAAAAGTGGTGATCACTTACTTCCAGTCCGTCTGTACATAAATTTGACTGAG	420			
Db	361 GGGAAACCAAAAGTGGTGATCACTTACTTCCAGTCCGTCTGTACATAAATTTGACTGAG	420			
Qy	421 GAACAGAGGGCGGAGTGGCCCTTTGCTTCCAAATTTCTGGCAGGAGATGSCCTCTTGCAG	480			

QY 361 GGGAAACCAAAAGTGGTATCACTTACTCCAGTCTCATGTCTACAATAAATTGACTGAG 420
Db 361 GGGAAACCAAAAGTGGTATCACTTACTCCAGTCTCATGTCTACAATAAATTGACTGAG 420
QY 421 GAAACAGAGGGCCGAGTGGCTTTGCTTCCAAATTTCTGGCAGGAGATGCCCTCTTGCAG 480
Db 421 GAAACAGAGGGCCGAGTGGCTTTGCTTCCAAATTTCTGGCAGGAGATGCCCTCTTGCAG 480
QY 481 ATTGAACCTCTGAAGCCAGTATGAGGGCCGGTACACTGTGAAGTTAAGAAATTCAGGG 540
Db 481 ATTGAACCTCTGAAGCCAGTATGAGGGCCGGTACACTGTGAAGTTAAGAAATTCAGGG 540
QY 541 CGCTACGTTGAGGACATGTCTATTAAGTCTTTAGTGAGACCATCCAAAGCCCAAGTGT 600
Db 541 CGCTACGTTGAGGACATGTCTATTAAGTCTTTAGTGAGACCATCCAAAGCCCAAGTGT 600
QY 601 GAGTTGGAAGGAGAGCTGACAGAAGAAAGTACCTGACTTTGTCAGTGTGAGTCACTCTCT 660
Db 601 GAGTTGGAAGGAGAGCTGACAGAAGAAAGTACCTGACTTTGTCAGTGTGAGTCACTCTCT 660
QY 661 GGCACAGAGCCCATTTGTGTATTAATGGCAGCGAATCCGAGAGAAAGAGGAGAGATGAA 720
Db 661 GGCACAGAGCCCATTTGTGTATTAATGGCAGCGAATCCGAGAGAAAGAGGAGAGATGAA 720
QY 721 CGTCTGCCCTCCAAATCTAGGATTTGACTACAAACCACTGACGAGATTTCTGTCAGAAAT 780
Db 721 CGTCTGCCCTCCAAATCTAGGATTTGACTACAAACCACTGACGAGATTTCTGTCAGAAAT 780
QY 781 CTTACCATGTCTACTCTGAGCTGTACAGTATGTACAAAGCATCGGCATGTTGCGAGGCA 840
Db 781 CTTACCATGTCTACTCTGAGCTGTACAGTATGTACAAAGCATCGGCATGTTGCGAGGCA 840
QY 841 AGCTGTGTGGTGGAGTAACTGTACAGTATGTACAAAGCATCGGCATGTTGCGAGGCA 900
Db 841 AGCTGTGTGGTGGAGTAACTGTACAGTATGTACAAAGCATCGGCATGTTGCGAGGCA 900
QY 901 GTGACAGGATAGTGGCTGGAGCCCTGCTGATTTTCTTGGTGTGCTGCTGATTAATCCGA 960
Db 901 GTGACAGGATAGTGGCTGGAGCCCTGCTGATTTTCTTGGTGTGCTGCTGATTAATCCGA 960
QY 961 AGGAAAGCAAAAGATATGAGGAGAGAGAGACCTTAATGAATTCGAGAGATGCT 1020
Db 961 AGGAAAGCAAAAGATATGAGGAGAGAGAGACCTTAATGAATTCGAGAGATGCT 1020
QY 1021 GAAAGCTCCAAAGCCGCTTGTGAAACCCAGCTCTCTTCTCAGAGCTCTCGGAGCTCA 1080
Db 1021 GAAAGCTCCAAAGCCGCTTGTGAAACCCAGCTCTCTTCTCAGAGCTCTCGGAGCTCA 1080
QY 1081 CGCTCTGGTTCTTCTCCTCACTCGCTTCCACAGCAAAATAGTGCTTCCAGAGCCAGCGGACA 1140
Db 1081 CGCTCTGGTTCTTCTCCTCACTCGCTTCCACAGCAAAATAGTGCTTCCAGAGCCAGCGGACA 1140
QY 1141 CTGTCAACTGAGCGAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCTAGTGGGG 1200
Db 1141 CTGTCAACTGAGCGAGCACCCAGCCAGGGCTGGCCACCCAGGCATACAGCTAGTGGGG 1200
QY 1201 CCAGAGGTGAGAGGTTCTGAACCAAAAGAGTCCACCATGTAAATCTGACCAAAAGCAGAA 1260
Db 1201 CCAGAGGTGAGAGGTTCTGAACCAAAAGAGTCCACCATGTAAATCTGACCAAAAGCAGAA 1260
QY 1261 ACCACACCCAGCATGATCCCGAGCAGAGAGAGCTTCCAAACCGGTCTGAAATTAACAATG 1320
Db 1261 ACCACACCCAGCATGATCCCGAGCAGAGAGAGCTTCCAAACCGGTCTGAAATTAACAATG 1320
QY 1321 GACTTGACTCCACGCTTTCTTAGAGTCAAGGCTTTGGACTCTTCTCGTCATTTGGAGC 1380
Db 1321 GACTTGACTCCACGCTTTCTTAGAGTCAAGGCTTTGGACTCTTCTCGTCATTTGGAGC 1380
QY 1381 TCAAGTCAACCGCCACACACACAGATGAGAGTCAATCTAAGTAGCAGTGTGAGCATTTGCACG 1440
Db 1381 TCAAGTCAACCGCCACACACACAGATGAGAGTCAATCTAAGTAGCAGTGTGAGCATTTGCACG 1440
QY 1441 GAAACAGATTTCAGATGAGCATTTTCTTATACAAATACCAAAACAAAGCAAAAGGATGTAAGCT 1500

Db 1441 GAAACAGATTTCAGATGAGCATTTTCTTATACAAATACCAAAACAAAGGATGTAAGCT 1500
QY 1501 GATTTCATCTGTAATAAGGCATCTTATTGTGTGCTTTTAGACCCAGAGTAAGGGAAGCAGGAG 1560
Db 1501 GATTTCATCTGTAATAAGGCATCTTATTGTGTGCTTTTAGACCCAGAGTAAGGGAAGCAGGAG 1560
QY 1561 TCCAAATCTATTGTGTGACAGGACCTGTGTGAGAAAGTTGGGGAAGAGTGTAGGTGAAT 1620
Db 1561 TCCAAATCTATTGTGTGACAGGACCTGTGTGAGAAAGTTGGGGAAGAGTGTAGGTGAAT 1620
QY 1621 ATACCTAAACCTTTTAATGTGGGATATTTGTATCAGTGTCTTGAATCACAATTTTCAAG 1680
Db 1621 ATACCTAAACCTTTTAATGTGGGATATTTGTATCAGTGTCTTGAATCACAATTTTCAAG 1680
QY 1681 AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTATTGGATTAATTA 1740
Db 1681 AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTATTGGATTAATTA 1740
QY 1741 GTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG 1800
Db 1741 GTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTACTG 1800
QY 1801 AGCTAAACCACTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTTCTGACTTAAC 1860
Db 1801 AGCTAAACCACTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTTCTGACTTAAC 1860
QY 1861 TTCAATTTGTCTAATAGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGAGATGGA 1920
Db 1861 TTCAATTTGTCTAATAGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGAGATGGA 1920
QY 1921 GAAAGTGAATGAGTTTCTCCACTATATCAATCTCACTATTTGTATTTGAGCCCAAAA 1980
Db 1921 GAAAGTGAATGAGTTTCTCCACTATATCAATCTCACTATTTGTATTTGAGCCCAAAA 1980
QY 1981 TAACTATGAAGGAGACAAATAATTTGACAAAAGATTTGACAAAGGATTTGAGAGCTTTCAT 2040
Db 1981 TAACTATGAAGGAGACAAATAATTTGACAAAAGATTTGACAAAGGATTTGAGAGCTTTCAT 2040
QY 2041 GATGTTATGAGGATTTGTGACAAACATTAAGAAATATATAATGGAGCAATTTGGATTTCC 2100
Db 2041 GATGTTATGAGGATTTGTGACAAACATTAAGAAATATATAATGGAGCAATTTGGATTTCC 2100
QY 2101 CCTCAAAATCAGATCCCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACA 2160
Db 2101 CCTCAAAATCAGATCCCTTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAATACA 2160
QY 2161 ACATGTCAATTTATCAACGCTCTTAGAAGAAATTTCTTAGAAGAAAGGATCTTAGGAAT 2220
Db 2161 ACATGTCAATTTATCAACGCTCTTAGAAGAAATTTCTTAGAAGAAAGGATCTTAGGAAT 2220
QY 2221 GCTGAAAGATTACCAACATACCATTAAGTCTCTTCTTCTGAGAAAATGTGAAACCCAG 2280
Db 2221 GCTGAAAGATTACCAACATACCATTAAGTCTCTTCTTCTGAGAAAATGTGAAACCCAG 2280
QY 2281 AATTGCAAGACTGGGTGGACTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA 2340
Db 2281 AATTGCAAGACTGGGTGGACTAGAAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAA 2340
QY 2341 GGAAGGTAGCCGGCATGTCAGGACCTGTAGGAAAATCCAGCAGGTGGAGTTGCA 2400
Db 2341 GGAAGGTAGCCGGCATGTCAGGACCTGTAGGAAAATCCAGCAGGTGGAGTTGCA 2400
QY 2401 GTGAGCCGAGATTATGCGATTGCACTCCAGCTGGGTGACAGAGCGGACTCCGCTCTC 2458
Db 2401 GTGAGCCGAGATTATGCGATTGCACTCCAGCTGGGTGACAGAGCGGACTCCGCTCTC 2458

RESULT 13
AK026068
LOCUS AK026068 2627 bp mRNA linear
DEFINITION Homo sapiens cDNA: FLJ22415 fis, clone HRC08561.
ACCESSION AK026068

Wed May 11 07:24:22 2005

VERSION	AK026068.1	GI:10438796	Db	393	GGGACTCACCTGAGATCAAGAGAGTGGCAGAGAGGAAAGGTCACTTTGGCCCTGCCACCAT	452
KEYWORDS	oligo capping; fis (full insert sequence).		Qy	301	CAACTGGGGCTTCAGAAAAAGACACCTCTGGATATTCAATGGCTGCTCACCGATAATGAA	360
SOURCE	Homo sapiens (human)		Db	453	CAACTGGGGCTTCAGAAAAAGACACCTCTGGATATTCAATGGCTGCTCACCGATAATGAA	512
ORGANISM	Homo sapiens		Qy	361	GGGACCAAAAGTGGTGTATCACTTACTTCCAGTGGTGTATCTTCAATAAATCTGACTGAG	420
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Db	513	GGGACCAAAAGTGGTGTATCACTTACTTCCAGTGGTGTATCTTCAATAAATCTGACTGAG	572
AUTHORS	1 Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.		Qy	421	GAACAGAGAGGGCCGAGTGGCTTTGCTTCCAAATTTCTGGCAGAGATGCTCTCTTGCG	480
TITLE	NEDO human cDNA sequencing project		Db	573	GAACAGAGAGGGCCGAGTGGCTTTGCTTCCAAATTTCTGGCAGAGATGCTCTCTTGCG	632
JOURNAL	Unpublished		Qy	481	ATTGAACCTCTGAAGCCCGAGTGGTGTATCACTTCTGAAGGTTTAAAGATTCAGGG	540
AUTHORS	2 (bases 1 to 2627) Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.		Db	633	ATTGAACCTCTGAAGCCCGAGTGGTGTATCACTTCTGAAGGTTTAAAGATTCAGGG	692
TITLE	Direct Submission		Qy	541	CGCTAGCTGGAGCCATGTCTTAAAGTCTTGTAGTGAACCATCCAGCCCAAGTGT	600
JOURNAL	Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fldcna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)		Db	693	CGCTAGCTGGAGCCATGTCTTAAAGTCTTGTAGTGAACCATCCAGCCCAAGTGT	752
COMMENT	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).		Qy	601	GAGTTGGAAGGAGCTGTACAGAGAGTGTACCTGACTTTTGCAGTGTGAGTCACTCTCT	660
FEATURES	Location/Qualifiers		Db	753	GAGTTGGAAGGAGCTGTACAGAGAGTGTACCTGACTTTTGCAGTGTGAGTCACTCTCT	812
source	1. :2627	/organism="Homo sapiens"	Qy	661	GGCAGAGAGCCATGTCTTAAAGTCTTGTAGTGAACCATCCAGCCCAAGTGT	720
	/mol_type="mRNA"	/db_xref="taxon:9606"	Db	813	GGCAGAGAGCCATGTCTTAAAGTCTTGTAGTGAACCATCCAGCCCAAGTGT	872
	/clone="HRC08561"	/cell_type="primary human renal epithelial cells"	Qy	721	CGTCTGCTCCAAATCTAGGATTTGACTAACCCCTGGACGAGTCTTCTGTCGAGAT	780
	/clone_lib="HRC"	/notes="cloning vector pME18SFL3"	Db	873	CGTCTGCTCCAAATCTAGGATTTGACTAACCCCTGGACGAGTCTTCTGTCGAGAT	932
	342..1463	/notes="unnamed protein product"	Qy	781	CTTACCAGTCTTACTCTGGAGTGTACAGTGTACAGAGGCAACGAACTGGGAGGAA	840
CDS	/notes="cloning vector pME18SFL3"	/codon_start=1	Db	933	CTTACCAGTCTTACTCTGGAGTGTACAGTGTACAGAGGCAACGAACTGGGAGGAA	992
	/notes="unnamed protein product"	/db_xref="GI:10438797"	Qy	841	AGCTGTGTGGAGTAACTGTACAGTGTATGATGATGATGATGATGATGATGATGATGAT	900
	/protein_id="BAB15347.1"	/translation="MSLLLLLVSVYVGLTHTEIKRVAEKEVLPCHQLHGLPEK	Db	993	AGCTGTGTGGAGTAACTGTACAGTGTATGATGATGATGATGATGATGATGATGATGAT	1052
	/db_xref="GI:10438797"	DTLDIELFDNKGNSQKVIYTSRSVYNNLTEQKGRVAFASFLAGDASLQIPLK	Qy	901	GTGACAGCATAGTGGTGTGGAGCCCTGCTGATTTTCTCTTGTGTGGTGTCTTAATCCGA	960
	/translation="MSLLLLLVSVYVGLTHTEIKRVAEKEVLPCHQLHGLPEK	PSDEGRYTKVNSGRVSWHVLKLVKVRSPKCELEGLTEGSDLTLOQSSSGTE	Db	1053	GTGACAGCATAGTGGTGTGGAGCCCTGCTGATTTTCTCTTGTGTGGTGTCTTAATCCGA	1112
	PSDEGRYTKVNSGRVSWHVLKLVKVRSPKCELEGLTEGSDLTLOQSSSGTE	PVYVWQRIEKGEDERLPPKRIYDINHPFVLLQNLWMSYGLVQCTAGNEAKGES	Qy	961	AGGAAAGCAAAAGAAAGATATGAGGAAAGAGAGACCTAATGAAATTCAGAGAGATGCT	1020
	PVYVWQRIEKGEDERLPPKRIYDINHPFVLLQNLWMSYGLVQCTAGNEAKGES	CVRVTVQYQISGIMVAGATGIVAGALLIFLLVLLIRKKERYEERPEIRRED	Db	1113	AGGAAAGCAAAAGAAAGATATGAGGAAAGAGAGACCTAATGAAATTCAGAGAGATGCT	1172
	CVRVTVQYQISGIMVAGATGIVAGALLIFLLVLLIRKKERYEERPEIRRED	AEAPKARLVKPSRSSSSRSSTSTANSASQRTLTSTDAPOPLGATQAYS	Qy	1021	GAAGCTCCAAAGCCCGTCTTGTGAAACCCAGAGTCTCTTCTTCTCAGGCTCTCGGAGTCA	1080
	AEAPKARLVKPSRSSSSRSSTSTANSASQRTLTSTDAPOPLGATQAYS	LVGPEVRGSPKPVHNLTKAETTPSMIPSQSRAFTV"	Db	1173	GAAGCTCCAAAGCCCGTCTTGTGAAACCCAGAGTCTCTTCTTCTCAGGCTCTCGGAGTCA	1232
ORIGIN			Qy	1081	CGCTCTGGTCTTCTCTCACTCGCTTCCAGCAAAATAGTGTCTTCCAGCCAGCGGACA	1140
Query Match	99.7%; Score 2450; DB 9; Length 2627;		Db	1233	CGCTCTGGTCTTCTCTCACTCGCTTCCAGCAAAATAGTGTCTTCCAGCCAGCGGACA	1292
Best Local Similarity	99.8%; Pred. No. 0;		Qy	1141	CTGTCAATGACGACGACACCCAGCGGCTGGCCACCCAGGAGCATACAGCTTAGTGGGG	1200
Matches 2453; Conservative	0; Mismatches 5; Indels 0; Gaps 0;		Db	1293	CTGTCAATGACGACGACACCCAGCGGCTGGCCACCCAGGAGCATACAGCTTAGTGGGG	1352
1	CGCGCGGAGCCATCTGCCCCCAGGGGACCGGGCGGGCGGGCGGGCTCCCGCCCGGCAC	60	Qy	1201	CCAGAGGTGAGAGGTTCTGAACAAAAGTGTCCACCATGCTTCTGACCAAGAGCAAA	1260
153	CGCGCGGAGCCATCTGCCCCCAGGGGACCGGGCGGGCGGGCTCCCGCCCGGCAC	212	Db	1353	CCAGAGGTGAGAGGTTCTGAACAAAAGTGTCCACCATGCTTCTGACCAAGAGCAAA	1412
61	ATGGCTGAGCCACCTCGCGGCGACCCCGAGGCGCGGCGCCAGCTCGCCGAGGTCCTG	120	Qy	1261	ACCAACCCAGCATGATCCCGAGCCAGAGAGGCTTCCAAACCGGTCTGTAATCAATG	1320
213	ATGGCTGAGCCACCTCGCGGCGACCCCGAGGCGCGGCGCCAGCTCGCCGAGGTCCTG	272	Db	1413	ACCAACCCAGCATGATCCCGAGCCAGAGAGGCTTCCAAACCGGTCTGTAATCAATG	1472
121	CGGAGCG	180	Qy	1321	GACTTGACTCCCAACCGTCTTCTAGGAGTCAAGGTTCTTGGAGCTCTTCTGCTCAATGGAGC	1380
273	CGGAGCG	332	Db	1473	GACTTGACTCCCAACCGTCTTCTAGGAGTCAAGGTTCTTGGAGCTCTTCTGCTCAATGGAGC	1532
181	CGGATCGGAGTGCCT	240	Qy			
333	GGATCGGAGTGCCT	392	Db			
241	GGGACTCACCTGAGATCAAGAGAGTGGCAGAGAGGAAAGGTCACTTTGGCCCTGCCACCAT	300	Qy			

QY 1381 TCAAGTCAACGACCAACAACAGATGAGAGTCACTTAAGTAGCAGTGAAGCATTTGCACG 1440
Db |||||
QY 1533 TCAAGTCAACGACCAACAACAAGATGAGAGTCACTTAAGTAGCAGTGAAGCATTTGCACG 1592
Db |||||
QY 1441 GAACAGATTCAGATGAGCATTTTCCCTTATACAAATACCAACCAAGCAAGAAAGGATGAAGCT 1500
Db |||||
QY 1593 GAACAGATTCAGATGAGCATTTTCCCTTATACAAATACCAACCAAGCAAGAAAGGATGAAGCT 1652
QY 1501 GATTCATCTGTAAGAGGATCTTATTTGTCCTTTAGACCAAGTAAGGAAAGCAGAG 1560
Db |||||
QY 1653 GATTCATCTGTAAGAGGATCTTATTTGTCCTTTAGACCAAGTAAGGAAAGCAGAG 1712
QY 1561 TCCAAATCTATTTGTGACAGGACCTGTGTGAGAGGTTGGGAAAGGAGTGAAGTGAAT 1620
Db |||||
QY 1713 TCCAAATCTATTTGTGACAGGACCTGTGTGAGAGGTTGGGAAAGGAGTGAAGTGAAT 1772
QY 1621 ATACCTAAACCTTTAAATGTGGATATTTTGTATCAGTGCCTTTGATTCACATTTTCAAG 1680
Db |||||
QY 1773 ATACCTAAACCTTTAAATGTGGATATTTTGTATCAGTGCCTTTGATTCACATTTTCAAG 1832
QY 1681 AGGAATGGATGCTGTGTTGTAATTTTCTATGCAATTTCTGCAAACTTATTGGATATTA 1740
Db |||||
QY 1833 AGGAATGGATGCTGTGTTGTAATTTTCTATGCAATTTCTGCAAACTTATTGGATATTA 1892
QY 1741 GTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACTGTCTACACCATGACTG 1800
Db |||||
QY 1893 GTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACTGTCTACACCATGACTG 1952
QY 1801 AGCTAACCACTTCTAAGAACTCCAAAAAGAAACATGTGTCTTCTATTCTGACTTAAC 1860
Db |||||
QY 1953 AGCTAACCACTTCTAAGAACTCCAAAAAGAAACATGTGTCTTCTATTCTGACTTAAC 2012
QY 1861 TTCAATTTGTCTAAGGTTGGATATTAATTTCAAGGAGTTGAAATAGTGGAGATGA 1920
Db |||||
QY 2013 TTCAATTTGTCTAAGGTTGGATATTAATTTCAAGGAGTTGAAATAGTGGAGATGA 2072
QY 1921 GAAGAGTGAATGAGTTTCTCCACTCTATCTACTTCTCACTATTTGTATGAGGCCAAAA 1980
Db |||||
QY 2073 GAAGAGTGAATGAGTTTCTCCACTCTATCTACTTCTCACTATTTGTATGAGGCCAAAA 2132
QY 1981 TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTTGTGAAGGACTTTCATCTTCAT 2040
Db |||||
QY 2133 TAACTATGAAGGAGACAAAAATTTGTGACAAAGGATTTGTGAAGGACTTTCATCTTCAT 2192
QY 2041 GATGTTATGAGGATTTGTGACAAACATTTAGAAATATATAATGAGCAATTTGTGATTTCC 2100
Db |||||
QY 2193 GATGTTATGAGGATTTGTGACAAACATTTAGAAATATATAATGAGCAATTTGTGATTTCC 2252
QY 2101 CCTCAAAATCAGATGCTCTAAGGACTTTTCTGCTAGATATTTCTGGAAGGAGAAATACA 2160
Db |||||
QY 2253 CCTCAAAATCAGATGCTCTAAGGACTTTTCTGCTAGATATTTCTGGAAGGAGAAATACA 2312
QY 2161 ACATGTCATTTATCAACGTCCTTAGAAAGATTTCTTAGAGAAAGGATCTAGGAAT 2220
Db |||||
QY 2313 ACATGTCATTTATCAACGTCCTTAGAAAGATTTCTTAGAGAAAGGATCTAGGAAT 2372
QY 2221 GCTGAAAGATTAACCAACATACCATTTATAGTCTCTTCTTCTGAGAAATGTGAACACAG 2280
Db |||||
QY 2373 GCTGAAAGATTAACCAACATACCATTTATAGTCTCTTCTTCTGAGAAATGTGAACACAG 2432
QY 2281 AATTGCAAGATCGGTGGATAGAAAGGAGATTTAGATCAGTTTCTCTTAATATGTCAA 2340
Db |||||
QY 2433 AATTGCAAGATCGGTGGATAGAAAGGAGATTTAGATCAGTTTCTCTTAATATGTCAA 2492
QY 2341 GGAAGGTACCGGGGATCGGTGACAGGACCTGTAGAGAAATTCACAGAGGTGAGGTTGCA 2400
Db |||||
QY 2493 GGAAGGTACCGGGGATCGGTGACAGGACCTGTAGAGAAATTCACAGAGGTGAGGTTGCA 2552
QY 2401 GTGAGCCGAGATTATGCCATTTGCACTCCAGCTGGGTGACAGAGGAGGACTCCGCTC 2458
Db |||||
QY 2553 GTGAGCCGAGATTATGCCATTTGCACTCCAGCTGGGTGACAGAGGAGGACTCCATCTC 2610
Db |||||

RESULT 14
CQ802458
LOCUS CQ802458 5120 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 1 from Patent EP1416279.
ACCESSION CQ802458
VERSION CQ802458.1 GI:47109435
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Buchholz, M., Gress, T., Loesch, S. and Weidle, U.
TITLE Methods for diagnosis and therapy of pancreatic cancer and
composition useful therein
JOURNAL Patent: EP 1416279-A 1 06-MAY-2004;
F. HOFMANN-LA ROCHE AG (CH)
FEATURES
source Location/Qualifiers
1..5120
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
366..1487
/note="unnamed protein product"
/codon_start=1
/protein_id="CAG28887.1"
/db_xref="GI:47109436"
/translation="MSLLLLLVSYVYVGLTHTTEIKRVAEEKVTLPCRHOLGLPEK
DTLDIEWLLDNEGNQKVITYSSRRHYNNLTTEQKGRVAFNSPLAGDASLOIEPLK
PSDEGRYTKRKNESGRVSHVILKVLPRSPKCELEGELTEGSDLTQCESGSGTE
PIVYVYRIEKEGEDERLPKIDYNHPGRVLLQNLMTSYGLYQTAGNEAKGES
CVAVTVQYVQSIGWAGAVTGI VAGALLIFLLVLLIRRKDKERYEEEPNREIRD
AEAPKALVLPSSSSSGSRSSRSTSTFANSASRSORTLSTDAAPQPLGATQAYS
LVGFEVRSBPVKVHNLTKAETTPSMIPQSRAFQTV"
ORIGIN
Query Match 99.6%; Score 2448.4; DB 6; Length 5120;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2452; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CGCGCGGAGGCCCATCTGCCCCCAGGGGCGACGGGGCGGGCGGGTCCCGCCCGGCAC 60
Db 177 CGCGCGGAGGCCCATCTGCCCCCAGGGGCGACGGGGCGGGCGGGTCCCGCCCGGCAC 236
QY 61 ATGCTGCGAGCACCTCGCGGCGACCCCGAGCGCGCGCCAGCTCGCCCGAGGTCGGT 120
Db 237 ATGCTGCGAGCACCTCGCGGCGACCCCGAGCGCGCGCCAGCTCGCCCGAGGTCGGT 296
QY 121 CGGAGGCGCGCGCGCGCGCGCGCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCG 180
Db 297 CGGAGGCGCGCGCGCGCGCGCGCAAGCAGCAGCTGAGCGGGGAAGCGCCCGCGTCCG 356
QY 181 GGGATCGGGATGTCCT 240
Db 357 GGGATCGGGATGTCCT 416
QY 241 GGGACTCACACTGAGATCAAGAGAGTGCAGAGAAAGGTCACCTTCCCTGCCACCAT 300
Db 417 GGGACTCACACTGAGATCAAGAGAGTGCAGAGAAAGGTCACCTTCCCTGCCACCAT 476
QY 301 CAACTGGGGCTTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATTAATGA 360
Db 477 CAACTGGGGCTTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATTAATGA 536
QY 361 GGGAAACCAAAAGTGGTGAATCACTTACTCAGTGTCTATGTCTACAAATTAATGCTGAG 420
Db 537 GGGAAACCAAAAGTGGTGAATCACTTACTCAGTGTCTATGTCTACAAATTAATGCTGAG 596
QY 421 GAACAGAGGCGCGGAGTGGCTTTGCTTCCAAATTTCTTGGCAGGAGATGCTCTCTTGCAG 480
Db 597 GAACAGAGGCGCGGAGTGGCTTTGCTTCCAAATTTCTTGGCAGGAGATGCTCTCTTGCAG 656

481 ATTGAACTCTGAAGCCAGTGTAGGGCCGGTACACCTGTAGGTTAAGAAATTCAGGG 540
Db
657 ATTGAACCTCTGAAGCCAGTGTAGGGCCGGTACACCTGTAGGTTAAGAAATTCAGGG 716
Qy
541 CGCTACGTGTGAGCCATGTCTATCTTAAAGTCTTGTAGTGACCATCCAGGCCCAAGTGT 600
Db
717 CGCTACGTGTGAGCCATGTCTATCTTAAAGTCTTGTAGTGACCATCCAGGCCCAAGTGT 776
Qy
601 GAGTTGGAAGGAGAGCTGACAGAAAGGAAGTGCCTGACTTTGGAGTGTGAGTCACTCTCT 660
Db
777 GAGTTGGAAGGAGAGCTGACAGAAAGGAAGTGCCTGACTTTGGAGTGTGAGTCACTCTCT 836
Qy
661 GGCACAGAGCCCATGTGTATCTGCGAGCGAATCCGAGAGAAAGAGGAGAGATGAA 720
Db
837 GGCACAGAGCCCATGTGTATCTGCGAGCGAATCCGAGAGAAAGAGGAGAGATGAA 896
Qy
721 CGTCTGCTCCCAATCTAGGATTGACTCAACACCACTCGGACGAGTTCTGCTCCAGAA 780
Db
897 CGTCTGCTCCCAATCTAGGATTGACTCAACACCACTCGGACGAGTTCTGCTCCAGAA 956
Qy
781 CTTACCATGTCTTCTGAGTGTACAGTGTGACAGAGCAACGAGCTGGGAAGGA 840
Db
957 CTTACCATGTCTTCTGAGTGTACAGTGTGACAGAGCAACGAGCTGGGAAGGA 1016
Qy
841 AGCTGTGTGCGAGTAACTGTACAGTATGTACAAAGCATCGGATGTTGCGAGGACA 900
Db
1017 AGCTGTGTGCGAGTAACTGTACAGTATGTACAAAGCATCGGATGTTGCGAGGACA 1076
Qy
901 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTTGGTGTGGCTCTAATCCGA 960
Db
1077 GTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTTGGTGTGGCTCTAATCCGA 1136
Qy
961 AGGAAGCAAGAAAGATATGAGAGAGAGAGACCTAATGAATTCGAGAGATGCT 1020
Db
1137 AGGAAGCAAGAAAGATATGAGAGAGAGAGACCTAATGAATTCGAGAGATGCT 1196
Qy
1021 GAAGCTCCAAAGCCGCTCTGTGAAACCCAGCTCTCTTCTCTCAAGGCTCTCGGAGCTCA 1080
Db
1197 GAAGCTCCAAAGCCGCTCTGTGAAACCCAGCTCTCTTCTCTCAAGGCTCTCGGAGCTCA 1256
Qy
1081 CGCTCTGGTCTTCTTCCACTCGCTCCAGCAAGATAGTGCCTCAGCAGCCAGCGGACA 1140
Db
1257 CGCTCTGGTCTTCTTCCACTCGCTCCAGCAAGATAGTGCCTCAGCAGCCAGCGGACA 1316
Qy
1141 CTGTCAACTGACGACGACCCAGCAGGCTGGCCACCAGGCATACAGCCTAGTGGGG 1200
Db
1317 CTGTCAACTGACGACGACCCAGCAGGCTGGCCACCAGGCATACAGCCTAGTGGGG 1376
Qy
1201 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAGACAGAA 1260
Db
1377 CCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAGACAGAA 1436
Qy
1261 ACCACACCCAGCATGATGCCAGCAGCAGAGAGCCCTCCAAACGGTCTGAATTAACAATG 1320
Db
1437 ACCACACCCAGCATGATGCCAGCAGCAGAGAGCCCTCCAAACGGTCTGAATTAACAATG 1496
Qy
1321 GACTTGACTCCCAAGCTCTTCTTAGGATCAGGGTCTTTGGACTCTTCTCTCATTTGGAGC 1380
Db
1497 GACTTGACTCCCAAGCTCTTCTTAGGATCAGGGTCTTTGGACTCTTCTCTCATTTGGAGC 1556
Qy
1381 TCAAGTCAACAGCACAACACCATGAGAGGTCAATCTAAGTAGCAGTGTGAGCAATTCGACG 1440
Db
1557 TCAAGTCAACAGCACAACACCATGAGAGGTCAATCTAAGTAGCAGTGTGAGCAATTCGACG 1616
Qy
1441 GAACAGATTGAGATGAGATTTCTTATACATACCAACAGCAAGCAAGGATGTAAGCT 1500
Db
1617 GAACAGATTGAGATGAGATTTCTTATACATACCAACAGCAAGCAAGGATGTAAGCT 1676
Qy
1501 GATTTCATCTGTAAGAGGCATCTTATTTGTCCTTTTAGACAGAGTAAGGAAAGCAGGAG 1560
Db
1677 GATTTCATCTGTAAGAGGCATCTTATTTGTCCTTTAGACAGAGTAAGGAAAGCAGGAG 1736
Qy
1561 TCCAAATCTATTTGTTGACACAGGACCTGTGTGAGAAAGTTGGGGAAAGGTGAGGTGAAT 1620

1737 TCCAAATCTATTTGTTGACACGAGCCGTGTGGTGAGAAAGTTGGGGAAAGGTGAGGTGAAT 1796
Qy
1621 ATACCTTAAACATTTTAATCTGGGATATTTTGTATCAGTCTTGTATTCAAAATTTTCAAG 1680
Db
1797 ATACCTTAAACATTTTAATCTGGGATATTTTGTATCAGTCTTGTATTCAAAATTTTCAAG 1856
Qy
1681 AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTTGATGATTTA 1740
Db
1857 AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTTGATGATTTA 1916
Qy
1741 GTTATTTAGACAGTCAAGCAGAAACCCACAGCCTTATTAACCTGTCTACACCATGTACTG 1800
Db
1917 GTTATTTAGACAGTCAAGCAGAAACCCACAGCCTTATTAACCTGTCTACACCATGTACTG 1976
Qy
1801 AGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTTATTTCTGACTTAAC 1860
Db
1977 AGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTTATTTCTGACTTAAC 2036
Qy
1861 TTTCAATTTGTATAGGTTTGGATATTTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA 1920
Db
2037 TTTCAATTTGTATAGGTTTGGATATTTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGA 2096
Qy
1921 GAAGAGTGAATGAGTTTCTCCCACTCTTACTAATCTCACTATTTGTATTGAGCCCAAAA 1980
Db
2097 GAAGAGTGAATGAGTTTCTCCCACTCTTACTAATCTCACTATTTGTATTGAGCCCAAAA 2156
Qy
1981 TAACTATGAAGAGAGACAAAAATTTGTGACAAAGGATTTGTGAAGAGCTTTCCATCTTCAT 2040
Db
2157 TAACTATGAAGAGAGACAAAAATTTGTGACAAAGGATTTGTGAAGAGCTTTCCATCTTCAT 2216
Qy
2041 GATGTTATAGGATTTGTGACAAACATTAATAATATAATAGGAGCAATTTGTGGATTTCC 2100
Db
2217 GATGTTATAGGATTTGTGACAAACATTAATAATATAATAGGAGCAATTTGTGGATTTCC 2276
Qy
2101 CCTCAATCAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGAGAGAAATATACA 2160
Db
2277 CCTCAATCAGATGCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGAGAGAAATATACA 2336
Qy
2161 ACATGTCATTTATCAACGCTCTTAGAAGAAATTTCTTAGAGAAAAAGGATCTAGGAAT 2220
Db
2337 ACATGTCATTTATCAACGCTCTTAGAAGAAATTTCTTAGAGAAAAAGGATCTAGGAAT 2396
Qy
2221 GCTGAAAGATTAACCAACATACCAATTAATAGTCTTCTTCTGAGAAAAATGTGAAACAG 2280
Db
2397 GCTGAAAGATTAACCAACATACCAATTAATAGTCTTCTTCTGAGAAAAATGTGAAACAG 2456
Qy
2281 AATTGCAAGACTGGGTGCACTAGAAAAAGGAGATTAGATCAAGTTTCTTCTTAATATGTCAA 2340
Db
2457 AATTGCAAGACTGGGTGCACTAGAAAAAGGAGATTAGATCAAGTTTCTTCTTAATATGTCAA 2516
Qy
2341 GGAAAGTAGCCGGCATGGTGCCAGGCACTGTAGGAAAAATCCAGCAGGTGGAGGTTGCA 2400
Db
2517 GGAAAGTAGCCGGCATGGTGCCAGGCACTGTAGGAAAAATCCAGCAGGTGGAGGTTGCA 2576
Qy
2401 GTGAGCCGAGATTAATGCCATTTGCACTCCAGCTGGGTGACAGAGGGGACTCCGCTCTC 2458
Db
2577 GTGAGCCGAGATTAATGCCATTTGCACTCCAGCTGGGTGACAGAGGGGACTCCATCTC 2634

RESULT 15

BC009371

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

BC009371 2298 bp mRNA linear PRI 29-JUN-2004
Homo sapiens adipocyte-specific adhesion molecule, mRNA (cDNA clone
MGC:14901 IMAGE:4122648), complete cds.

BC009371

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2298)

Wed May 11 07:24:22 2005

1921 CCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAATA 1980
2159 CAACATGTCTATTTATCAACGCTCTTAGAAGAAATTTCTTCTAGAGAAAAGGGATCTAGGA 2218
1981 CAACATGTCTATTTATCAACGCTCTTAGAAGAAATTTCTTCTAGAGAAAAGGGATCTAGGA 2040
2219 ATGCTGAAAGATTTACCCAAACATACCATTTATAGTCTCTTCTTCTGAGAAAATGTGAACC 2278
2041 ATGCTGAAAGATTTACCCAAACATACCATTTATAGTCTCTTCTTCTGAGAAAATGTGAACC 2100
2279 AGAATTGCAAGACTGGGTGGA CTAGAAAAGGAGATTTAGATCAGTTTCTTCTTAAATATGTC 2338
2101 AGAATTGCAAGACTGGGTGGA CTAGAAAAGGAGATTTAGATCAGTTTCTTCTTAAATATGTC 2160
2339 AAGGAAGGTAGCCGGGCATGCTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGTTG 2398
2161 AAGGAAGGTAGCCGGGCATGCTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGTTG 2220
2399 CAGTGAGCCGAGATTTATGCGCATTTGCGACTCCAGCCTGGGTGACAGAGCGGACTCCGCTCTC 2458
2221 CAGTGAGCCAAAGATTTATGCCATTTGCACTCCAGCCTGGGTGACAGAGCGGACTCCATCTC 2280

Search completed: May 6, 2005, 07:09:31
Job time : 10415 secs

841 CTGAAGCTCCAAAAGCCGCTTGTGAACCCAGCTCTCTTCTCCTCAGGCTCTCGGAGCT 900
1079 CACGCTCTGGTCTTCTCCACCTCGCTCCACAGCAATAGTGCCTCAGCAGCCAGCGGA 1138
901 CACGCTCTGGTCTTCTCCTCCACTCGCTCCACAGCAATAGTGCCTCAGCAGCCAGCGGA 960
1139 CACTGTCAACTGAGCAGCAGCAGCCAGCAGGCTGGCCACCCAGGATACAGCCTAGTGG 1198
961 CACTGTCAACTGAGCAGCAGCAGCCAGCAGGCTGGCCACCCAGGATACAGCCTAGTGG 1020
1199 GGCAGAGGTGAGAGTTCTGAA CCAAGAAAGTCCACCATGCTAATCTTGACCAAGCAG 1258
1021 GGCAGAGGTGAGAGTTCTGAA CCAAGAAAGTCCACCATGCTAATCTTGACCAAGCAG 1080
1259 AAACCAACCCAGCAGATGATCCAGCAGCAGCAGAGCCTTCCAAACGGTCTGAATTACAA 1318
1081 AAACCAACCCAGCAGATGATCCAGCAGCAGCAGAGCCTTCCAAACGGTCTGAATTACAA 1140
1319 TGGACTTGACTCCACGCTTCTTAGAGAGTCAGGCTCTTGGACTCTTCTCGTCAATTGGA 1378
1141 TGGACTTGACTCCACGCTTCTTAGAGAGTCAGGCTCTTGGACTCTTCTCGTCAATTGGA 1200
1379 GCTCAAGTCAACAGCAGCAGCAGCAGATCAGAGGTCACTAAGTAGCAGTCAAGTTCGA 1438
1201 GCTCAAGTCAACAGCAGCAGCAGCAGCAGATCAGAGGTCACTAAGTAGCAGTCAAGTTCGA 1260
1439 CGGAACAGATTCAGATGAGCATTTCTTATACATACCAACAGCAAGCAAGAGGTGAAG 1498
1261 CGGAACAGATTCAGATGAGCATTTCTTATACATACCAACAGCAAGCAAGAGGTGAAG 1320
1499 CTGATTCATCTGTAAAAGGCATCTTATTTGTGCTTTTAGACCAGAGTAGGGAAGCAGG 1558
1321 CTGATTCATCTGTAAAAGGCATCTTATTTGTGCTTTTAGACCAGAGTAGGGAAGCAGG 1380
1559 AGTCCAAATCTATTTGTGACAGGACCTGTGTGAGAGGTTGGGGAAGGTGAGGTGA 1618
1381 AGTCCAAATCTATTTGTGACAGGACCTGTGTGAGAGGTTGGGGAAGGTGAGGTGA 1440
1619 ATATACCTTAAACCTTTTAAATGCTGGATATTTGTATCAGTGCCTTCAATTCACATTTCA 1678
1441 ATATACCTTAAACCTTTTAAATGCTGGATATTTGTATCAGTGCCTTCAATTCACATTTCA 1500
1679 AGAGGAAATGGGATGCTGTTGTAAAATTTCTGCAATTTCTGCAATTTATTTGATAT 1738
1501 AGAGGAAATGGGATGCTGTTGTAAAATTTCTGCAATTTCTGCAATTTATTTGATAT 1560
1739 TAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTTACCTGTCTACCATGTAC 1798
1561 TAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTTACCTGTCTACCATGTAC 1620
1799 TGAGCTAACCACTTCTAAGAAAATCCAAAGGAAACATGCTGCTTCTTCTGACTTA 1858
1621 TGAGCTAACCACTTCTAAGAAAATCCAAAGGAAACATGCTGCTTCTTCTGACTTA 1680
1859 ACTTCATTTGCTATAGGTTTGGATATTAATTTCAAGGGAGTTGAAAATAGTGGAGATG 1918
1681 ACTTCATTTGCTATAGGTTTGGATATTAATTTCAAGGGAGTTGAAAATAGTGGAGATG 1740
1919 GAGAAAGATCAATGAGTTTCTCCACTCTATATCTCACTATTTCTGATTTGAGCCCAA 1978
1741 GAGAAAGATCAATGAGTTTCTCCACTCTATATCTCACTATTTCTGATTTGAGCCCAA 1800
1979 AATAACTATGAAGGAGCAGCAAAAATTTGTGACAAAGGATTTGCAAGAGCTTTCCATCTTC 2038
1801 AATAACTATGAAGGAGCAGCAAAAATTTGTGACAAAGGATTTGCAAGAGCTTTCCATCTTC 1860
2039 ATGATGTTATGAGGATTTGTCACAAACATTAGAAAATATATATGAGCAATTTGATGAT 2098
1861 ATGATGTTATGAGGATTTGTCACAAACATTAGAAAATATATATGAGCAATTTGATGAT 1920
2099 CCCCTCAAATCAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAATA 2158

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2005, 22:30:03 ; Search time 7133 Seconds
(without alignments)
13116.778 Million cell updates/sec

Title: US-09-978-544A-58

Perfect score: 2458

Sequence: 1 gcgcgggagccatctgcc.....acagagcgggactcgtctc 2458

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1792.4	72.9	1892	3	CRG22259 full-length
2	1134.4	46.2	2931	3	AK033723 Mus muscu
3	1126.4	45.8	4017	3	AK028983 Mus muscu
4	1020.2	41.5	1945	3	AK080481 Mus muscu
5	977.6	39.8	1162	5	BX395411 BX395411
6	894	36.4	1036	9	AY406755 Homo sapi
7	806.4	32.8	979	5	BX334131 BX334131
8	741.4	30.2	758	5	BU621985 UI-H-FH1-
9	731	29.7	732	5	BX113005 BX113005
10	708.2	28.8	1039	9	AY406757 Mus muscu
11	699.8	28.5	719	5	BQ008520 UI-H-EOL-
12	686.8	27.9	706	6	CB265996 1004901 H
13	683.6	27.8	820	1	AL598458 DKF2p313H
14	679.8	27.7	716	2	AW963657 EST375730
15	677.6	27.6	737	4	BM680006 UI-B-EOL-
16	664.2	27.0	673	7	CV028233 6696 Full
17	636	25.9	662	5	BQ010255 UI-H-EOL-
18	634	25.8	658	4	BM728789 UI-B-EOL-
19	631.6	25.7	653	7	CK003476 AGENCOURT
20	618	25.1	948	5	BUI149052 AGENCOURT
21	609.2	24.8	925	9	AY406756 Pan trogl
22	604.8	24.6	608	5	BX475999 DKF2p686L
23	603.4	24.5	606	8	AQ380425 RPC111-15
24	595.2	24.2	627	4	BI254835 602974095

25	594.8	24.2	870	2	BF304909
26	593.2	24.1	874	5	BQ437365 AGENCOURT
27	582.4	23.7	584	5	BP291711 BP291711
28	581.2	23.6	592	4	BM683516 UI-B-EOL-
29	579	23.6	621	4	BM723837 UI-B-EOL-
30	571	23.2	583	5	BP328793 BP328793
31	568.4	23.1	781	7	CK365261 AGENCOURT
32	561.4	22.8	586	4	BI259594 602968364
33	559	22.7	776	7	CN455933 UI-M-HNO-
34	557	22.7	980	5	BU520401 AGENCOURT
35	555.8	22.6	573	2	BF056275 7k03e06.x
36	554	22.5	554	6	CB141641 K-EST0195
37	548.2	22.3	668	2	BE272669 601105042
38	545.8	22.2	569	5	BP206251 BP206251
39	543.6	22.1	688	6	CAS13515 UI-R-FJO-
40	525.8	21.4	530	2	BF592856 7j95e06.x
41	510	20.7	599	6	CA395814 c969e08.y
42	506	20.6	1074	6	CA978231 AGENCOURT
43	502	20.4	991	4	BG254336 602368894
44	489.4	19.9	516	5	BU742705 UI-B-EOL-
45	488	19.9	501	5	BX484121 DKF2p686G
46	472.4	19.2	483	2	AW614786 hh40g10.x
47	465.6	18.9	553	2	AW385555 RC3-LT002
48	464.6	18.9	489	5	BU740253 UI-B-EOL-
49	453	18.4	556	2	AW161204 au79g08.y
50	452.4	18.4	502	2	BE291115 PMO-GN001
51	451.4	18.4	1049	4	BG173260 602336750
52	449.8	18.3	482	2	AW084936 xc65g08.x
53	446.4	18.2	812	2	BF106994 601824349
54	444.4	18.1	527	2	BE272517 601104854
55	441.2	17.9	779	7	CK364736 AGENCOURT
56	436	17.7	440	1	A1038014 ox29e06.x
57	433.2	17.6	667	4	BG723094 602690661
58	427	17.4	525	4	BM722786 UI-B-EOL-
59	424	17.2	576	5	BP255217 BP255217
60	422.2	17.2	435	1	A1720414 as81d10.x
61	418	17.0	532	4	BM718472 UI-B-EOL-
62	414	16.8	414	1	A1962508 wq41n01.x
63	410.4	16.7	633	6	CB123619 K-EST0172
64	409	16.6	413	1	A1091707 oo23h12.x
65	406.8	16.6	411	1	A1654893 wb52b06.x
66	406.2	16.5	641	7	C0649082 ILLUMIGEN
67	399.6	16.2	517	1	AA387226 vc21e09.r
68	390.4	15.9	1006	3	AK018527 Mus muscu
69	388.4	15.8	783	4	BI183873 UNL-P-FJO-
70	380.8	15.5	772	6	CAS13406 UI-R-FJO-
71	380	15.5	392	1	A1001922 ov23a07.s
72	374.6	15.2	483	1	A1021505 ub12f10.x
73	374	15.2	638	2	AW647243 EST325786
74	371.8	15.1	910	6	CA979507 AGENCOURT
75	349.4	14.2	352	1	A1656765 tt47f04.x
76	349	14.2	519	5	BX280758 BX280758
77	346.8	14.1	481	1	A1815701 au49g04.y
78	346.8	14.1	665	2	BB640218 BB640218
79	341.8	13.9	440	1	AA386948 vc23g09.r
80	340.6	13.9	800	7	CO402483 AGENCOURT
81	329.8	13.4	621	4	BG088526 H3154B11-
82	320.4	13.0	666	4	BM728708 UI-B-EJ0-
83	320	13.0	498	2	BF723456 mab31c09
84	314.2	12.8	691	5	BU328742 603495163
85	314	12.8	407	1	AA387234 vc23g09.r
86	313.8	12.8	595	1	AA386757 vcl17h05.r
87	308	12.5	332	1	AA318060 EST20256
88	306.2	12.5	400	1	AA387020 vc22d04.r
89	304.4	12.4	642	2	BB613387 BB613387
90	303.2	12.3	928	6	CA468113 AGENCOURT
91	298.6	12.1	426	5	BY354962 BY354962
92	296.2	12.1	328	1	AA373427 EST85507
93	295.8	12.0	603	1	AL697730 DKF2p686J
94	280.8	11.4	384	6	CB703066 AMGNNUC.T
95	280.4	11.4	288	1	AL701536 DKF2p686K
96	277.6	11.3	423	6	CB797124 AMGNNUC.S
97	276.6	11.3	932	6	BY720702 BY720702

Wed May 11 07:24:22 2005

98	269.4	11.0	916	2	BF382295	601815210	171	112	4.6	400	5	BY001911	BY001911
99	267.8	10.9	862	6	CB229958	AGENCOURT	172	111.8	4.5	701	4	BJ727044	BJ727044
100	267.4	10.9	545	6	CB611674	AMGNNUC:N	173	111.2	4.5	796	7	C0554492	AGENCOURT
101	264.6	10.8	359	6	BY770574	BY770574	174	109.4	4.5	825	6	CA512305	CA512305
102	263.2	10.7	356	5	BY132537	BY132537	175	107.2	4.4	412	6	CB801593	CB801593
103	252.2	10.3	334	3	CA208153	CA208153	176	105.8	4.3	146	5	BY355306	BY355306
104	245	10.0	351	6	CB780871	AMGNNUC:M	177	100.4	4.1	1116	6	CD511850	CD511850
105	242.8	9.9	257	6	CD706076	EST22603	178	100.8	4.1	414	6	CB801043	CB801043
106	234.4	9.5	608	2	BB637486	BB637486	179	99.2	4.0	399	6	CB706485	CB706485
107	232.2	9.4	724	6	CA506854	CA506854	180	95.2	3.9	519	2	BF719430	BF719430
108	229.2	9.0	349	5	BY141240	BY141240	181	92.8	3.8	461	6	CB737344	CB737344
109	220.8	9.0	341	9	CB5634631	CB5634631	182	90.8	3.7	781	2	BB619481	BB619481
110	220.6	9.0	110	3	BY2115052	BY2115052	183	90.8	3.7	794	5	HU380648	HU380648
111	210.4	8.6	825	5	BY354782	BY354782	184	90.2	3.7	797	7	CK1313816	CK1313816
112	209.4	8.5	292	5	BY148334	BY148334	185	89	3.6	796	7	CO914438	CO914438
113	208	8.5	296	5	AG2277718	AG2277718	186	88.6	3.6	597	7	BE6477336	BE6477336
114	208	8.5	449	4	AA207536	AA207536	187	86.6	3.5	757	7	CR437468	CR437468
115	201.8	8.2	254	1	AG075988	AG075988	188	86.4	3.5	515	5	BQ033849	BQ033849
116	201.4	8.2	674	4	BG075988	BG075988	189	85.6	3.5	512	4	BG228735	BG228735
117	200	8.1	600	4	CD763532	CD763532	190	84.8	3.4	432	2	BB689334	BB689334
118	199.8	8.1	717	6	CD763564	CD763564	191	84	3.4	561	2	BB619036	BB619036
119	199.8	8.1	429	4	BI338029	BI338029	192	83.2	3.4	943	2	BF121151	BF121151
120	198.8	8.1	429	4	CAW557819	CAW557819	193	80.8	3.3	522	8	AQ628854	AQ628854
121	198.2	8.1	650	2	BY355110	BY355110	194	80	3.3	705	7	CO804488	CO804488
122	197.6	8.0	264	5	BP426567	BP426567	195	80	3.3	927	2	BF120157	BF120157
123	194.8	7.9	278	5	AA781908	AA781908	196	77.4	3.1	435	2	BB690324	BB690324
124	185.4	7.7	380	1	BB250997	BB250997	197	77	3.1	889	7	CF585131	CF585131
125	185.4	7.5	623	2	BE863209	BE863209	198	75.8	3.1	370	6	CB425698	CB425698
126	183.2	7.5	311	2	BF524900	BF524900	199	75.4	3.1	404	5	BY296935	BY296935
127	182.2	7.4	421	2	BB569025	BB569025	200	75	3.1	825	7	CO810180	CO810180
128	177.6	7.2	273	2	BY355174	BY355174	201	74	3.0	509	8	AQ383377	AQ383377
129	175.8	7.2	235	5	CB587783	CB587783	202	72.4	2.9	780	7	CV104986	CV104986
130	174.6	7.1	747	6	BG094669	BG094669	203	72	2.9	107	2	BF919782	BF919782
131	170	6.9	541	4	BG115335	BG115335	204	72	2.9	414	1	AI852886	AI852886
132	168.8	6.9	637	4	CB433361	CB433361	205	71.6	2.9	396	9	CG572195	CG572195
133	167.6	6.8	568	6	CB460835	CB460835	206	71.6	2.9	496	2	BF566850	BF566850
134	167.6	6.8	686	6	CG550224	CG550224	207	71.6	2.9	532	8	AQ180796	AQ180796
135	165.2	6.7	270	9	CG550224	CG550224	208	71.6	2.9	513	9	CG588080	CG588080
136	163.6	6.7	242	5	AG160534	AG160534	209	71.6	2.9	648	9	AG180437	AG180437
137	160	6.5	854	9	AG160534	AG160534	210	71.6	2.9	683	6	BY749634	BY749634
138	159	6.5	597	8	CF585130	CF585130	211	71.6	2.9	716	6	BY749634	BY749634
139	158	6.4	992	7	BY354925	BY354925	212	71.6	2.9	799	7	CK841576	CK841576
140	155.8	6.3	199	5	BY713773	BY713773	213	71.6	2.9	822	3	AK089373	AK089373
141	153.4	6.2	637	6	BY713773	BY713773	214	71.2	2.9	487	9	CG661343	CG661343
142	152.2	6.2	895	7	CR441829	CR441829	215	71.2	2.9	533	9	CG634965	CG634965
143	147	6.0	454	2	BE645799	BE645799	216	70.8	2.9	548	6	CB178748	CB178748
144	147	6.0	456	1	AI125838	AI125838	217	70.8	2.9	511	8	AQ415751	AQ415751
145	147	6.0	490	5	BI834022	BI834022	218	70.8	2.9	597	4	BG680294	BG680294
146	147	6.0	534	4	BI834022	BI834022	219	70.6	2.9	658	7	CK004796	CK004796
147	146.4	6.0	879	5	BY739967	BY739967	220	70.4	2.9	154	2	BF919899	BF919899
148	146.2	5.9	841	7	CR433237	CR433237	221	70.4	2.9	205	2	AI707744	AI707744
149	146	5.9	465	1	AI620230	AI620230	222	70.4	2.9	322	1	AA634147	AA634147
150	145.2	5.9	638	6	CB459048	CB459048	223	70.4	2.9	340	1	AA634147	AA634147
151	145.2	5.9	880	7	CF378876	CF378876	224	70.2	2.9	520	9	CG645291	CG645291
152	143.8	5.9	469	1	AA923519	AA923519	225	70	2.8	193	2	AW050680	AW050680
153	141	5.7	834	5	BY739949	BY739949	226	69.6	2.8	423	2	BG685958	BG685958
154	138.2	5.6	596	6	CA506971	CA506971	227	69.6	2.8	910	4	BG533568	BG533568
155	138.2	5.6	831	5	BY739949	BY739949	228	69.4	2.8	183	8	AZ494567	AZ494567
156	134.2	5.5	574	7	CR437467	CR437467	229	69.4	2.8	235	1	AA077881	AA077881
157	134	5.5	690	5	BQ033848	BQ033848	230	69.2	2.8	369	8	AQ357543	AQ357543
158	134	5.5	735	9	AG605123	AG605123	231	69.2	2.8	462	1	AA548477	AA548477
159	129.8	5.3	272	2	BB577671	BB577671	232	69.2	2.8	553	8	AQ793624	AQ793624
160	128.2	5.2	864	5	BU115914	BU115914	233	69	2.8	740	6	CA308944	CA308944
161	127	5.2	772	4	BI833948	BI833948	234	68.8	2.8	166	5	BX500034	BX500034
162	126.8	5.2	899	3	AK033766	AK033766	235	68.8	2.8	204	8	AQ050965	AQ050965
163	126.8	5.2	672	5	BQ179203	BQ179203	236	68.8	2.8	294	2	BQ065600	BQ065600
164	126.6	5.2	723	5	BQ179203	BQ179203	237	68.8	2.8	318	5	BQ535892	BQ535892
165	126.6	5.2	434	6	CB433923	CB433923	238	68.8	2.8	373	4	BQ031344	BQ031344
166	126.4	5.1	600	6	CB433923	CB433923	239	68.8	2.8	397	8	BM873691	BM873691
167	124.4	5.0	634	2	BF406857	BF406857	240	68.8	2.8	404	8	AQ0596495	AQ0596495
168	124	5.0	634	2	BF406857	BF406857	241	68.8	2.8	421	5	BX952963	BX952963
169	121.8	4.9	707	7	CN529862	CN529862	242	68.8	2.8	430	8	AQ414005	AQ414005
170	119.4	4.9	402	4	BY001911	BY001911	243	68.8	2.8	435	1	AI460009	AI460009

244	68.8	2.8	443	8	AQ082191	AQ082191	RPC11-11-55	317	67.8	2.8	330	2	BF916935	BF916935	IL3-UT011
245	68.8	2.8	460	5	AQ537631	AQ537631	RPC1-11-3	318	67.8	2.8	379	4	BM692443	BM692443	UI-E-CK1-
246	68.8	2.8	461	5	BQ707757	BQ707757	AGENCOURT	319	67.8	2.8	393	1	AA452832	AA452832	xx3609.8
247	68.8	2.8	468	2	AW819485	AW819485	RC5-ST029	320	67.8	2.8	457	1	AI355414	AI355414	QC6004.x
248	68.8	2.8	481	2	BF800435	BF800435	PMO-CI004	321	67.8	2.8	471	7	T60156	T60156	YC2209.81
249	68.8	2.8	482	2	AQ554340	AQ554340	RPC1-11-4	322	67.8	2.8	478	1	AA827686	AA827686	od5605.8
250	68.8	2.8	521	2	AW089898	AW089898	xd13c11.x	323	67.8	2.8	487	6	CD722309	CD722309	o10806.y
251	68.8	2.8	533	7	CR557070	CR557070	DKFp459H	324	67.8	2.8	569	4	BM791176	BM791176	K-EST0071
252	68.8	2.8	546	5	BA482626	BA482626	DKFp686P	325	67.8	2.8	581	7	CN275405	CN275405	17000600
253	68.8	2.8	551	2	AW955841	AW955841	EST367911	326	67.8	2.8	660	8	AQ728131	AQ728131	HS 5457 B
254	68.8	2.8	562	8	AQ792364	AQ792364	HS 5255 B	327	67.8	2.8	698	9	AG162589	AG162589	Pan trogl
255	68.8	2.8	567	5	BA484525	BA484525	DKFp686G	328	67.8	2.8	831	9	AQ898815	AQ898815	HS 3130 A
256	68.8	2.8	572	5	BUS75115	BUS75115	AGENCOURT	329	67.6	2.8	839	1	AA098381	AA098381	mo08909.r
257	68.8	2.8	583	2	BE067790	BE067790	MR4-BT035	330	67.6	2.8	440	5	BA493466	BA493466	DKFp2781D
258	68.8	2.8	593	6	CA396069	CA396069	cs73f06.y	331	67.6	2.8	603	7	CM411917	CM411917	170005322
259	68.8	2.8	616	6	CB105625	CB105625	K-EST0130	332	67.4	2.7	185	1	AA229705	AA229705	rc35607.r
260	68.8	2.8	620	8	B72425	B72425	RPC111-8M22	333	67.4	2.7	302	6	CD236715	CD236715	FNPABF08
261	68.8	2.8	622	6	CB105935	CB105935	K-EST0135	334	67.4	2.7	339	1	AA508902	AA508902	rg90802.8
262	68.8	2.8	642	7	W26032	W26032	1998 Human	335	67.4	2.7	407	1	AL707526	AL707526	DKFp2686F
263	68.8	2.8	645	6	CB105892	CB105892	K-EST0135	336	67.4	2.7	424	2	BB687081	BB687081	BB687081
264	68.8	2.8	646	6	CB105609	CB105609	K-EST0130	337	67.4	2.7	444	1	AA229614	AA229614	rc35607.8
265	68.8	2.8	652	8	AQ197632	AQ197632	CIT-HSP-2	338	67.4	2.7	505	8	AQ050547	AQ050547	RPC1-11-3
266	68.8	2.8	663	9	AG135290	AG135290	Pan trogl	339	67.4	2.7	583	1	AI907878	AI907878	RC-BT155-
267	68.8	2.8	666	8	AQ039496	AQ039496	CIT-HSP-2	340	67.4	2.7	659	9	AG076908	AG076908	Pan trogl
268	68.8	2.8	668	7	CR541174	CR541174	DKFp459I	341	67.4	2.7	697	6	CD237763	CD237763	FNPAPC04
269	68.8	2.8	673	4	BM728941	BM728941	UI-E-E01-	342	67.4	2.7	1114	4	BA496410	BA496410	602538006
270	68.8	2.8	685	4	BI193100	BI193100	602947363	343	67.2	2.7	126	4	BA680909	BA680909	60262873
271	68.8	2.8	694	9	AG153290	AG153290	Pan trogl	344	67.2	2.7	191	5	BQ028390	BQ028390	UI-H-C00-
272	68.8	2.8	699	9	AG169710	AG169710	Pan trogl	345	67.2	2.7	194	7	CB360138	CB360138	170004706
273	68.8	2.8	723	9	AG144298	AG144298	Pan trogl	346	67.2	2.7	205	4	BQ223397	BQ223397	na776h04.
274	68.8	2.8	728	5	BUS85371	BUS85371	AGENCOURT	347	67.2	2.7	205	8	AQ229162	AQ229162	HS-2033.A
275	68.8	2.8	729	5	CD239732	CD239732	FNPBXH08	348	67.2	2.7	209	1	AA482273	AA482273	aa3605.8
276	68.8	2.8	729	9	AG144300	AG144300	Pan trogl	349	67.2	2.7	237	4	BF942997	BF942997	QV0-NN114
277	68.8	2.8	760	8	AF101697	AF101697	UI-E-E01-	350	67.2	2.7	243	5	BQ311431	BQ311431	QV4-BN026
278	68.8	2.8	813	4	BM040897	BM040897	603614593	351	67.2	2.7	245	7	H82306	H82306	yu79c05.r1
279	68.8	2.8	813	6	CD356377	CD356377	AGENCOURT	352	67.2	2.7	263	8	AQ543831	AQ543831	RPC1-11-3
280	68.8	2.8	824	6	CD245106	CD245106	AGENCOURT	353	67.2	2.7	283	1	AA664528	AA664528	nu67c11.8
281	68.8	2.8	917	5	BUS49275	BUS49275	AGENCOURT	354	67.2	2.7	310	5	BUS64518	BUS64518	AGENCOURT
282	68.8	2.8	1501	2	BF694757	BF694757	602080846	355	67.2	2.7	311	8	AQ280752	AQ280752	CITBT-E1-
283	68.8	2.8	1501	3	AF318360	AF318360	Homo sapi	356	67.2	2.7	315	1	AI244356	AI244356	Q176B08.x
284	68.8	2.8	1501	3	AF318360	AF318360	Homo sapi	357	67.2	2.7	316	5	BUS41803	BUS41803	AGENCOURT
285	68.4	2.8	587	5	BA060645	BA060645	mj71g05.r	358	67.2	2.7	320	2	BF771774	BF771774	RC4-UT001
286	68.4	2.8	520	5	BM931240	BM931240	UI-E-EJ1-	359	67.2	2.7	321	8	B56654	B56654	CIT-HSP-216
287	68.4	2.8	524	5	BUS743089	BUS743089	UI-E-EJ1-	360	67.2	2.7	324	2	AW849935	AW849935	IL3-CT021
288	68.4	2.8	557	2	BE143857	BE143857	MR0-HT016	361	67.2	2.7	325	1	AI285521	AI285521	qu79g10.x
289	68.4	2.8	594	2	BE143624	BE143624	MR0-HT016	362	67.2	2.7	328	1	AL596983	AL596983	DKFp2313L
290	68.4	2.8	620	1	AA792150	AA792150	vn51d12.r	363	67.2	2.7	336	1	AI243793	AI243793	qu64e08.x
291	68.2	2.8	623	7	N66705	N66705	yz33a07.s1	364	67.2	2.7	344	1	AA303007	AA303007	EST114046
292	68.2	2.8	421	1	AI866970	AI866970	wn13g03.x	365	67.2	2.7	344	1	BF871137	BF871137	CM0-ET012
293	68.2	2.8	500	9	CS567582	CS567582	OST194038	366	67.2	2.7	345	4	BF957224	BF957224	QV4-NN114
294	68.2	2.8	539	6	CD683597	CD683597	EST117 hu	367	67.2	2.7	355	1	AI903462	AI903462	RC-BT029-
295	68.2	2.8	543	1	AUI56877	AUI56877	AUI56877	368	67.2	2.7	359	1	AJ346429	AJ346429	sHR-00001
296	68.2	2.8	556	7	CN353345	CN353345	170006001	369	67.2	2.7	372	1	AI366464	AI366464	ao83c05.x
297	68.2	2.8	707	7	CN353347	CN353347	170006001	370	67.2	2.7	375	1	AA644226	AA644226	ab63f02.8
298	68.2	2.8	735	7	CN353343	CN353343	170005999	371	67.2	2.7	376	8	AQ479840	AQ479840	RPC1-11-2
299	68.2	2.8	766	5	BA645492	BA645492	DKFp781B	372	67.2	2.7	378	2	BF928469	BF928469	IL2-NT030
300	68.2	2.8	811	5	BUS82844	BUS82844	AGENCOURT	373	67.2	2.7	378	8	AM340844	AM340844	xr31e03.x
301	68.2	2.8	817	2	BUS86991	BUS86991	601439535	374	67.2	2.7	378	8	BS4076	BS4076	CIT-HSP-201
302	68.2	2.8	885	5	BUS21120	BUS21120	AGENCOURT	375	67.2	2.7	379	2	BF897355	BF897355	IL2-MT017
303	68.2	2.8	911	4	BG618992	BG618992	602616510	376	67.2	2.7	382	6	CD519195	CD519195	AGENCOURT
304	68.2	2.8	912	2	BE877891	BE877891	601489371	377	67.2	2.7	382	8	B73217	B73217	RPC111-1102
305	68.2	2.8	923	3	BF028995	BF028995	601764479	378	67.2	2.7	383	1	AV760918	AV760918	AV760918
306	68.2	2.8	288	1	AI214755	AI214755	qg67f07.x	379	67.2	2.7	384	5	BUS93876	BUS93876	AGENCOURT
307	68.2	2.8	343	1	AI301263	AI301263	qn04g06.x	380	67.2	2.7	388	2	AW518030	AW518030	xx65h01.x
308	68.2	2.8	407	1	AI262205	AI262205	qk09c10.x	381	67.2	2.7	389	9	CS550630	CS550630	OST156892
309	68.2	2.8	495	1	AL041619	AL041619	DKFp434K	382	67.2	2.7	390	8	B89531	B89531	RPC111-27M1
310	68.2	2.8	568	8	B93784	B93784	CIT-HSP-216	383	67.2	2.7	391	4	BG604247	BG604247	EDFLR14-7
311	68.2	2.8	839	4	BG401100	BG401100	602465166	384	67.2	2.7	398	2	BF989630	BF989630	RC6-MT016
312	68.2	2.8	5785	3	HSN802309	HSN802309	AGENCOURT	385	67.2	2.7	399	5	BQ288046	BQ288046	ik38g02.x
313	67.8	2.8	218	1	AA298345	AA298345	EST114026	386	67.2	2.7	399	9	AG191348	AG191348	Pan trogl
314	67.8	2.8	263	2	BF919865	BF919865	QV2-NT014	387	67.2	2.7	405	2	BE147762	BE147762	RC1-HT022
315	67.8	2.8	305	1	AA372949	AA372949	EST84898	388	67.2	2.7	405	6	CD558708	CD558708	AGENCOURT
316	67.8	2.8	318	1	AA828153	AA828153	od71d09.8	389	67.2	2.7	409	2	BF913650	BF913650	MR3-UT010

C 390	67.2	2.7	417	8	AQ094582	AQ094582 HS 3026 B	463	67.2	2.7	695	7	CF126693	CF126693 UI-HF-ETO
C 391	67.2	2.7	420	7	H59356	Yr27e05.x1	464	67.2	2.7	696	9	AG177244	AG177244 Pan trogl
C 392	67.2	2.7	427	2	AW872676	hm26d11.x	C 465	67.2	2.7	697	5	BU675951	BU675951 UI-CF-DUI
C 393	67.2	2.7	439	1	AQ313193	CLT-HSP-2	C 466	67.2	2.7	698	8	AQ315050	AQ315050 RPC111-94
C 394	67.2	2.7	442	1	AI017825	ou99f08.x	C 467	67.2	2.7	710	6	CN265201	CN265201 170004245
C 395	67.2	2.7	444	1	AV730244	AV730244	C 468	67.2	2.7	711	6	CD642905	CD642905 AGENCOURT
C 396	67.2	2.7	451	1	AI653493	lq95a01.x	C 469	67.2	2.7	726	5	AL042927	AL042927 DKFZp434K
C 397	67.2	2.7	453	2	AW872575	hm24a03.x	470	67.2	2.7	726	5	BX114589	BX114589
C 398	67.2	2.7	455	2	BE139252	xt66f09.x	471	67.2	2.7	732	5	BU162405	BU162405 AGENCOURT
C 399	67.2	2.7	455	8	B34340	HS-1024-B1-	C 472	67.2	2.7	740	7	CN369185	CN369185 170006003
C 400	67.2	2.7	457	8	AQ225816	HS 2014 A	473	67.2	2.7	749	1	AV729132	AV729132 AV729132
C 401	67.2	2.7	458	4	BF943855	QV0-NN114	474	67.2	2.7	750	9	AG031699	AG031699 Pan trogl
C 402	67.2	2.7	460	4	BM679571	UI-E-E00-	475	67.2	2.7	751	5	BU853245	BU853245 AGENCOURT
C 403	67.2	2.7	467	5	BU735183	UI-E-DW0-	476	67.2	2.7	753	7	CR559922	CR559922 DKFZp459M
C 404	67.2	2.7	477	1	AI132909	HA1491 HU	C 477	67.2	2.7	759	7	CN369186	CN369186 170006001
C 405	67.2	2.7	477	8	AQ770714	HS 5368 B	C 478	67.2	2.7	766	9	AG187061	AG187061 Pan trogl
C 406	67.2	2.7	485	1	AA214042	zr58g04_s	479	67.2	2.7	781	3	BU852976	BU852976 AGENCOURT
C 407	67.2	2.7	487	2	AW865946	QV3-SN002	480	67.2	2.7	803	6	CB310287	CB310287 AGENCOURT
C 408	67.2	2.7	489	1	BQ775109	UI-H-PH0-	481	67.2	2.7	805	4	BG740566	BG740566 AGENCOURT
C 409	67.2	2.7	489	5	AQ353821	RPC111-11	C 482	67.2	2.7	839	5	BU933808	BU933808 AGENCOURT
C 410	67.2	2.7	489	8	AQ353821	UI-HF-BL0	C 483	67.2	2.7	841	5	BQ428106	BQ428106 AGENCOURT
C 411	67.2	2.7	491	2	AW575605	HS 5291 B	C 484	67.2	2.7	864	5	BU854568	BU854568 AGENCOURT
C 412	67.2	2.7	504	8	AQ827059	HS 5291 B	C 485	67.2	2.7	877	2	BE674825	BE674825 AGENCOURT
C 413	67.2	2.7	514	5	CK905224	ih08b06.y	C 486	67.2	2.7	895	2	BE378912	BE378912 601237984
C 414	67.2	2.7	515	7	CR546036	DKFZp4701	C 487	67.2	2.7	900	2	BF130627	BF130627 601819217
C 415	67.2	2.7	515	7	BM309841	ih08b06.y	C 488	67.2	2.7	914	5	BQ430335	BQ430335 AGENCOURT
C 416	67.2	2.7	517	4	BM309841	ih08b06.y	C 489	67.2	2.7	967	3	CR618817	CR618817 full-1eng
C 417	67.2	2.7	517	8	AQ349863	RPC111-11	C 490	67.2	2.7	977	5	BM364209	BM364209 EX364209
C 418	67.2	2.7	519	5	EX494499	DKFZp7790	C 491	67.2	2.7	1003	4	BG428273	BG428273 602498945
C 419	67.2	2.7	520	8	AQ877271	HS 2142 B	C 492	67.2	2.7	1057	4	BM466476	BM466476 AGENCOURT
C 420	67.2	2.7	526	2	BE301068	ba84g06.x	C 493	67.2	2.7	1077	5	BQ892454	BQ892454 AGENCOURT
C 421	67.2	2.7	527	2	AW975244	ESW387352	C 494	67.2	2.7	1142	5	BM906035	BM906035 AGENCOURT
C 422	67.2	2.7	528	8	AQ389659	RPC111-14	C 495	67.2	2.7	1407	3	CR619477	CR619477 full-1eng
C 423	67.2	2.7	531	8	AQ416815	RPC111-11	C 496	67.2	2.7	1693	3	BC051262	BC051262 Homo sapi
C 424	67.2	2.7	539	8	AQ474892	CITBI-EI-	497	67.2	2.7	2399	3	CR749223	CR749223 Homo sapi
C 425	67.2	2.7	542	5	EX646083	DKFZp781D	498	67.2	2.7	3016	3	BC068461	BC068461 Homo sapi
C 426	67.2	2.7	543	1	AA902371	UI-CF-PN0	C 500	67.2	2.7	379	1	AA442105	AA442105 zw55g06.f
C 427	67.2	2.7	550	8	AQ174291	HS 3209 B	C 501	67.2	2.7	478	8	AQ121544	AQ121544 HS 3079 B
C 428	67.2	2.7	554	6	CA312702	UI-CF-PN0	C 502	67.2	2.7	554	7	AV693393	AV693393 AV693393
C 429	67.2	2.7	556	1	AL597016	DKFZp331P	C 503	67.2	2.7	590	1	CN273689	CN273689 170006000
C 430	67.2	2.7	567	1	AV718449	DKFZp686N	C 504	67.2	2.7	681	9	AG186161	AG186161 Pan trogl
C 431	67.2	2.7	569	5	EX489045	DKFZp686N	C 505	67.2	2.7	734	6	CA426088	CA426088 UI-H-DFO-
C 432	67.2	2.7	569	7	CN275283	RPC111-2	C 506	67.2	2.7	734	6	CA426088	CA426088 UI-H-DFO-
C 433	67.2	2.7	569	8	AQ483938	RPC111-2	C 507	67.2	2.7	1031	5	CR762822	CR762822 DKFZp469B
C 434	67.2	2.7	575	8	AL705993	DKFZp686C	C 508	66.8	2.7	518	7	EX936797	EX936797 DKFZp781K
C 435	67.2	2.7	575	8	AQ353841	RPC111-10	C 509	66.8	2.7	628	5	EX936797	EX936797 DKFZp781K
C 436	67.2	2.7	582	1	AA179944	zpl6b02.s	C 510	66.8	2.7	651	9	AG074730	AG074730 Pan trogl
C 437	67.2	2.7	584	6	CB105902	UI-H-FE1-	C 511	66.8	2.7	667	9	AG001476	AG001476 Homo sapi
C 438	67.2	2.7	592	6	CA425008	UI-H-FE1-	C 512	66.8	2.7	691	9	AG001476	AG001476 Homo sapi
C 439	67.2	2.7	601	6	CA425008	UI-H-FE1-	C 513	66.8	2.7	908	4	BF980862	BF980862 602304069
C 440	67.2	2.7	601	8	AQ029370	RPC111-37	C 514	66.8	2.7	3820	3	HSM803830	HSM803830
C 441	67.2	2.7	603	1	AV761561	AV761561	C 515	66.8	2.7	3820	3	HSM803831	HSM803831
C 442	67.2	2.7	605	1	AL699226	DKFZp686L	C 516	66.8	2.7	168	1	AA018183	AA018183 za553c05.s
C 443	67.2	2.7	605	4	BG109474	QV0-NN114	C 517	66.6	2.7	289	4	BM665481	BM665481 UI-E-CL1-
C 444	67.2	2.7	606	4	BF950181	UI-H-DH0-	C 518	66.6	2.7	313	2	AW183121	AW183121 xg56b10.x
C 445	67.2	2.7	615	6	CA437649	UI-H-DH0-	C 519	66.6	2.7	337	2	AM183121	AM183121 xg56b10.x
C 446	67.2	2.7	620	6	CA441227	UI-H-DH0-	C 520	66.6	2.7	353	1	AJ346587	AJ346587 SHC-00001
C 447	67.2	2.7	622	6	BQ029620	UI-H-DH0-	C 521	66.6	2.7	560	8	AG0633079	AG0633079 Pan trogl
C 448	67.2	2.7	627	6	CA441204	UI-H-DH0-	C 522	66.6	2.7	581	2	BE147090	BE147090 PMO-HT022
C 449	67.2	2.7	627	9	AG083884	Pan trogl	C 523	66.6	2.7	611	1	AL048607	AL048607 DKFZp586O
C 450	67.2	2.7	629	5	BX507857	DKFZp686D	C 524	66.6	2.7	635	5	BX646163	BX646163 DKFZp781L
C 451	67.2	2.7	635	8	BZ607926	WHACW54TR	C 525	66.6	2.7	643	4	BG536137	BG536137 602564230
C 452	67.2	2.7	635	9	AG094989	Pan trogl	C 526	66.6	2.7	647	2	AW029547	AW029547 wx13c10.x
C 453	67.2	2.7	636	7	CR739103	CR739103	C 527	66.6	2.7	663	9	AG090835	AG090835 AGENCOURT
C 454	67.2	2.7	637	8	AQ073576	CITBI-EI-	C 528	66.6	2.7	669	7	CK002319	CK002319 Pan trogl
C 455	67.2	2.7	660	9	AG043336	Pan trogl	C 529	66.6	2.7	684	8	AQ896165	AQ896165 HS 3148 B
C 456	67.2	2.7	668	9	AG067502	Pan trogl	C 530	66.6	2.7	891	5	BQ220373	BQ220373 AGENCOURT
C 457	67.2	2.7	671	9	AG166478	Pan trogl	C 531	66.4	2.7	201	2	BF919902	BF919902 QV2-NT014
C 458	67.2	2.7	676	1	AV720475	Pan trogl	C 532	66.4	2.7	238	1	AL036037	AL036037 DKFZp564B
C 459	67.2	2.7	676	1	AG119886	Pan trogl	C 533	66.4	2.7	285	1	AA600368	AA600368 ag04h04.s
C 460	67.2	2.7	679	9	AG119886	Pan trogl	C 534	66.4	2.7	315	2	BF589789	BF589789 nac24g05
C 461	67.2	2.7	686	7	CN263594	170004240	C 535	66.4	2.7	397	1	AA167556	AA167556 zpl5a11.y
C 462	67.2	2.7	688	9	AG182837	Pan trogl							

536	66.4	2.7	412	1	AL712425	AL712425	DKF2p686P	609	66	2.7	758	5	BQ772300	BQ772300	UI-H-EZ1-
C 537	66.4	2.7	432	8	AQ881297	AQ881297	HS_5450_B	C 610	66	2.7	4462	3	HSM01306	HSM01306	UI-H-EZ1-
C 538	66.4	2.7	460	8	AQ191097	AQ191097	HS_2195_A	C 611	65.8	2.7	240	1	AA078678	AA078678	Homo sapi
C 539	66.4	2.7	480	1	AA968680	AA968680	Oq76e04_B	C 612	65.8	2.7	304	2	BF842006	BF842006	RC2-HT107
C 540	66.4	2.7	490	4	AA968680	AA968680	Oq76e04_B	C 613	65.8	2.7	310	5	BQ772300	BQ772300	AGENCOURT
C 541	66.4	2.7	480	1	AA968680	AA968680	Oq76e04_B	C 614	65.8	2.7	340	1	AA668961	AA668961	ab92d04_B
C 542	66.4	2.7	505	6	CB045122	CB045122	NISC_9C08	C 615	65.8	2.7	379	2	AA668961	AA668961	RC2-CT016
C 543	66.4	2.7	507	7	CB045122	CB045122	NISC_9C08	C 616	65.8	2.7	401	1	AA668961	AA668961	RC2-CT016
C 544	66.4	2.7	515	4	BT111323	BT111323	id94a06_x	C 617	65.8	2.7	423	1	AA551582	AA551582	nk73b10_B
C 545	66.4	2.7	518	2	BF920038	BF920038	QV2-NIT014	C 618	65.8	2.7	441	5	AA218835	AA218835	zq15a11_B
C 546	66.4	2.7	544	6	CB050531	CB050531	NISC_9J118	C 619	65.8	2.7	442	1	AA218835	AA218835	AGENCOURT
C 547	66.4	2.7	544	6	CB050531	CB050531	NISC_9J118	C 620	65.8	2.7	461	1	BF904211	BF904211	IL5-WT025
C 548	66.4	2.7	550	8	AQ768907	AQ768907	HS_3160_B	C 621	65.8	2.7	481	1	AV728513	AV728513	AV728513
C 549	66.4	2.7	601	1	AL706293	AL706293	DKF2p686A	C 622	65.8	2.7	481	1	AI791227	AI791227	Oe21g10_Y
C 550	66.4	2.7	608	1	AV710572	AV710572	AV710572	C 623	65.8	2.7	501	2	AW846021	AW846021	RC2-CT016
C 551	66.4	2.7	659	4	BM050683	BM050683	G0363447	C 624	65.8	2.7	502	8	AQ424903	AQ424903	CIT81-EI-
C 552	66.4	2.7	680	8	AQ779683	AQ779683	HS_5571_B	C 625	65.8	2.7	527	8	AQ142553	AQ142553	HS_2222_B
C 553	66.4	2.7	691	8	AQ779683	AQ779683	HS_5571_B	C 626	65.8	2.7	563	5	BU787683	BU787683	io33a10_Y
C 554	66.4	2.7	723	7	CO247221	CO247221	AGENCOURT	C 627	65.8	2.7	601	5	BM969096	BM969096	UI-CF-ENO
C 555	66.4	2.7	728	9	AG031015	AG031015	Pan trogl	C 628	65.8	2.7	680	1	AL043217	AL043217	DKF2p434I
C 556	66.2	2.7	216	1	AI866422	AI866422	wk18b05_x	C 629	65.8	2.7	691	9	AG091588	AG091588	Pan trogl
C 557	66.2	2.7	314	7	TA7324	TA7324	yp10d02.r1	C 630	65.8	2.7	697	6	CD366151	CD366151	UI-H-F7I-
C 558	66.2	2.7	322	1	AA531580	AA531580	nj65a07_s	C 631	65.8	2.7	760	7	CK000274	CK000274	AGENCOURT
C 559	66.2	2.7	331	7	R06502	R06502	Yf09e08.r1	C 632	65.8	2.7	783	9	AG002281	AG002281	Homo sapi
C 560	66.2	2.7	356	7	H60188	H60188	Yr38e08.r1	C 633	65.8	2.7	888	2	BE881616	BE881616	601490034
C 561	66.2	2.7	357	1	AA641122	AA641122	nr28g09.r	C 634	65.8	2.7	1136	4	BM805582	BM805582	AGENCOURT
C 562	66.2	2.7	374	7	TA7324	TA7324	yp10d02.r1	C 635	65.8	2.7	116	8	AQ052915	AQ052915	RPC111-53
C 563	66.2	2.7	374	7	TA7324	TA7324	yp10d02.r1	C 636	65.6	2.7	146	5	BU564070	BU564070	AGENCOURT
C 564	66.2	2.7	376	8	BA9905	BA9905	CIT-HSP-517	C 637	65.6	2.7	151	7	R58559	R58559	GA154_Fetal
C 565	66.2	2.7	416	8	AQ104140	AQ104140	HS_3109_A	C 638	65.6	2.7	154	1	AA074342	AA074342	zm15g03_B
C 566	66.2	2.7	418	6	CB068479	CB068479	is20d09_x	C 639	65.6	2.7	155	1	AA984848	AA984848	am93h09_B
C 567	66.2	2.7	432	8	AQ230834	AQ230834	HS_2036_B	C 640	65.6	2.7	159	1	AA837087	AA837087	om18g09_B
C 568	66.2	2.7	460	1	AA223174	AA223174	zr07h02_B	C 641	65.6	2.7	182	1	AA879215	AA879215	nw85d07_B
C 569	66.2	2.7	480	8	BA4929	BA4929	HS-1060-A2-	C 642	65.6	2.7	195	5	BX956140	BX956140	DKF2p781G
C 570	66.2	2.7	507	8	AL199583	AL199583	RPC111-62	C 643	65.6	2.7	197	7	F18105	F18105	HSPD02679_H
C 571	66.2	2.7	510	1	AA131035	AA131035	zo16g07_x	C 644	65.6	2.7	200	2	BE042792	BE042792	ho28e11_x
C 572	66.2	2.7	519	7	CN276779	CN276779	170006001	C 645	65.6	2.7	205	2	AW081911	AW081911	xb57b05_x
C 573	66.2	2.7	529	8	CN413917	CN413917	170005328	C 646	65.6	2.7	205	8	AQ079592	AQ079592	CIT-HSP-2
C 574	66.2	2.7	529	8	AQ532233	AQ532233	RPC1-11-3	C 647	65.6	2.7	209	4	BG271955	BG271955	na160h05_F
C 575	66.2	2.7	537	8	AZ254548	AZ254548	HSC_00142	C 648	65.6	2.7	214	1	AI818231	AI818231	wk77d02_x
C 576	66.2	2.7	544	1	AU147773	AU147773	AU147773	C 649	65.6	2.7	223	7	F16569	F16569	HSPD01067_H
C 577	66.2	2.7	554	8	AQ886149	AQ886149	HS_5532_A	C 650	65.6	2.7	231	1	AA586571	AA586571	no56a04_B
C 578	66.2	2.7	565	2	BF736618	BF736618	QV3-KT001	C 651	65.6	2.7	232	2	AA586580	AA586580	no56c04_B
C 579	66.2	2.7	571	5	BP244213	BP244213	BP244213	C 652	65.6	2.7	234	2	AA901478	AA901478	RC0-NN101
C 580	66.2	2.7	574	5	BP244174	BP244174	BP244174	C 653	65.6	2.7	237	1	AI691091	AI691091	tx90e05_x
C 581	66.2	2.7	578	7	CK818584	CK818584	ic30a05_Y	C 654	65.6	2.7	246	1	AL705469	AL705469	DKF2p686B
C 582	66.2	2.7	613	6	CD721986	CD721986	o104a05_Y	C 655	65.6	2.7	245	6	CB296732	CB296732	220030_re
C 583	66.2	2.7	614	8	AQ343417	AQ343417	RPC111-12	C 656	65.6	2.7	249	5	EX482868	EX482868	DKF2p686F
C 584	66.2	2.7	629	2	BE894890	BE894890	601434074	C 657	65.6	2.7	253	2	BF854778	BF854778	PM0-FN008
C 585	66.2	2.7	633	6	CA394377	CA394377	CA394377	C 658	65.6	2.7	260	2	BE009406	BE009406	PM0-BN016
C 586	66.2	2.7	640	9	AG130047	AG130047	Pan trogl	C 659	65.6	2.7	266	2	BE000221	BE000221	MRO-BN007
C 587	66.2	2.7	642	7	CN483194	CN483194	hw29d11_Y	C 660	65.6	2.7	267	5	BU588787	BU588787	AGENCOURT
C 588	66.2	2.7	664	5	BO005623	BO005623	UI-H-ED0-	C 661	65.6	2.7	268	1	AA318189	AA318189	EST20237
C 589	66.2	2.7	707	8	AQ540349	AQ540349	RPC1-11-3	C 662	65.6	2.7	269	2	AW819470	AW819470	RC5-ST029
C 590	66.2	2.7	752	7	CN642328	CN642328	ILLUMIGEN	C 663	65.6	2.7	270	1	AA829490	AA829490	od06g04_B
C 591	66.2	2.7	763	1	AU130337	AU130337	AU130337	C 664	65.6	2.7	271	1	AI821013	AI821013	yb78d11_Y
C 592	66.2	2.7	765	8	AQ415694	AQ415694	RPC1-11-2	C 665	65.6	2.7	271	1	AA468198	AA468198	nc76a09_B
C 593	66.2	2.7	804	7	CK000918	CK000918	AGENCOURT	C 666	65.6	2.7	277	1	AA887897	AA887897	nq99f09_B
C 594	66.2	2.7	824	5	BU153976	BU153976	AGENCOURT	C 667	65.6	2.7	281	1	AI821303	AI821303	yb78d11_x
C 595	66.2	2.7	832	8	AQ743503	AQ743503	HS_5482_B	C 668	65.6	2.7	281	1	AA630672	AA630672	ae65g02_B
C 596	66.2	2.7	878	5	BQ709593	BQ709593	AGENCOURT	C 669	65.6	2.7	282	7	CN277598	CN277598	170006001
C 597	66.2	2.7	900	5	BO672362	BO672362	AGENCOURT	C 670	65.6	2.7	283	1	AA635105	AA635105	ab48g01_x
C 598	66.2	2.7	902	6	CD514546	CD514546	AGENCOURT	C 671	65.6	2.7	283	1	AA503119	AA503119	ng76f05_B
C 599	66.2	2.7	933	5	BU941276	BU941276	AGENCOURT	C 672	65.6	2.7	283	2	AW074242	AW074242	xb09h01_x
C 600	66.2	2.7	969	4	BG030587	BG030587	602297946	C 673	65.6	2.7	283	8	AQ069621	AQ069621	HS_2268_B
C 601	66.2	2.7	1067	5	BU172793	BU172793	AGENCOURT	C 674	65.6	2.7	284	1	AA487726	AA487726	aa55c10_r
C 602	66.2	2.7	1659	4	BM803793	BM803793	AGENCOURT	C 675	65.6	2.7	288	2	BF825369	BF825369	RC4-HN003
C 603	66.2	2.7	1860	3	BC019841	BC019841	Homo sapi	C 676	65.6	2.7	289	4	BF962997	BF962997	QV2-HN004
C 604	66	2.7	371	1	AA578486	AA578486	nl66e09_s	C 677	65.6	2.7	292	5	QZ233132	QZ233132	AGENCOURT
C 605	66	2.7	689	5	AX507284	AX507284	DKF2p779N	C 678	65.6	2.7	298	1	AL589429	AL589429	DKF2p451D
C 606	66	2.7	691	9	AG170656	AG170656	Pan trogl	C 679	65.6	2.7	299	1	AV750361	AV750361	AV750361
C 607	66	2.7	692	5	BX508106	BX508106	DKF2p686K	C 680	65.6	2.7	300	1	AA838190	AA838190	cel1902_B
C 608	66	2.7	721	6	CA439967	CA439967	UI-H-D10-	C 681	65.6	2.7	300	1	AA480792	AA480792	ne86d09_B

65.6	2.7	301	8	AQ067363	HS_2237_A	C 755	65.6	2.7	397	8	AQ172310	HS_3183_A
65.6	2.7	305	2	BE147116	PM2-HT022	C 756	65.6	2.7	399	2	BF763657	CM0-CS006_A
65.6	2.7	307	1	TS537538	tp04g08.x	C 757	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 758	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 759	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 760	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 761	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 762	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 763	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 764	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 765	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 766	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 767	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 768	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 769	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 770	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 771	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 772	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 773	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 774	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 775	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 776	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 777	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 778	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 779	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 780	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 781	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 782	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 783	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 784	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 785	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 786	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 787	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 788	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 789	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 790	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 791	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 792	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 793	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 794	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 795	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 796	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 797	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 798	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 799	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 800	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 801	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 802	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 803	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 804	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 805	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 806	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 807	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 808	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 809	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 810	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 811	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 812	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 813	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 814	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 815	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 816	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 817	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 818	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 819	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 820	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 821	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 822	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 823	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 824	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 825	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 826	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 827	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 828	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 829	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 830	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 831	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 832	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 833	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 834	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 835	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 836	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 837	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 838	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 839	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 840	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 841	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 842	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 843	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 844	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 845	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 846	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 847	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 848	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 849	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 850	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 851	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 852	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 853	65.6	2.7	400	1	AL706658	DKF2p686F
65.6	2.7	307	1	TS537538	tp04g08.x	C 854	65.6	2.7	400	1	AL706658	

c 974	65.6	2.7	604	8	AQ388703	RPC11-15	AQ388703	RPC11-15	c1047	65.6	2.7	683	9	AG083107	Pan trogl
c 975	65.6	2.7	605	5	BX480255	DKF2p686M	BX480255	DKF2p686M	1048	65.6	2.7	683	9	AG086352	Pan trogl
c 976	65.6	2.7	605	7	CK002451	AGENCOURT	CK002451	AGENCOURT	c1049	65.6	2.7	684	4	BM786256	K-EST0064
c 977	65.6	2.7	605	8	AQ347764	RPC11-13	AQ347764	RPC11-13	c1050	65.6	2.7	684	4	BM786256	K-EST0064
c 978	65.6	2.7	606	8	AQ508672	RPC1-11-3	AQ508672	RPC1-11-3	c1051	65.6	2.7	687	8	BZ603817	WHAR70TR
c 979	65.6	2.7	609	1	AV658701	AV658701	AV658701	AV658701	c1052	65.6	2.7	687	8	AQ383155	WHAR11-13
c 980	65.6	2.7	609	6	CA438175	UI-H-DIO-	CA438175	UI-H-DIO-	c1053	65.6	2.7	688	1	AV700812	AV700812
c 981	65.6	2.7	609	6	CD701702	EST18226	CD701702	EST18226	1054	65.6	2.7	688	1	AV726885	AV726885
c 982	65.6	2.7	612	5	BQ708675	AGENCOURT	BQ708675	AGENCOURT	1055	65.6	2.7	688	1	AV726885	AV726885
c 983	65.6	2.7	613	9	AG150419	Pan trogl	AG150419	Pan trogl	1056	65.6	2.7	689	2	BF677006	602084239
c 984	65.6	2.7	616	7	CR539154	DKF2p459E	CR539154	DKF2p459E	c1057	65.6	2.7	690	2	BE251460	601109342
c 985	65.6	2.7	619	7	CR5314072	170004551	CR5314072	170004551	c1058	65.6	2.7	690	2	BE251460	601109342
c 986	65.6	2.7	623	6	CD172351	170006000	CD172351	170006000	c1059	65.6	2.7	690	2	BE251460	601109342
c 987	65.6	2.7	623	6	CD172351	170006000	CD172351	170006000	c1060	65.6	2.7	690	2	BE251460	601109342
c 988	65.6	2.7	627	6	CD172351	170006000	CD172351	170006000	c1061	65.6	2.7	690	2	BE251460	601109342
c 989	65.6	2.7	628	4	BG430787	602498557	BG430787	602498557	1062	65.6	2.7	690	2	BE251460	601109342
c 990	65.6	2.7	628	8	BZ608925	WHAAAG53TR	BZ608925	WHAAAG53TR	1063	65.6	2.7	690	2	BE251460	601109342
c 991	65.6	2.7	628	8	BZ608925	WHAAAG53TR	BZ608925	WHAAAG53TR	1064	65.6	2.7	690	2	BE251460	601109342
c 992	65.6	2.7	630	2	BE393707	601310933	BE393707	601310933	1065	65.6	2.7	690	2	BE251460	601109342
c 993	65.6	2.7	632	7	CR524786	602574045	CR524786	602574045	c1066	65.6	2.7	690	2	BE251460	601109342
c 994	65.6	2.7	633	2	BF530460	602071588	BF530460	602071588	c1067	65.6	2.7	690	2	BE251460	601109342
c 995	65.6	2.7	635	2	BF530460	602071588	BF530460	602071588	c1068	65.6	2.7	690	2	BE251460	601109342
c 996	65.6	2.7	636	9	AG156196	Pan trogl	AG156196	Pan trogl	c1069	65.6	2.7	690	2	BE251460	601109342
c 997	65.6	2.7	637	6	CA428427	UI-H-DF0-	CA428427	UI-H-DF0-	1070	65.6	2.7	690	2	BE251460	601109342
c 998	65.6	2.7	637	6	CA428427	UI-H-DF0-	CA428427	UI-H-DF0-	c1071	65.6	2.7	690	2	BE251460	601109342
c 999	65.6	2.7	641	4	BG546863	602574045	BG546863	602574045	1072	65.6	2.7	690	2	BE251460	601109342
1000	65.6	2.7	641	4	BG546863	602574045	BG546863	602574045	c1073	65.6	2.7	690	2	BE251460	601109342
1001	65.6	2.7	643	5	BX507867	602574045	BX507867	602574045	1074	65.6	2.7	690	2	BE251460	601109342
1002	65.6	2.7	644	8	AQ083136	RPC11-15	AQ083136	RPC11-15	1075	65.6	2.7	690	2	BE251460	601109342
1003	65.6	2.7	644	8	AQ083136	RPC11-15	AQ083136	RPC11-15	c1076	65.6	2.7	690	2	BE251460	601109342
1004	65.6	2.7	647	4	BM0453378	Pan trogl	BM0453378	Pan trogl	c1077	65.6	2.7	690	2	BE251460	601109342
1005	65.6	2.7	647	4	BM0453378	Pan trogl	BM0453378	Pan trogl	c1078	65.6	2.7	690	2	BE251460	601109342
1006	65.6	2.7	648	5	BG689165	UI-CF-EC1	BG689165	UI-CF-EC1	c1079	65.6	2.7	690	2	BE251460	601109342
1007	65.6	2.7	652	2	BE062635	QVO-BT026	BE062635	QVO-BT026	c1080	65.6	2.7	690	2	BE251460	601109342
1008	65.6	2.7	652	9	AG038075	Pan trogl	AG038075	Pan trogl	c1081	65.6	2.7	690	2	BE251460	601109342
1009	65.6	2.7	653	1	AV763430	AV763430	AV763430	AV763430	1082	65.6	2.7	690	2	BE251460	601109342
1010	65.6	2.7	653	4	BG401563	602466208	BG401563	602466208	1083	65.6	2.7	690	2	BE251460	601109342
1011	65.6	2.7	654	9	AG153173	Pan trogl	AG153173	Pan trogl	1084	65.6	2.7	690	2	BE251460	601109342
1012	65.6	2.7	655	2	BE152248	QVA-HT031	BE152248	QVA-HT031	1085	65.6	2.7	690	2	BE251460	601109342
1013	65.6	2.7	655	9	AG119870	Homo sapi	AG119870	Homo sapi	1086	65.6	2.7	690	2	BE251460	601109342
1014	65.6	2.7	656	9	AG117705	Pan trogl	AG117705	Pan trogl	c1087	65.6	2.7	690	2	BE251460	601109342
1015	65.6	2.7	657	8	AQ490406	RPC1-11-2	AQ490406	RPC1-11-2	c1088	65.6	2.7	690	2	BE251460	601109342
1016	65.6	2.7	658	8	AQ490406	RPC1-11-2	AQ490406	RPC1-11-2	1089	65.6	2.7	690	2	BE251460	601109342
1017	65.6	2.7	658	9	AG183574	Pan trogl	AG183574	Pan trogl	c1090	65.6	2.7	690	2	BE251460	601109342
1018	65.6	2.7	659	9	AG183574	Pan trogl	AG183574	Pan trogl	1091	65.6	2.7	690	2	BE251460	601109342
1019	65.6	2.7	660	5	BG928994	AGENCOURT	BG928994	AGENCOURT	c1092	65.6	2.7	690	2	BE251460	601109342
1020	65.6	2.7	662	9	AG104573	Pan trogl	AG104573	Pan trogl	c1093	65.6	2.7	690	2	BE251460	601109342
1021	65.6	2.7	667	9	AG067534	Pan trogl	AG067534	Pan trogl	1094	65.6	2.7	690	2	BE251460	601109342
1022	65.6	2.7	668	8	B65896	CIT-HSP-202	B65896	CIT-HSP-202	1095	65.6	2.7	690	2	BE251460	601109342
1023	65.6	2.7	668	9	AG045483	Pan trogl	AG045483	Pan trogl	1096	65.6	2.7	690	2	BE251460	601109342
1024	65.6	2.7	668	9	AG056389	Pan trogl	AG056389	Pan trogl	c1097	65.6	2.7	690	2	BE251460	601109342
1025	65.6	2.7	669	8	BZ602285	WHAAK07TR	BZ602285	WHAAK07TR	c1098	65.6	2.7	690	2	BE251460	601109342
1026	65.6	2.7	671	8	AG171555	Pan trogl	AG171555	Pan trogl	c1099	65.6	2.7	690	2	BE251460	601109342
1027	65.6	2.7	672	8	AG158237	Pan trogl	AG158237	Pan trogl	c1100	65.6	2.7	690	2	BE251460	601109342
1028	65.6	2.7	673	8	AQ055484	CIT-HSP-202	AQ055484	CIT-HSP-202	c1101	65.6	2.7	690	2	BE251460	601109342
1029	65.6	2.7	673	8	BZ774131	mcv86b10	BZ774131	mcv86b10	1102	65.6	2.7	690	2	BE251460	601109342
1030	65.6	2.7	674	1	AL704227	Pan trogl	AL704227	Pan trogl	c1103	65.6	2.7	690	2	BE251460	601109342
1031	65.6	2.7	674	4	BM787549	K-EST0066	BM787549	K-EST0066	1104	65.6	2.7	690	2	BE251460	601109342
1032	65.6	2.7	676	5	BQ068872	UI-H-EIO-	BQ068872	UI-H-EIO-	c1105	65.6	2.7	690	2	BE251460	601109342
1033	65.6	2.7	677	4	BM653399	UI-E-CQ-	BM653399	UI-E-CQ-	1106	65.6	2.7	690	2	BE251460	601109342
1034	65.6	2.7	677	4	BM653399	UI-E-CQ-	BM653399	UI-E-CQ-	1107	65.6	2.7	690	2	BE251460	601109342
1035	65.6	2.7	678	2	CA389370	ca80e04.y	CA389370	ca80e04.y	1108	65.6	2.7	690	2	BE251460	601109342
1036	65.6	2.7	678	2	BE888430	601512801	BE888430	601512801	1109	65.6	2.7	690	2	BE251460	601109342
1037	65.6	2.7	679	1	AV703259	AV703259	AV703259	AV703259	1110	65.6	2.7	690	2	BE251460	601109342
1038	65.6	2.7	679	1	AV703259	AV703259	AV703259	AV703259	c1111	65.6	2.7	690	2	BE251460	601109342
1039	65.6	2.7	679	9	AG171895	Pan trogl	AG171895	Pan trogl	1112	65.6	2.7	690	2	BE251460	601109342
1040	65.6	2.7	681	4	BM686581	UI-E-CQ-	BM686581	UI-E-CQ-	c1113	65.6	2.7	690	2	BE251460	601109342
1041	65.6	2.7	681	4	BM686581	UI-E-CQ-	BM686581	UI-E-CQ-	1114	65.6	2.7	690	2	BE251460	601109342
1042	65.6	2.7	681	9	AG083589	Pan trogl	AG083589	Pan trogl	c1115	65.6	2.7	690	2	BE251460	601109342
1043	65.6	2.7	682	5	BG630852	UI-H-FLO-	BG630852	UI-H-FLO-	1116	65.6	2.7	690	2	BE251460	601109342
1044	65.6	2.7	682	6	CD692088	EST8627 h	CD692088	EST8627 h	1117	65.6	2.7	690	2	BE251460	601109342
1045	65.6	2.7	682	7	CN268696	170005321	CN268696	170005321	1118	65.6	2.7	690	2	BE251460	601109342
1046	65.6	2.7	683	1	AI246528	qn64d04.x	AI246528	qn64d04.x	c1119	65.6	2.7	690	2	BE251460	601109342

c1120	65.6	2.7	840	4	BM007773	603617231	1193	55.4	2.7	1198	7	CK230542	ILLUMIGEN
c1121	65.6	2.7	843	6	CD653622	AGENCY	1194	65.4	2.7	1341	2	BE901529	601677409
1122	65.6	2.7	855	1	AL119158	DKF2p761L	1195	65.4	2.7	2540	3	CR593742	full1-leng
1123	65.6	2.7	859	2	BE973838	601680645	c1196	65.2	2.7	430	8	B53903	CIT-HSP-201
1124	65.6	2.7	859	4	BG751356	602730109	c1197	65.2	2.7	474	8	AQ208089	HS-2007-B
1125	65.6	2.7	864	4	BG110162	602279794	c1198	65.2	2.7	477	8	AQ225545	HS-2007-B
c1126	65.6	2.7	864	4	BG429844	602494863	c1199	65.2	2.7	583	5	BP873354	BP873354
c1127	65.6	2.7	866	4	BG541161	602569938	c1200	65.2	2.7	585	8	AQ149696	HS-3178-A
c1128	65.6	2.7	872	5	BQ646204	AGENCY	c1201	65.2	2.7	848	8	AQ742505	HS-5383-B
c1129	65.6	2.7	876	6	CB993955	AGENCY	c1202	65.2	2.7	933	5	BQ897609	AGENCY
1130	65.6	2.7	884	6	BG164850	602340574	c1203	65.2	2.7	983	5	BX345380	BX345380
c1131	65.6	2.7	884	6	CD514466	AGENCY	c1204	65.2	2.7	1027	1	AL553966	AL553966
c1132	65.6	2.7	887	5	BUI92436	AGENCY	1205	65.2	2.7	1067	4	BG681437	602628105
1133	65.6	2.7	895	5	BQ882091	AGENCY	1206	65.2	2.7	1143	4	BQ260656	602372222
c1134	65.6	2.7	897	5	BX352404	BX352404	1207	65	2.6	131	2	BG934873	IL2-NT019
1135	65.6	2.7	898	4	BG260135	602371230	c1208	65	2.6	236	7	CN274979	170006000
c1136	65.6	2.7	903	5	BQ232733	AGENCY	1209	65	2.6	513	8	AQ190314	HS-3223-A
1137	65.6	2.7	907	4	BG539458	602568080	c1210	65	2.6	558	8	AQ144286	HS-3080-A
1138	65.6	2.7	917	5	BUI74148	AGENCY	c1211	65	2.6	576	6	CB555237	MMSF0014-
c1139	65.6	2.7	919	5	BX452209	AGENCY	1212	65	2.6	610	8	BH609665	HIV19C04-
c1140	65.6	2.7	925	5	BQ706870	AGENCY	1213	65	2.6	636	9	AG065252	Pan trogl
c1141	65.6	2.7	928	5	BQ648991	AGENCY	1214	65	2.6	644	8	AQ051710	RPC111-50
1142	65.6	2.7	929	4	BG496851	602538859	1215	65	2.6	662	9	AG131186	Pan trogl
c1143	65.6	2.7	930	5	BQ710436	AGENCY	1216	65	2.6	665	9	AG063672	Pan trogl
1144	65.6	2.7	948	5	BQ711182	AGENCY	c1217	65	2.6	679	7	CN265762	170004247
c1145	65.6	2.7	955	2	BE379442	601237395	1218	65	2.6	696	1	AV377614	AV377614
1146	65.6	2.7	959	5	BQ705924	AGENCY	1219	65	2.6	702	9	AG093052	Pan trogl
1147	65.6	2.7	960	4	BG110235	602279888	1220	65	2.6	746	5	BQ432822	AGENCY
1148	65.6	2.7	964	4	BG032579	602301496	c1221	65	2.6	758	5	BM989947	UI-H-D10-
c1149	65.6	2.7	971	4	BM802467	AGENCY	1222	65	2.6	775	8	AQ745181	HS-5502-A
1150	65.6	2.7	972	1	AL562711	AL562711	c1223	65	2.6	778	6	CA413180	UI-H-E20-
c1151	65.6	2.7	972	1	BQ710512	AGENCY	1224	65	2.6	902	5	BQ712086	AGENCY
1152	65.6	2.7	983	5	BU554100	AGENCY	1225	65	2.6	907	5	BQ710417	AGENCY
c1153	65.6	2.7	985	1	AL044339	DKF2p434A	1226	65	2.6	907	5	BQ710417	AGENCY
1154	65.6	2.7	985	5	BM907182	AGENCY	c1227	64.8	2.6	186	1	AA599550	ag08a04.8
c1155	65.6	2.7	988	5	BM905391	AGENCY	c1228	64.8	2.6	257	2	BF840495	RC6-HT100
1156	65.6	2.7	988	5	BQ711330	AGENCY	c1229	64.8	2.6	304	1	AI278087	qms7h07.X
c1157	65.6	2.7	1005	3	AL590991	full-leng	1230	64.8	2.6	366	2	BF768769	QV4-IT000
1158	65.6	2.7	1020	1	AL528645	AL528645	1231	64.8	2.6	396	6	C15893	C15893
c1159	65.6	2.7	1032	4	BM562790	AGENCY	c1232	64.8	2.6	405	8	AQ661775	HS-2137-A
1160	65.6	2.7	1053	1	AL567196	AL567196	1233	64.8	2.6	426	1	AA226715	nc27h03.8
c1161	65.6	2.7	1080	5	BX405271	BX405271	c1234	64.8	2.6	430	8	AQ228480	CIT-HSP-2
c1162	65.6	2.7	1086	4	BM803038	AGENCY	c1235	64.8	2.6	460	8	AQ120671	HS-3076-A
1163	65.6	2.7	1119	1	AV761458	AV761458	c1236	64.8	2.6	464	1	AI955807	wt59h02.X
c1164	65.6	2.7	1140	4	BG435095	602507103	c1237	64.8	2.6	472	8	AQ420543	RPC1-11-1
1165	65.6	2.7	1144	1	AL565655	AL565655	c1238	64.8	2.6	474	8	AQ227389	HS-2017-B
c1166	65.6	2.7	1162	4	BG541442	602570872	c1239	64.8	2.6	500	1	AI732911	oe21g10.X
c1167	65.6	2.7	1169	7	CF265102	AGENCY	c1240	64.8	2.6	507	8	AQ140467	HS-3116-A
1168	65.6	2.7	1197	4	BM465161	AGENCY	1241	64.8	2.6	537	5	BQ364679	MR0-SN004
c1169	65.6	2.7	1219	3	BC037851	Homo sapi	1242	64.8	2.6	542	4	BG285703	602380748
c1170	65.6	2.7	1227	3	CR590140	full-leng	c1243	64.8	2.6	547	2	AW575719	UI-HF-BM0
c1171	65.6	2.7	1469	3	CR604873	full-leng	c1244	64.8	2.6	554	8	AQ623864	HS-5376-A
1172	65.6	2.7	1553	3	BC038707	Homo sapi	c1245	64.8	2.6	562	1	AU144711	AU144711
c1173	65.6	2.7	1654	3	CR607248	full-leng	1246	64.8	2.6	571	5	BQ722916	AGENCY
c1174	65.6	2.7	1684	3	CR593666	full-leng	1247	64.8	2.6	629	5	BQ673768	AGENCY
c1175	65.6	2.7	1723	3	CR592582	full-leng	1248	64.8	2.6	649	9	AG042323	Pan trogl
c1176	65.6	2.7	1803	3	CR600765	full-leng	1249	64.8	2.6	681	9	AG139477	Pan trogl
1177	65.6	2.7	2285	3	CR749362	Homo sapi	c1250	64.8	2.6	682	5	BQ774596	UI-H-FH0-
c1178	65.6	2.7	2531	3	BC020559	Homo sapi	1251	64.8	2.6	727	5	EX952052	DKF2p7810
1179	65.6	2.7	2999	3	BC035096	Homo sapi	1252	64.8	2.6	761	5	BUI71042	AGENCY
c1180	65.6	2.7	3038	3	BC040590	Homo sapi	c1253	64.8	2.6	5689	3	HS0806132	HS0806132
c1181	65.6	2.7	3162	3	BC056195	Homo sapi	1254	64.6	2.6	96	2	BF130198	RC1818222
1182	65.6	2.7	4374	3	CR749480	Homo sapi	c1255	64.6	2.6	115	2	BE156738	RC0-HT036
c1183	65.4	2.7	276	4	BT091290	Homo sapi	1256	64.6	2.6	173	6	CD5211332	AGENCY
c1184	65.4	2.7	424	1	AL701204	DKF2p686G	c1257	64.6	2.6	213	1	AI864813	wk04f10.X
c1185	65.4	2.7	445	8	AQ177677	HS-2209-B	1258	64.6	2.6	212	7	R65651	Y126902.r1
c1186	65.4	2.7	461	8	AA0511522	HS-5074-B	c1259	64.6	2.6	229	2	BF817886	RC4-CI019
1187	65.4	2.7	462	1	AA055029	ab03h12.X	c1260	64.6	2.6	237	1	AA975335	on37g11.8
c1188	65.4	2.7	470	5	BX492195	DKF2p7810	1261	64.6	2.6	243	8	AQ275593	RPC1-g-17
1189	65.4	2.7	523	1	AI732179	ac94e12.X	c1262	64.6	2.6	268	2	BF893595	RC3-MT013
c1190	65.4	2.7	563	8	AQ888215	HS-3069-A	c1263	64.6	2.6	309	4	BM504093	h20908.X
c1191	65.4	2.7	591	5	BU626398	UI-H-DF0-	1264	64.6	2.6	321	5	EX478293	DKF2p686N
1192	65.4	2.7	821	2	BE902562	601675096	1265	64.6	2.6	339	2	BF771019	IL5-IT002

c1266	64.6	2.6	340	2	AW468372	he37a08.x	1339	64.6	2.6	686	6	CA391921	cs20c07.y
c1267	64.6	2.6	341	2	BF899031	PM2-MT020	1340	64.6	2.6	886	7	AG069175	Pan trogl
c1268	64.6	2.6	344	8	AQ063249	CIT-HSP-2	1342	64.6	2.6	692	8	CN298996	170004240
c1269	64.6	2.6	348	2	BF916919	IL3-DT011	1343	64.6	2.6	692	8	AQ385010	RPC111-15
c1270	64.6	2.6	360	7	T41259	ya33g05.s1	1343	64.6	2.6	700	8	AQ241749	CITBI-EI-
c1271	64.6	2.6	361	1	AA662994	ac52c12.s	c1344	64.6	2.6	701	8	BM724359	UI-E-E01-
c1272	64.6	2.6	365	8	B76591	RPC111-15N1	c1345	64.6	2.6	705	8	AQ380615	RPC111-16
c1273	64.6	2.6	366	1	A1266133	qp64b03.x	1346	64.6	2.6	713	8	AQ541479	RPC11-11.3
c1274	64.6	2.6	382	1	AV728928	AV728928	c1347	64.6	2.6	715	9	AG008263	AG008263 Homo sapi
c1275	64.6	2.6	391	4	BM853440	K-ESN0135	1348	64.6	2.6	715	9	AG149945	Pan trogl
c1276	64.6	2.6	392	1	A1246796	qx72a01.x	1349	64.6	2.6	743	9	BM679680	UI-E-E00-
c1277	64.6	2.6	395	8	AQ219404	HS 3245.B	1350	64.6	2.6	746	9	AG115333	AG115333 Pan trogl
c1278	64.6	2.6	396	2	BF805095	IL5-C1015	1351	64.6	2.6	746	9	BM79680	UI-E-E00-
c1279	64.6	2.6	406	2	BF842127	NR1-HT106	c1352	64.6	2.6	747	6	CB998346	CB998346 AGENCOURT
c1280	64.6	2.6	408	1	AA487142	ab19c10.s	1353	64.6	2.6	769	5	BQ435687	BQ435687 AGENCOURT
c1281	64.6	2.6	415	1	AA640053	RP40b06.s	1354	64.6	2.6	841	1	AG121859	AG121859
c1282	64.6	2.6	417	8	AQ395085	CITBI-EI-	1355	64.6	2.6	841	1	AG121859	AG121859
c1283	64.6	2.6	421	1	AA593375	hm0810.s	1356	64.6	2.6	898	8	AG089490	AG089490
c1284	64.6	2.6	421	1	AV742636	AV742636	c1357	64.6	2.6	932	5	EX433879	EX433879
c1285	64.6	2.6	430	1	BM504315	ih20g08.y	1358	64.6	2.6	932	5	EX433879	EX433879
c1286	64.6	2.6	431	4	B32106	HS-1014-B1-	c1359	64.6	2.6	932	5	EX433879	EX433879
c1287	64.6	2.6	432	8	AQ816321	HS 4551.A	1360	64.6	2.6	932	5	EX433879	EX433879
c1288	64.6	2.6	433	8	AQ463870	HS 5080.A	c1361	64.6	2.6	932	5	EX433879	EX433879
c1289	64.6	2.6	433	8	AQ477517	CITBI-EI-	1362	64.6	2.6	932	5	EX433879	EX433879
c1290	64.6	2.6	441	1	AA838227	ce37d03.s	c1363	64.6	2.6	932	5	EX433879	EX433879
c1291	64.6	2.6	453	6	CA392280	cs23c03.y	1364	64.6	2.6	932	5	EX433879	EX433879
c1292	64.6	2.6	453	6	CA392282	ce23ff10.y	c1365	64.6	2.6	932	5	EX433879	EX433879
c1293	64.6	2.6	463	8	AQ322261	HS 5465.B	1366	64.6	2.6	932	5	EX433879	EX433879
c1294	64.6	2.6	464	2	AW439851	hb8g09.x	c1367	64.6	2.6	932	5	EX433879	EX433879
c1295	64.6	2.6	465	8	AQ798837	HS 2169.B	c1368	64.6	2.6	932	5	EX433879	EX433879
c1296	64.6	2.6	468	7	H69089	yr-86f07.s1	c1369	64.6	2.6	932	5	EX433879	EX433879
c1297	64.6	2.6	472	2	AW502047	UI-HF-BR0	c1370	64.6	2.6	932	5	EX433879	EX433879
c1298	64.6	2.6	490	8	AQ123703	HS 3104.B	c1371	64.6	2.6	932	5	EX433879	EX433879
c1299	64.6	2.6	494	2	AW975259	EST387367	1372	64.6	2.6	932	5	EX433879	EX433879
c1300	64.6	2.6	494	1	AA486819	ab19c10.s	1373	64.6	2.6	932	5	EX433879	EX433879
c1301	64.6	2.6	496	1	AQ203711	HS 3103.A	c1374	64.6	2.6	932	5	EX433879	EX433879
c1302	64.6	2.6	499	8	AQ167088	HS 3151.B	1375	64.6	2.6	932	5	EX433879	EX433879
c1303	64.6	2.6	503	5	BH152879	UP-297-17	c1376	64.6	2.6	932	5	EX433879	EX433879
c1304	64.6	2.6	504	8	BN152039	328755612	c1377	64.6	2.6	932	5	EX433879	EX433879
c1305	64.6	2.6	510	7	CN268053	170005518	c1378	64.6	2.6	932	5	EX433879	EX433879
c1306	64.6	2.6	511	7	CN268053	170005518	1379	64.6	2.6	932	5	EX433879	EX433879
c1307	64.6	2.6	521	1	AA160481	zo73c07.s	1380	64.6	2.6	932	5	EX433879	EX433879
c1308	64.6	2.6	526	8	AQ358759	HS 5030.A	c1381	64.6	2.6	932	5	EX433879	EX433879
c1309	64.6	2.6	529	8	AQ213006	HS 3214.B	c1382	64.6	2.6	932	5	EX433879	EX433879
c1310	64.6	2.6	537	2	BE067037	PM4-BT034	c1383	64.6	2.6	932	5	EX433879	EX433879
c1311	64.6	2.6	538	1	AU146344	AU146344	c1384	64.6	2.6	932	5	EX433879	EX433879
c1312	64.6	2.6	539	1	AU158859	AU158859	1385	64.6	2.6	932	5	EX433879	EX433879
c1313	64.6	2.6	542	8	AQ552243	CITBI-EI-	c1386	64.6	2.6	932	5	EX433879	EX433879
c1314	64.6	2.6	543	8	AQ552243	CITBI-EI-	c1387	64.6	2.6	932	5	EX433879	EX433879
c1315	64.6	2.6	546	2	BE143522	MR0-HT016	1388	64.6	2.6	932	5	EX433879	EX433879
c1316	64.6	2.6	549	2	BE143522	MR0-HT016	c1389	64.6	2.6	932	5	EX433879	EX433879
c1317	64.6	2.6	551	5	EX481896	DKFZp686A	1390	64.6	2.6	932	5	EX433879	EX433879
c1318	64.6	2.6	563	8	AQ441812	HS 5106.B	c1391	64.6	2.6	932	5	EX433879	EX433879
c1319	64.6	2.6	570	8	BH1244	CIT-HSP-202	1392	64.6	2.6	932	5	EX433879	EX433879
c1320	64.6	2.6	584	4	BM264460	rs35a10.x	c1393	64.6	2.6	932	5	EX433879	EX433879
c1321	64.6	2.6	590	2	AW972628	EST384719	1394	64.6	2.6	932	5	EX433879	EX433879
c1322	64.6	2.6	596	5	BQ017745	UI-H-ED0-	c1395	64.6	2.6	932	5	EX433879	EX433879
c1323	64.6	2.6	601	5	EX508613	DKFZp686M	1396	64.6	2.6	932	5	EX433879	EX433879
c1324	64.6	2.6	603	7	CN298997	170004181	c1397	64.6	2.6	932	5	EX433879	EX433879
c1325	64.6	2.6	615	2	BE150420	RC1-HT026	1398	64.6	2.6	932	5	EX433879	EX433879
c1326	64.6	2.6	616	7	CR548465	DKFZp4591	c1399	64.6	2.6	932	5	EX433879	EX433879
c1327	64.6	2.6	637	8	AQ529716	RPC11-11.3	1400	64.6	2.6	932	5	EX433879	EX433879
c1328	64.6	2.6	642	8	B59854	CIT-HSP-345	c1401	64.6	2.6	932	5	EX433879	EX433879
c1329	64.6	2.6	648	8	B2611349	WHA001TR	c1402	64.6	2.6	932	5	EX433879	EX433879
c1330	64.6	2.6	653	7	CR789476	DKFZp459A	c1403	64.6	2.6	932	5	EX433879	EX433879
c1331	64.6	2.6	654	7	CN264409	170004243	c1404	64.6	2.6	932	5	EX433879	EX433879
c1332	64.6	2.6	656	7	CF146868	UI-HF-CB0	c1405	64.6	2.6	932	5	EX433879	EX433879
c1333	64.6	2.6	660	9	AG078171	Pan trogl	1406	64.6	2.6	932	5	EX433879	EX433879
c1334	64.6	2.6	670	9	CN255774	170006000	c1407	64.6	2.6	932	5	EX433879	EX433879
c1335	64.6	2.6	678	9	AG181920	Pan trogl	c1408	64.6	2.6	932	5	EX433879	EX433879
c1336	64.6	2.6	679	9	AG128822	Pan trogl	c1409	64.6	2.6	932	5	EX433879	EX433879
c1337	64.6	2.6	683	8	AQ267639	RPC111-75	1410	64.6	2.6	932	5	EX433879	EX433879
c1338	64.6	2.6	683	9	AG125117	Pan trogl	c1411	64.6	2.6	932	5	EX433879	EX433879

[illegible]

Db	1299	CCAGAGGTGAGAGGTTCTTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAGACGAA	1358
Qy	1261	ACCACACCCAGCATGATCCCGAGCCAGCAGAGCCTTCCAAACGGTCTGAAATTTACAATG	1320
Db	1359	ACCACACCCAGCATGATCCCGAGCCAGCAGAGCCTTCCAAACGGTCTGAAATTTACAATG	1418
Qy	1321	GACTTGACTCCCCACGCTTTCCTTAGGAGTCAGGGTCTTTGGAGCTCTTCTCGTCATTGAGC	1380
Db	1419	GACTTGACTCCCCACGCTTTCCTTAGGAGTCAGGGTCTTTGGAGCTCTTCTCGTCATTGAGC	1478
Qy	1381	TCAAGTCACCCAGCCACACAACCCAGATGAGAGTGCATCTAAGTAGCAGTGAGCATTTGCCAG	1440
Db	1479	TCAAGTCACCCAGCCACACAACCCAGATGAGAGTGCATCTAAGTAGCAGTGAGCATTTGCCAG	1538
Qy	1441	GAACAGAGTCAGATGAGCATTTTTCCTTATACAATACCAACCAAGCAAGCAAGATGTAAGCT	1500
Db	1539	GAACAGAGTCAGATGAGCATTTTTCCTTATACAATACCAACCAAGCAAGCAAGATGTAAGCT	1598
Qy	1501	GATTTCATCTGTAAAAAGGCATCTTATTTGTGCTTTAGACAGAGTAAGGGAAGCAGGAG	1560
Db	1599	GATTTCATCTGTAAAAAGGCATCTTATTTGTGCTTTAGACAGAGTAAGGGAAGCAGGAG	1658
Qy	1561	TCCAAATCTATTTGTTGACACGAGCAGCTGTGGTGAGAGGTTGGGGAAGAGTGAGTGAAT	1620
Db	1659	TCCAAATCTATTTGTTGACACGAGCAGCTGTGGTGAGAGGTTGGGGAAGAGTGAGTGAAT	1718
Qy	1621	ATACCTTAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAAATTTTCAAG	1680
Db	1719	ATACCTTAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAAATTTTCAAG	1778
Qy	1681	AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTATGGAATTTA	1740
Db	1779	AGGAAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAAACTTATGGAATTTA	1838
Qy	1741	GTTATTCAGACAGTCAACGAGAACCCAGCCTTATTACACCTGCTTACACCAT	1794
Db	1839	GTTATTCAGACAGTCAACGAGAACCCAGCCTTATTACACCTGCTTACACCAT	1892
RESULT 2			
AK033723			
LOCUS	2931 bp mRNA linear HTC 03-APR-2004		
DEFINITION	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130232017 product:ADIPOCYTE-SPECIFIC PROTEIN 5, full insert sequence.		
ACCESSION	AK033723		
VERSION	AK033723.1 GI:26329414		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subcloning of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.		

Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2931)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES

Location/Qualifiers
1..2931
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:9130232017"
/db_xref="caxon:10090"
/clones="9130232017"
/sex="male"
/tissue type="cecum"
/clone_libs="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

374..1495
/note="unnamed protein product; ADIPOCYTE-SPECIFIC PROTEIN
5 (SPTR|Q920S5, evidence: FASTV, 99.7%ID, 100%length,
match=119)

putative"
/codon_start=1
/protein_id="BAC28446.1"
/db_xref="GI:26329415"
/translation="MSLFFLMVSYVGTGLTHTEIKRVABEKVTLPCHHQLGLPEKD
TLDEWLLTDNEGKQVITYSSRYNNLTVEOKRVAFASFLAGDSLIQIPLKP
SDGEYTKVKNRYVWVSHVILKVLVPPSKPKCELEGPTEGSDTLTQCESAGTKP
IVYVQRIREKGEDEHLPPKSRIDYNNPGRVLLQNLTMASGLYQCTAGNEAKESC
VVRVTVQVQSIGWAGVAVTGIVAGALLIFLLIWLIRKRSKDRYEEDRPREIRBDA
EAPRRLVKPSSSSGSRSSRSGSSSTRSTGNSRSQRTLSSEAAFPQPGPLAPQAYS

CDS

ORIGIN
Query Match
Best Local Similarity 46.2%; Score 1134.4; DB 3; Length 2931;
Matches 1774; Conservative 0; Mismatches 506; Indels 96; Gaps 24;
QY 16 CTGCCCCCAGGGGCGAGGGGCGGGGCGGGGCTCCCGCCGCGACATGGCTGACGCCACC 75
DB 206 CAGCGCGCAGGGGAGCCCGGGCGCGGGGC---CAGCGCGCGACATGGCTGACGCC-CC 260
QY 76 TCGCGCGCAGCCCGCAGGCGCGCGCCAGCTCGCCGCGAGGTCGCTCGAGGCGCGCGGCC 135
DB 261 CCGCGCGCAGCCCGCAGGCGCGCGCCCTGCTCACAGAGGTCGCTCGGCTGGGCTCGGTC 320
QY 136 GCCCGGAGCCCAAGCAGCAACTGAGCGGGGAGGCGCGCGCTCCGGGATCGGATGTC 195
DB 321 GCCCTGAGCCAGGCTGC-GCTGAGCGGGAGTGCCCGTGTCCGGAGATCGGATGTC 379
QY 196 CTCCT 255
DB 380 CTCCTC---TTCTCTCTGCTAGTATCTTATTTATTTGGAACGCTGGGAACCTCACACTGAG 436
QY 256 ATCAAGAGAGTGGCAGAGGAAAGGTCACTTTGCGCTGCCACCATCAACTGCGGCTTCCA 315
DB 437 ATCAAGAGAGTGGCAGAGGAAAGGTCACTTTGCGCTGCCACCATCAACTGCGGCTTCCA 496
QY 316 GAAAAAGACACTCTCTGGATATTGAAATGGCTGCTCACCCGATTAATGAAGGGAACCAAAAAGTG 375
DB 497 GAGAAAGACACCTCTGGACATTGANTGCTGCTCACCGATATGAAGGGAACCAAAAAGTG 556
QY 376 GTGATCACTTACTCCAGTCGTCATCTTCAATTAATTAAGTAAAGTTCAGGCGCTACGTGGAGC 435
DB 557 GTTATTACGTATTCCAGCGCTCATGTCTACAATAACTTGAACGAGGAGCAGAAAGGCCGA 616
QY 436 GTGCGCTTTCCTTCCAATTTCTTGGCAGGAGATGCTCTTGCAGATTGAACTCTGAGG 495
DB 617 GTGCGCTTTCCTTCCAATTTCTTGGCAGGAGATGCTCTTGCAGATTGAGCCTCTGAAA 676
QY 496 CCCAGTGTATGAGGCGCGGTACACCTGTAAAGTTAAGTAATTCAGGCGCTACGTGGAGC 555
DB 677 CCCAGTGTATGAGGCGAGATACACCTGCAGAGTGAAGATTGAGGACGCTATGTCTGGAGC 736
QY 556 CATGTCACTTTAAAAGTCTTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGAGAG 615
DB 737 CATGTCACTTTGAAAGTGTAGTGAGACCATCCAAGCCCAAGTGTGAGCTGGAAGGAGAG 796
QY 616 CTGACAGAGGAAGTGAACCTTTCAGTGTGAGTATCTCTTGGCAGCAGAGGCCATT 675
DB 797 CCGACCGAAGGAAGTGAACCTTTCAGTGTGAGTATCTCTTGGCAGCAGAGGCCATT 856
QY 676 GTGTATTACTGGCAGCGAATCCGAGAGAAAGAGGAGGAGGATGAACGCTGCTCTCCCAAA 735
DB 857 GTGTATTATTGGCAGCGAATCCGAGAGAAAGAGGAGGAGGATGAACACCTGCCACCCAAA 916
QY 736 TCTAGGATTGACTACAAACACCTTGGACGAGTCTTCTGTGAGAAATCTTTACCATGTCCTAC 795
DB 917 TCCAGAAATTGATTACAAACACCTTGGCGAGTGTGCTGTGCAGAAATCTCACCATGSCCTCC 976
QY 796 TCTGGACTGTACCAAGTGCACAGCAGGCGAAGCAAGCTGGGAAGGAAAGCTGTGTGTGCGA 855
DB 977 TCTGGGCTTTACCAAGTGCACAGCAGGCGAAGCAAGCTGGGAAGGAGGAGCTGTGTGTGACGG 1036
QY 856 GTAACCTGTACAGTATGTACAAAGCATCGGCATGGTTGTCAGGAGCGAGTGCACAGGCGATAGTG 915
DB 1037 GTGACTGTACAGTATGTGACAGCATTTGGCATGGTGGCAGGAGCGAGTGCACAGGCGATAGTG 1096
QY 916 GCTGGAGCCCTGCTGATTTTCTCTTGTGTGGCTGTCTTAATCCGAAGGAAAGACAAAGAA 975
DB 1097 GCAGGAGCCCTGCTCATTTTCTCTGTATGGCTGTCTTAATACGAAGGAAAGGAAAGAC 1156
QY 976 AGATATGAGGAAGAGAGACCTTAATGAATTCGAGAAAGATGCTGAAGAGCTTCAAAAGCC 1035

Wed May 11 07:24:22 2005

1157 AGATACGAGGAAGACAGACACCTAATGAATCCGAGAGAGCGCGAGAGGCCCGGAGCC 1216
 1036 CGTCTTGTGAAGCCAGCTCTCTTCTCAGAGCTCGGAGCTCAGCTCTGGTCTTCTTC 1095
 1217 GCGCTTGTGAAGCTAGCTCTCTTCTCAGGCTCCGAGCTCAGCTCTGGCTCTCTCC 1276
 1096 TCACCTCGCTCCACGCAATAGTGCCTCAGCAGCGGAGGACACTGTCACTACAGCCA 1155
 1277 TCCACCGCTCCACCGGAACAGTGCCTCCAGAAGCCAGCGAGCTGTGAGTGAAGCA 1336
 1156 GCACC--CCAGCCAGGCTGGCCACCAGGCATACAGCTAGTGGGGCCAGAGGTGAGA 1212
 1337 GCGCGCAGCAGCGCGGCTAGCCCGAGGACATACAGCTCTAGGACCGGAAGTGA 1396
 1213 GGTCTGACCAAGAAAGTCCACCATGCTAATCTGACCAAGAGCAAAACCCACCCAGC 1272
 1397 GGTCTGACCAAGAAAGTCCACCATGCTAATCTGACCAAGAGCAAAACCCACCCAGC 1456
 1273 ATGATCCCGCAGCAGCAGGCTTCCAAAGCTTCCAAAGCTTCTGACTTGAAGTGGCTCC 1332
 1457 ACAAGCCCGCAGCAGCAAGGCTTCCAAAGCTTCTGACTTGAAGTGGCTTGAAT--T 1514
 1333 AGCTTTCTAGAGTACAGGCTTCTTGGACTTCTTCTGACTTCTGCTATTTGGAGCTCAAGTCA--CC 1390
 1515 GCGCTTGGCCCAAGTCAAGTCTTACCTAGTCTAGTCTGAGTCTGCTCCACAGCCAGCA 1574
 1391 AGCCACACACACAGATGAGAGGCTATCTTAGTACGATGAGGATTCACGGAACAGATTC 1450
 1575 AGCCCTCAGCAGATACGATCTCACTTAAGTAGCTGCGAAGATGGCAGCCAG--TTC 1633
 1451 AGATGACATTTCTTATAC--ATACCAACAAAGCAAAAGGATGTAAGTGA--TTCAT 1507
 1634 TGATGATGCTCTTATATAGATACCAACAAACAAACAGGAGGAGGCTGACCATCT 1693
 1508 CTGTAAAAAGCATTTATTTGCTTTAGACAGAGTAAGGAAAGCAGGAGTCCAAT 1567
 1694 ATCTAAAGCAGCTCACTGTGCTTCAG--CAGAGTGGAGGAGGCGGCCAAGC 1752
 1568 CTATTTGTTACAGGACCTGTGTGTGAGAGGTTGGGGAAAGGTGAGTGAATATACCTA 1627
 1753 TTATTT-----TGTGAAATAAAGGAAAGGTGAGGCTGCAACACCTG 1796
 1628 AAATCTTTAATGTGGATTTTGTATCAGTCTTTCATTCACAAATTTTCAAGAGGAAT 1687
 1797 AAACATCTTACCTAGATGTTGCAAGTCA-----CCACAGTCAAGAAGAAGCG 1844
 1688 GGGATCTGTTGTAAATTTCTATGCAATTTCTCAAACTTATTTGGATTATAG--TTAT 1745
 1845 GGAATCTGTAGATCAATTTCTATTTCTGCAAAATTTATTTGGATTATGTTGATAT 1904
 1746 TCAGACAGTCAAG--CAGAACCCACAGCCTTAT--TACACCTGTCTACACCATGTACTGAG 1802
 1905 TCAGATAGTCAAAACAGAGAGCCGCTTATATATACCTATCTGCAACATGTACTGGG 1964
 1803 CTAAACATCTTAAGAACTCCAAAGAGGAA-----ACATGTGTC 1843
 1965 AGAATCTGTTTAAAGATTCATTTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2024
 1844 TTCTATTCTGACTTAATCTTATTTGTATAGGTTTGGATATTAATTTCAAGGGGAGGTTG 1903
 2025 TTCTACTTTGACTTGAATCTTGTGTGTAAGGTTTGAAGCTTGTGGGAGGAGTTGC 2084
 1904 AAATAGTGGAGATGGAGAGAGTGAATGAGTTTCTCCACTCTATATCAATCTCACTAT 1963
 2085 AATGTGGAGACAGAGAAAGGAGCTTTCTTCTTACCTCATCAACAGCAATCTTCCCTAT 2144
 1964 TTGTATTGAGCCCAAAATACTATGAAGGAGCAAA-----AATTTGTGCAAGGAT 2017
 2145 TTCCGTCGAAACCTTAAATATATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2204
 2018 TGTGAAGAGCTTCCATCTTCTCATGATGTTATGAGGATTTGTGACCAACAT--TAGAATAT 2076
 2205 TCTGAAGAGCTTTC---CTTTTGTATATTCAGAGGCTTGACACAGATATCAAGAGAT 2261

2077 APTATGGAGCAATTTGTGATTTCCCTCAAT-----CAGATGCTCTTAAGGACTTTCCTG 2132
 2262 ATCCGGGGCAGTGTGGCTCTTTATTCATTTGACTGACTCCCTTAAAGACTTCTCTG 2321
 2133 CTAGATATTTCTGGAAGGAGAAAT-----ACAAATGTCATTTATCAACGTCCTTAGAAA 2188
 2322 CTGGATGTTTCTAGGAGAAACAAATACTCACTACATGTCACCTTAATGATGTCCTTAGGG 2381
 2189 GAATCTTCTAGAGAAAGGATCTAGAAATGCTGAAAGATTACCCCAACATCATAT 2248
 2382 ACAGTCTCTAGAG--AAAGTCTCTCAGGATGTTGAAAGATCCCTTTGCATACCATTC 2439
 2249 AGTCTCTTCTTCTGAGAAATGTTGAAACCAAGATTCGAGCTGGGTGGACTAGAAAGG 2308
 2440 CTGCTCTCTTCTTCTGGAACCAAGACCAACAGATTTCAAGACTGCTTGGATAGAGAGG 2499
 2309 GAGATTAGATCAGTCTTCTTCTTAATATGTCMAAGGA 2344
 2500 GAGAGTAGACC---TTTCTCTCAGTAGTCAAGGA 2532

RESULT 3
 AK028983
 LOCUS
 DEFINITION
 Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:473247P04 product:ADIPCYTE-SPECIFIC PROTEIN 5, full insert sequence.

ACCESSION
 AK028983
 VERSION
 AK028983.1 GI:26081115
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2
 Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-Format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

REFERENCE	6 (bases 1 to 4017)	Qy	376	GTGATCACTTACTCTCAGTCTGTCATGTCTTAACTTGA	435
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	Db	525	GTTATTACGATTTCAGCCGTCATGTCTTACAACTTAACTTGA	584
TITLE	Direct Submission	Qy	436	GTGGCTTTGCTTCCAAATTTCTCGCAGGAGATCCCTCTTGCAGATTGA	495
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]	Db	585	GTGGCTTTGCTTCCAACTTCTCGCAGGAGATGCTCTCCCTGCAGATTGAG	644
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.	Qy	496	CCCAAGTATGAGGCGCGGTACACCTGTAAGGTAAAGAAATTCAGGGCGCTAC	555
FEATURES	Location/Qualifiers	Db	645	CCCAAGTATGAGGCGCGGTACACCTGTAAGGTAAAGAAATTCAGGGCGCTAC	704
source	1. 4017 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM.DB:4732477P04" /db_xref="taxon:10090" /clone="4732477P04" /tissue_type="skin" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="10 days neonate"	Qy	556	CATCTCATTTAAAAGTCTTAGTGAGACCATCAAGCCAAAGTGTGAGTTGGA	615
misc_feature	343..1463 /note="AD1POCYTE-SPECIFIC PROTEIN 5 (SPTR Q920S5, evidence: FASTY, 99.7%ID, 100%length, match=1119) putative"	Db	705	CATGTCACTTTGAAAGTGCTAGTGAGACCATCAAGCCAAAGTGTGAGCTG	764
ORIGIN	Query Match 45.8%; Score 1126.4; DB 3; Length 4017; Best Local Similarity 74.7%; Pred. No. 2.4e-285; Matches 1777; Conservative 0; Mismatches 501; Indels 100; Gaps 25;	Qy	616	CTGACAGAGGAGTGAACCTGACCTTTTCAGTGTCAGTTCATCTCTGGCACA	675
		Db	765	CCGACCAAGGAAGTGAACCTGACCTGCGGTGTGAGTCTGCTCTGGAAC	824
		Qy	676	GTGTATTACTGGCAGCGAATCCGAGAGAAAGAGGAGGATGAACGTCTGCT	735
		Db	825	GTGTATTATTGGCAGCGAATCCGAGAGAAAGGAGGAGGATGAACCTTCC	884
		Qy	736	TCTAGGATTGACTACAAACCCCTGGACGAGTTCTGTGCGAGAAATTTTAC	795
		Db	885	TCCAGAAATTTGATTACAAACCAACCCCTGGCGGAGTGTCTGTCAGAAAT	944
		Qy	796	TCTGGACTGACCTGAGTGCACAGCAGGCAACGAACTGGGAGGAAAGTGTG	855
		Db	945	TCTGGGCTTTTACCAAGTGCACAGCAGGCAACGAACTGGGAGGAGGAGT	1004
		Qy	856	GTAATCTGTACAGTATGTACAAAGCATCGGCATGTGTGCGAGCAGATGAC	915
		Db	1005	GTGACTGTACAGTATGTGCGAGGCAATTTGGCATGTGTGCGAGGAGCAGT	1064
		Qy	916	GCTGGAGCCCTGCTGATTTTCTCTTGGTGTGCTTAATCCGAAAGGAAAGA	975
		Db	1065	GCAGGAGCCCTGCTCAATTTTCTCTGATATGGTGTCTTAATACGAAGGAA	1124
		Qy	976	AGATATGAGGAGGAGAGACCTTAATGAAATTCGAGAGATGCTGAGCTCCA	1035
		Db	1125	AGATACAGGAGGAGGAGACCTTAATGAAATTCGAGAGACGCGGAGCCGC	1184
		Qy	1036	CGTCTGTGAAACCCAGCTCTCTCTCAGGCTCTCGAGCTCACGCTCTGGT	1095
		Db	1185	CGCTTGTGAAGCTTAGCTCTCTCTCAGGCTCCCGAGCTCACGCTCTGG	1244
		Qy	1096	TCCAATCGCTCCACAGCAATATAGTGCCTCAGCAGCAGCGGACACTGT	1155
		Db	1245	TCCACCGCTCCACCGGAAACAGTGCCTCCAGAAAGCCAGCGGAGCTGT	1304
		Qy	1156	GCACC---CCAGCCAGGCTGGCCACCCAGCATACAGCTTAGTGGGCGAG	1212
		Db	1305	CGCCGCGAGCAGCCCGGCTAGCCCGCAGCATACAGCTCATAGGACCGGA	1364
		Qy	1213	GGTTCTGAACCAAGAAAGTCCACATGTCTGACCAAGCAGAAACACACCC	1272
		Db	1365	GGTTCTGAACCAAGAAAGTCCACATGTCTGACCAAGCAGAAACACAC	1424
		Qy	1273	ATGATCCCCAGCCAGCAGAGCCTTCCAAACCGGTCTGAATTAACAATGA	1332
		Db	1425	ACACGCCAGCCAGCAGAAAGCTTCCAAACCTGTCTGACTTAGAGTGA	1482
		Qy	1333	ACGCTTCTTAGAGTACAGGTCTTTTGGACTCTTCTGTCATTTGGAGTCA	1390
		Db	1483	CGCTTGTCCCAAGTCAAGATCTTAGCTAGTCACTGGAGCTGTCCACG	1542
		Qy	1391	AGCCACACACACAGATGAGAGGTTCATCTAAGTAGCAGTGAGCTTGCAC	1450
		Db	1543	AGCCCCCTCAGCCAGATAGTCTCACTTAAGTAGCTGAGAAATGGCACG	1601

source	1..1945	/organism="Mus musculus"	
		/mol_type="mRNA"	
		/strain="C57BL/6J"	
		/db_xref="PANTOM.DB:A730044A20"	
		/db_xref="taxon:10090"	
		/clone="A730044A20"	
		/tissue_type="cerebellum"	
		/clone_lib="RIKEN full-length enriched mouse cDNA library"	
		/dev_stages="7 days neonate"	
misc_feature	327..1450		
		/note="ADIPOCYTE-SPECIFIC PROTEIN 5 (SPTR Q92085, evidence: FASTY, 99.7%ID, 100*length, match=1119) putative"	
ORIGIN			
Query Match	41.5%;	Score 1020.2;	DB 3; Length 1945;
Best Local Similarity	79.4%;	Pred. No. 2e-257;	
Matches 1448; Conservative	0;	Mismatches 318; Indels 57; Gaps 18;	
Qy	16	CTGCCCCCAGGGGACACGGGGCGCGGGCGCGGCTCCCGCCCGGCACATGGCTGCAGCCACC	75
Db	160	CAGCGCAGGGGACCCCGGCGCGGGCGCAGGGCCC-----GCACATGGCTGCAGCC-CC	213
Qy	76	TCGGCGGACCCCGAGGGCGCGCGCCACAGCTGCGCCGAGGTCCGTTCGAGGCGCCCGGCCC	135
Db	214	CCGCGCGACCCCGAGGGCGCGCGCCCTGCTGCACAGAAAGTCCGTTCGCTGGGCTCGGTC	273
Qy	136	GCCCGGAGCCACAGCACAGCTGAGCGGGGAAGCCCGCGCTGCGGGGATCGGGATGTGCC	195
Db	274	GCCCTGCAGCAGCGGTGC-GCTGAGCGGGGAAGTGCCTGCTCCGAGATCGGGATGTGCC	332
Qy	196	CTCCTCCTTCTCCTCTTGTCTAGTTTCCTACTATGTTGGAACTTTGGGAGCTCACACTGAG	255
Db	333	CTCTTC---TTCCTCTGGCTAGTATCCTATTATGTTGGAACGCTGGGAACTCACACTGAG	389
Qy	256	ATCAAGAGAGTGGCAGAGGAAAAAGGTCACTTTTGGCCCTGCCACCAATCAACTGGGGCTTCCA	315
Db	390	ATCAAGAGAGTGGCAGAGGAAAAAGTTACCTTTGCCCTGTCAACATCAACTGGGGCTTCCC	449
Qy	316	GMAAAGACACTCTGGATATTGAATGCTGCTCAACGATATGAGGGGACCAAAAGTG	375
Db	450	GAGAAAGACACCTTGGACATTGGAATGGCTGCTCAACGATATGAAGGGGAACCAAAAGTG	509
Qy	376	GTGATCACTTACTCCAGTCGTCACTGTCTACAATACTTGACTGAGGAAACAGAAGGGCGGA	435
Db	510	GTTATTAGTATTCCAGCGCTCATGTCTACANTAACTTGACCGAGGAGCAGNAGGGCCGA	569
Qy	436	GTGGCCTTTGCTTCCAAATTTCTTGGCAGGAGATGCCTCTCTTTGCAGATTGAACCTCTGAAG	495
Db	570	GTGGCCTTCGCTTCCAACTTCTTGGCAGGAGATGCTTCCCTGTCAGATTGAGCCTCTGAAA	629
Qy	496	CCNAGTATGAGGGCCGGTACACCTGTAAAGTTAAGAAATTCAGGGCCGTACGTGTGGAGC	555
Db	630	CCCAGTATGAAGGCGCATACACTGCAAGGTGAAGAAATTCAGGACCGTATGTCTGGAGC	689
Qy	556	CATGTCACTTTAAAAGTCTTAGTGAGACCATCCAAAGCCCAAAGTGTGAGTTTGGAAAGGAG	615
Db	690	CATGTCACTTTGAAAGTGCTAGTGAGACCATCCAAAGCCCAAAGTGTGAGTTGGAAGGAG	749
Qy	616	CTGACAGAAGGAGTGACTGACTTTTGCAGTGTGAGTCACTCTCTGGCAGACGCCATT	675
Db	750	CCGACCGAAGGAGTGACCTGACGCTGCAGTGTGAGTCTGCGCTCTGGAACTTAAGCCCAT	809
Qy	676	GTGTATTCTGGCAGCGAATCCGAGAGNAGAGGGAGGAGNGATGAACGTCTGCCTCTCCAAA	735
Db	810	GTGTATTATTGGCAGCGAAATCCGGGAAAGGAGGGGAAGATGAACCTCTGCCACCCAAA	869
Qy	736	TCTAGGATTGACTACAAACCCCTGGACGAGTTCTGCTGCGAGAATCTTACCATGTCTCTAC	795
Db	870	TCCAGAATTGATTACAACAACCTTGGCCGAGTGTGCTGCAAGAATCTCAACATGGCCTCC	929
Qy	796	TCTGGACTGTACCAG-TGCACAGCAGGCAACGAAGCTGGGAAGGAAGAGCTGTGTGGTGCG	854

QY	1070	CTCGAGCTCAGCGTCTGTTCTTCTCCCTCACTGGCTCCACAGCAAAATAGTGCTCACGCA	1129		
Db	723	CTCGG-GGTGACGCTCTGGTCTTCTCACTGGCTCCACAGCAAAATAGTGCTCACGCA	665		
QY	1130	GCACGGGACACTGTCAACTGACGAGGACCCGAGCCAGGCGTGGCCACCCAGGCAATACA	1189		
Db	664	GCACGGGACACTGTCAACTGACGAGGACCCGAGGCGTGGCCACCCAGGCAATACA	605		
QY	1190	GCTAGTGGGGCAGAGGTGAGAGGTTCTGAACCAAAAGAAAGTCCACATGCTTAATCTGA	1249		
Db	604	GCTAGTGGGGCAGAGGTGAGAGGTTCTGAACCAAAAGAAAGTCCACATGCTTAATCTGA	545		
QY	1250	CCAAAGCAGAAACCAACCCAGCATGATCCCGCCGAGA-GCAGAGCGTTCCTCAAAACGGTC	1308		
Db	544	CCAAAGCAGAAACCAACCCAGCATGATCCCGCCGAGA-GCAGAGCGTTCCTCAAAACGGTC	485		
QY	1309	TGAATTACATGACCTTGAATCCCAACGCTTCTCTAGGAGTCAAGGCTCTTTGGAGCTCTTCT	1368		
Db	484	TGAATTACATGACCTTGAATCCCAACGCTTCTCTAGGAGTCAAGGCTCTTTGGAGCTCTTCT	425		
QY	1369	CGTCATTTGGAGCTCAAGTCAACGACCAACACGAGATGAGAGGTCATCTAAGTAGCAGT	1428		
Db	424	CGTCATTTGGAGCTCAAGTCAACGACCAACACGAGATGAGAGGTCATCTAAGTAGCAGT	365		
QY	1429	GAGCATTTGCAGGAAACAGATTCAGATGAGCATTTCTTATACATACCAACACAGCAAA	1488		
Db	364	GAGCATTTGCAGGAAACAGATTCAGATGAGCATTTCTTATACATACCAACACAGCAAA	305		
QY	1489	AGGATGTAAGCTGATTCATCTGTAAAAGGCACTTTATTGTGCTTTTAGACACAGAGTAAG	1548		
Db	304	AGGATGTAAGCTGATTCATCTGTAAAAGGCACTTTATTGTGCTTTTAGACACAGAGTAAG	245		
QY	1549	GCAGGAGGAGTCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAA	1608		
Db	244	GCAGGAGGAGTCCAAATCTATTGTTGACAGGACCTGTGTGAGAGGTTGGGAAA	185		
QY	1609	GGTGAGGTGAATATACCTTAAACCTTTAAATGTGGGATATTTTATCAGTGTCTTGAATC	1668		
Db	184	GGTGAGGTGAATATACCTTAAACCTTTAAATGTGGGATATTTTATCAGTGTCTTGAATC	125		
QY	1669	ACAATTTTCAAGAGGAAATGGAGTCTGTTGTAATTTTCTATGCAATTTCTGCAAACTT	1728		
Db	124	ACAATTTTCAAGAGGAAATGGAGTCTGTTGTAATTTTCTATGCAATTTCTGCAAACTT	65		
QY	1729	ATTGGAATATTAGTATTTCAGACAGTCAAGCAGAACCCACAGCCTTAT	1776		
Db	64	ATTGGAATATTAGTATTTCAGACAGTCAAGCAGAACCCACAGCCTTAT	17		
RESULT 6					
LOCUS	AY406755	1036 bp	DNA linear		
DEFINITION	Homo sapiens HCM2663 gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY406755				
VERSION	AY406755.1	GI:39762726			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1036) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferreria, S., Wang, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1036)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,				

```

BX395411/c      1162 bp      mRNA      linear      EST 01-MAY-2004
LOCUS          BX395411 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION     cDNA clone CS0DD007YF18 3-PRIME, mRNA sequence.

ACCESSION      BX395411
VERSION        BX395411.2 GI:46921137
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1162)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30628536.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6140.x

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DD007DC09NP1&c=6140.x.

FEATURES             Location/Qualifiers
     1..1162
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clones="CS0DD007YF18"
        /tissue types="NEUROBLASTOMA COT 50-NORMALIZED"
        /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR v
        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match           39.8%; Score 977.6; DB 5; Length 1162;
Best Local Similarity 93.1%; Pred. No. 3e-246;
Matches 1050; Conservative 22; Mismatches 50; Indels 6; Gaps 5;

Qy   652 TCATCTCTGGCACAGCCCATGTGTATTACTTCGCGAGCAATCCGAGAGAAGAGGA 711
Db   1141 TAATCTWACYTTGGACAGRCCTTTTATTAHTGGMAGSGAA-CGGABAGAARGGGA 1083

Qy   712 GAGGATGAACGCTGCCTCCCNAATCTAGGATTGACTACACCACCTCGAGCAGTTCTG 771
Db   1082 G-RGWTGAACCTVTCTCCCAAATYTAGGATTTAAMAAYAACNACCTTGACGGAGTCTG 1024

Qy   772 CTGCAGAAATCTTACCATGTCCTACTCTGCAGTGTACAAGTGCACAGCAGCAACGAGCT 831
Db   1023 CTGCAAAATTTTACCTTGTCCTACTCTGTMGTGTACCACTGAA-CAGCAGGCAACGAGCT 964

Qy   832 GGGAGGAGAAAGCTGTGTGGTGCAGTAACTGTACAGTATGTACAAAGCATCGGCATGGTT 891
Db   963 GGGAGGAGAAAGCTTTTGTGGTGCAGTATGTACAGTATGTACAAAGCACCAGCATGTT 904

Qy   892 GCAGGAGCAGTGA--CAGGCATAGTGGCTGGAGCCCTGCTGATTTTCTTGTGTGGC 949
Db   903 GCRGDGCCAATTACAGGCATTAGTGGCTGGAGCCCTGCTGATTTTCTTGTGTGGC 844

Qy   950 TGCTTAATCCGAAGGAAAGACAAGAAGATATGAGGAAGAGAGACTTAATAAATTC 1009
Db   843 TGCTTAATCCGAAGGAAAGACAAGAAGATATGAGGAAGAGAGACTTAATAAATTC 784

Qy   1010 GAGAGATGCTGAAGCTCCAAGACCCTGCTTGTGAAACCCAGTCTCTTCCTCAGCT 1069
Db   783 GAGAAGATGCTGAAGCTCCAAGACCCTGCTTGTGAAACCCRGCTCTCTTCCTCAGCT 724

```



```
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850 USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
    source
        Location/Qualifiers
            1..1036
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                <!.>1036
                /locus_tag="HCM2663"
    gene
    ORIGIN
        Query Match      36.4%; Score 894; DB 9; Length 1036;
        Best Local Similarity 86.3%; Pred. No. 3.4e-224;
        Matches 894; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 218 TTTCTACTATGTTGGAACCTTGGGACTTCACACTGAGATCAAGAGAGTGGCAGAGGAAA 277
Db 1 TTTCTACTATGTTGGAACCTTGGGACTTCACACTGAGATCAAGAGAGTGGCAGAGGAAA 60

Qy 278 AGGTCACTTTGCCCTGGCCACCATCAACTGGGCTTCCAGAAAAAGACACTCTGGATATTG 337
Db 61 AGGTCACTTTGCCCTGGCCACCATCAACTGGGCTTCCAGAAAAAGACACTCTGGATATTG 120

Qy 338 AATGGCTCTCACCAGTAATGAAGGAACCAAAAAGTGGTGATCACTTACTCCAGTCCTC 397
Db 121 AATGGCTCTCACCAGTAATGAAGGAACCAAAAAGTGGTGATCACTTACTCCAGTCCTC 180

Qy 398 ATGTCTACAATAACTTGTACTGAGGAACAGAGGGCCGAGTGGCCCTTTCCTTCCAATTTCC 457
Db 181 ATGTCTACAATAACTTGTACTGAGGAACAGAGGGCCGAGTGGCCCTTTCCTTCCAATTTCC 240

Qy 458 TGGCAGGAGATGCCTCTTGCAGATTGAACCTCTGAAAGCCAGCGATGATGAGGCGCGGTACA 517
Db 241 TGGCAGGAGATGCCTCTTGCAGATTGAACCTCTGAAAGCCAGCGATGATGAGGCGCGGTACA 300

Qy 518 CTTGTAGGTTAAGNATTCAGGGCGCTACGTGTGGAGCCATGTCTATTAAGTCTTAG 577
Db 301 CTTGTAGGTTAAGNATTCAGGGCGCTACGTGTGGAGCCATGTCTATTAAGTCTTAG 360

Qy 578 TGAGACCATCAAGCCCAAGTGTAGTTGGAAGGAGAGCTGACAGAAGGAAGTGAACCTGA 637
Db 361 TGAGACCATCAAGCCCAAGTGTAGTTGGAAGGAGAGCTGACAGAAGGAAGTGAACCTGA 420

Qy 638 CTTTGCAGTGTGAGTATCCTCTGGCAGACAGGCCATTGTGTATTACTGGCAGCGAATCC 697
Db 421 CTTTGCAGTGTGAGTATCCTCTGGCAGACAGGCCATTGTGTATTACTGGCAGCGAATCC 480

Qy 698 GAGAGAAAGAGGAGAGATGAACGTCTGCCTCCCAAACTAGAGTTGACTACAAACACC 757
Db 481 GAGAGAAAGAGGAGAGATGAACGTCTGCCTCCCAAACTAGAGTTGACTACAAACACC 540

Qy 758 CTGACAGATTCTGCTGAGAAATCTTACCATGCTCTCTGACTGTGACCTGACAGTGCACAG 817
Db 541 CTGACAGATTCTGCTGAGAAATCTTACCATGCTCTCTGACTGTGACCTGACAGTGCACAG 600

Qy 818 CAGGCAACGAAGCTGGGAAGAAAGCTGTGTGGTGCAGAGTAACCTGTACAGTATGTACAAA 877
Db 601 CAGGCAACGAAGCTGGGAAGAAAGCTGTGTGGTGCAGAGTAACCTGTACAGTATGTACAAA 660

Qy 878 GCATCGGCATGGTTCAGGAGCAGTGA CAGGCATAGTGGCTGGAGCCCTGCTGATTTTCC 937
Db 661 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy 938 TCTTGGTGTGCTGCTAATCCGAGGAAGACAAAGAAAGATATGAGGAAGAGAGAC 997
Db 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
```

```
998 CTAATGAAATTCGAGAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCT 1057
781 NNNNNNNNNNNNAGAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCTCT 840

Qy 1058 CTTCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCCACTCGTCCACAGCAATA 1117
Db 841 CTTCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCCACTCGTCCACAGCAATA 900

Qy 1118 GTGCTCTCAGCAGCAGCGGACACTGTCAACTGACGACGACCCAGCAGCGGCTGGCCA 1177
Db 901 GTGCTCTCAGCAGCAGCGGACACTGTCAACTGACGACGACCCAGCAGCGGCTGGCCA 960

Qy 1178 CCCAGGCATACAGCTAGTGGGGCAGAGGTGAGAGTTCTGAACCAAGAAGTCCACC 1237
Db 961 CCCAGGCATACAGCTAGTGGGGCAGAGGTGAGAGTTCTGAACCAAGAAGTCCACC 1020

Qy 1238 ATGCTAATCTGACCAA 1253
Db 1021 ATGCTAATCTGACCAA 1036

RESULT 7
BX334131
LOCUS BX334131 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DD007F18 5-PRIME, mRNA sequence.
ACCESSION BX334131
VERSION BX334131.2 GI:46262369
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 979)
AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 1, 2003 this sequence version replaced gi:30308253.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6140.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CS0DD007DC09QPI&c=6140.r.
FEATURES
    source
        1..979
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DD007F18"
            /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
            /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo (dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and EcoR V sites of the pCMVSPORT 6
            vector. Library was normalized."
    ORIGIN
        Query Match      32.8%; Score 806.4; DB 5; Length 979;
        Best Local Similarity 98.3%; Pred. No. 4.4e-201;
        Matches 855; Conservative 2; Mismatches 8; Indels 5; Gaps 4;

Qy 1 GCGCCGGAGGCCCATCTGCCCCAGGGGACAGGGCGCGGGCGGGTCCCGCCCGGCAC 60
Db 98 GCGCCGGAGGCCCATCTGCCCCAGGGGACAGGGCGCGGGCGGGTCCCGCCCGGCAC 157

Qy 61 ATGCTGAGCCACCTCGCGGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGTCCGT 120
```


Db	398	ATGAGCATTTCCTTTATACAAACAGACAAAAGGATGTAAAGCTGATTCATCTGTA	339
Qy	1513	AAAAGGCATCTTATTGTGCGCTTTAGACACAGAGTAAGCGAAAGCAGGAGTCCAAATCTATT	1572
Db	338	AAAAGGCATCTTATTGTGCGCTTTAGACACAGAGTAAGCGAAAGCAGGAGTCCAAATCTATT	279
Qy	1573	TGTTGACACGAGCACTGTGGTGAGAAAGTGTGGGAAAGCTGAGGTGAATATACCTTAAAACT	1632
Db	278	TGTTGACACGAGCACTGTGGTGAGAAAGTGTGGGAAAGCTGAGGTGAATATACCTTAAAACT	219
Qy	1633	TTTAAATGTGGGATATTTTGTATCAGTGCCTTTGATTCAAAATTTTCAAGAGGAAATGGGAT	1692
Db	218	TTTAAATGTGGGATATTTTGTATCAGTGCCTTTGATTCAAAATTTTCAAGAGGAAATGGGAT	159
Qy	1693	GCTGTTTGTAAATTTCTATGCATTTCTGCAACTTATTGGATTTATTAGTTATTCAGACA	1752
Db	158	GCTGTTTGTAAATTTCTATGCATTTCTGCAACTTATTGGATTTATTAGTTATTCAGACA	99
Qy	1753	GTCAGCAGAACCCACAGCCTTTATTACCTGTCTACCATGTACTGAGCTAACCACTT	1812
Db	98	GTCAGCAGAACCCACAGCCTTTATTACCTGTCTACCATGTACTGAGCTAACCACTT	39
Qy	1813	CTAAGAAACTCCAAAAAGGAAACA	1837
Db	38	CTAAGAAACTCCAAAAAGGAAACA	14

RESULT 9					
BX113005					
LOCUS	732 bp	mRNA	linear	EST 07-FEB-2003	
DEFINITION	Soares	total_fetus	Nb2HF8_9w	Homo sapiens	cdna clone
	INAGP998G114207			IMAGE:1657762,	mRNA sequence.

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1. (bases 1 to 1039) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trics
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2. (bases 1 to 1039) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
AUTHORS	Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..1039
gene	/organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>1039 /locus_tag="HCM2663"
ORIGIN	
Query Match	28.8%; Score 708.2; DB 9; Length 1039;
Best Local Similarity	75.6%; Pred. No. 3.7e-175;
Matches	786; Conservative 0; Mismatches 250; Indels 3; Gaps 1;
QY	218 TTTCTCTACTATGTTGGAACTTTGGGAGCTCACCTGAGATCAAGAGAGTGGCAGAGGAA 277
Db	1 TATCCTATTATGTTGGACGCTGGGAACTCACCTGAGATCAAGAGAGTGGCAGAGGAA 60
QY	278 AGGTCACTTTGGCTGCGACATCAACTCTGGGCTTCCAGAAAAAGACACACTCTGGATATTG 337
Db	61 AGGTACCTTTGGCTGCGCTGTACCACTCAACTGGGCTTCCCGAAGAGACACCCCTGGACATTG 120
QY	338 AATGGCTGTCTACCGATAATGAAGGAAACCAAAAAAGTGGTGAATCACTTACTCAGTCGTC 397
Db	121 AATGGCTGTCTACCGATATGAAGGAAACCAAAAAAGTGGTATTATCATATTTCCAGCCGTC 180
QY	398 ATGTCTACAATAACTTGACTTGAGGAACAGAGGGCGAGTGCGCTTCCTTCCAAATTTCC 457
Db	181 ATGTCTACAATAACTTGACCGAGGACGAGAGGGCGAGTGCGCTTCCTTCCAAATTTCC 240
QY	458 TGGCAGAGATGCTCCTCTGCAGATTGAACCTCTGAAGCCCAAGTGAAGGGCCCGGTACA 517
Db	241 TGGCAGAGATGCTCCTCTGCAGATTGAAGCCCAAGTGAAGGGCCCGGTACA 300
QY	518 CCTGTAAAGTTAAGAAATTACGGGCGTACGTGTGGAGCCATGTCATCTTTAAAGTCTTAG 577
Db	301 CCTGCAAGTTGAAGAAATTACGGAGCGTATGCTGGAGCCATGTCATCTTTAAAGTCTTAG 360
QY	578 TGAGACCATCCAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAAGAGTGAACCTGA 637
Db	361 TGAGACCATCCAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAAGAGTGAACCTGA 420
QY	638 CTTTTCAGTGTGAGTCACTCTCTGGCACAGAGCCCATTTGTATTACTTGGCAGCGAATCC 697
Db	421 CCGTCGAGTGTGAGTCTCGCTCTGGAATAGGCCCATTTGTATTATTATTTGGCAGCGAATCC 480
QY	698 GAGAGAAAGGGGAGAGATGAAGCTGTGCTGCCCTCCCAATCTTAGGATTGACTACAAACACC 757
Db	481 GGGAGAAAGGGGAGAGATGAACCTGTGCCACCCCAATCCAGAAATGATTATCAACAACCC 540


```
/clone_lib="NCI_CGAP_ED1"
/Note="Organ: Left Pubic Bone; Vector: p7T73-Pac
(Pharmacia) with a modified polylinker; Site 1: Ecor I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an Ecor I adaptor, digested with Not
I, and cloned directionally into p7T73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG TISSUE=chondrosarcoma
TAG LIB=UI-H-ED1
TAG_SEQ=CGTCAGGCT"

ORIGIN
Query Match      28.5%; Score 699.8; DB 5; Length 719;
Best Local Similarity 99.7%; Pred. No. 5.5e-173;
Matches 701; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1095 CTCACCTCGCTCCACAGCAATAGTGCCTCAGCAGCCAGCGGACACTGTCACTGACGC 1154
Db 719 CTCACCTCGCTCCACAGCAATAGTGCCTCAGCAGCCAGCGGACACTGTCACTGACGC 660

Qy 1155 AGCACCCAGCAGCGCTGGCCACCCAGGCATACAGCCTAGTGGGCCAGAGGTCAGAGG 1214
Db 659 AGCACCCAGCAGCGCTGGCCACCCAGGCATACAGCCTAGTGGGCCAGAGGTCAGAGG 600

Qy 1215 TTCTGAACCAAGAAGTCCACCATGCTTAATCTGACCAAAAGCAGAAACACACCCAGCAT 1274
Db 599 TTCTGAACCAAGAAGTCCACCATGCTTAATCTGACCAAAAGCAGAAACACACCCAGCAT 540

Qy 1275 GATCCCGCAGCAGAGAGGCTTCCAAACCGTCTGAATTAACAATGACTGCTCCAC 1334
Db 539 GATCCCGCAGCAGAGAGGCTTCCAAACCGTCTGAATTAACAATGACTGCTCCAC 480

Qy 1335 GCTTTCTTAGAGTCAGGCTCTTGGACTCTTCTGCTATTTGGAGCTCAAGTCCACGACC 1394
Db 479 GCTTTCTTAGAGTCAGGCTCTTGGACTCTTCTGCTATTTGGAGCTCAAGTCCACGACC 420

Qy 1395 ACACAAACAGATGAGAGTCTATCTAAGTAGCAGTGAGCATTTGCACGGAACAGATTTCAGAT 1454
Db 419 ACACAAACAGATGAGAGTCTATCTAAGTAGCAGTGAGCATTTGCACGGAACAGATTTCAGAT 360

Qy 1455 GAGCATTTTCTTATACAAATACCAAAACAGCAAAAGGATGTAAGCTGATTCATCTGTAAA 1514
Db 359 GAGCATTTTCTTATACAAATACCAAAACAGCAAAAGGATGTAAGCTGATTCATCTGTAAA 300

Qy 1515 AAGCATCTTATTTGCTTTAGACAGAGTAAGGGAAGCAGGAGTCCAAATCTATTG 1574
Db 299 AAGCATCTTATTTGCTTTAGACAGAGTAAGGGAAGCAGGAGTCCAAATCTATTG 240

Qy 1575 TTGACCAAGGACTGTGGTGGAAGGTTGGGGAAGGTCAGGTGAATATACCTTAAACTTT 1634
Db 239 TTGACCAAGGACTGTGGTGGAAGGTTGGGGAAGGTCAGGTGAATATACCTTAAACTTT 180

Qy 1635 TAATGTGGGATTAATTTGATCAGTCTTTGATTCACAAATTTTCAAGAGGAAATGGGATGC 1694
Db 179 TAATGTGGGATTAATTTGATCAGTCTTTGATTCACAAATTTTCAAGAGGAAATGGGATGC 120

Qy 1695 TGTTGTAAATTTTCTATGCAATTTCTGCAACTTATTTGGATATATAGTTATTCAGACAGT 1754
Db 119 TGTTGTAAATTTTCTATGCAATTTCTGCAACTTATTTGGATATATAGTTATTCAGACAGT 60

Qy 1755 CAAGCAGAAACCCACAGCCTTATTAACACCTGTCTACCCATGTA 1797
Db 59 CAAGCAGAAACCCACAGCCTTATTAACACCTGTCTACCCATGTA 17
```

```
RESULT 12
CB265996      706 bp      mRNA      linear      EST 20-FEB-2003
LOCUS      1004901 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
DEFINITION      cDNA 5', mRNA sequence.
ACCESSION      CB265996
VERSION      CB265996.1 GI:28440584
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Mammalia; Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 706)
AUTHORS      Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
TITLE      EST analysis of human adipose gene expression
JOURNAL      Unpublished (2002)
COMMENT      Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGGAAGCGGCCATTTGTGTGGT
BACKWARD: AATACGACTACTATAGGGCGAATTGG
Seq primer: GTTGGTACCCGGGAATTC.
FEATURES
Location/Qualifiers
1..706
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Male and Female"
/tissue_type="Adipose"
/clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
/note="Vector: lambdaTriplex"

ORIGIN
Query Match      27.9%; Score 686.8; DB 6; Length 706;
Best Local Similarity 98.3%; Pred. No. 1.5e-169;
Matches 694; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 810 GTGCACAGCAGGCAACGAAGCTGGGAAGGAAGTGTGTGTGGAGTAACCTGTACAGTA 869
Db 1 GTGCACAGCAGGCAACGAAGCTGGGAAGGAAGTGTGTGTGGAGTAACCTGTACAGTA 60

Qy 870 TGTACAAGCATCGGCATGTTGCAGGAGCAGTCACAGGCATAGTGGCTGGAGCCCTGCT 929
Db 61 TGTACAAGCATCGGCATGTTGCAGGAGCAGTCACAGGCATAGTGGCTGGAGCCCTGCT 120

Qy 930 GATTTTCTCTTGTGTGGCTGCTTAATCCGAAGGAAGACAAAGAAAGATATGAGGAAGA 989
Db 121 GATTTTCTCTTGTGTGGCTGCTTAATCCGAAGGAAGACAAAGAAAGATATGAGGAAGA 180

Qy 990 AGAGAGACCTTAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTTTGTGAAACC 1049
Db 181 AGAGAGACCTTAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTTTGTGAAACC 240

Qy 1050 CAGTCTCTCTCTCAGGCTCTCGAGCTCAGCTCTGCTTCTTCTCCCTCCCTCCAC 1109
Db 241 CAGTCTCTCTCTCAGGCTCTCGAGCTCAGCTCTGCTTCTTCTCCCTCCCTCCAC 300

Qy 1110 AGCAATAGTGCCTCAGCAGCCAGCGGACACTCTCAACTGACGACGACCCAGCCAGG 1169
Db 301 AGCAATAGTGCCTCAGCAGCCAGCGGACACTCTCAACTGACGACGACCCAGCCAGG 360

Qy 1170 GCTGGCCACCCAGGCATACAGCCTTAGTGGGCGCAGAGGTGAGAGGTTCTTGAAACCAAGAA 1229
Db 361 GCTGGCCACCCAGGCATACAGCCTTAGTGGGCGCAGAGGTGAGAGGTTCTTGAAACCAAGAA 420

Qy 1230 AGTCCACCATGCTTAATCTGACCAAGCAGAAACACACCCAGCATGATCCCCAGCCAGAG 1289
Db 421 AGTCCACCATGCTTAATCTGACCAAGCAGAAACACACCCAGCATGATCCCCAGCCAGAG 480
```


Db	245	TCACAAATTTTCAAGAGGAATGGGATGCTGTTTGTAAATTTTCTATGCAATTTCTGCAGAC	304
Qy	1727	TTATTGGATTATTAGTATTATCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTC	1786
Db	305	TTATTGGATTATTAGTATTATCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTC	364
Qy	1787	TACACCATGCTACTGAGCTAAACCACTTTCTAAGAAATCCCAAAAGGAAACAATGTGTCTTC	1846
Db	365	TACACCATGCTACTGAGCTAAACCACTTTCTAAGAAATCCCAAAAGGAAACAATGTGTCTTC	424
Qy	1847	TATTCTGACTTAACTTCATTGTCTATAGGTTTGGATATTAATTTCAAGGGAGTTGAAA	1906
Db	425	TATTCTGACTTAACTTCATTGTCTATAGGTTTGGATATTAATTTCAAGGGAGTTGAAA	484
Qy	1907	TAGTGGGAGATGCGAAGAGTGAATCAGTTTCTCCACCTCTATATACTAATCTCACTATTG	1966
Db	485	TAGTGGGAGATGCGAAGAGTGAATCAGTTTCTCCACCTCTATATACTAATCTCACTATTG	544
Qy	1967	TATTGAGCCCAAAATAAATCTATGAAAGGACAAAATTTGTGACAAAGGATTTGGAAGAG	2026
Db	545	TATTGAGCCCAAAATAAATCTATGAAAGGACAAAATTTGTGACAAAGGATTTGGAAGAG	604
Qy	2027	CTTTCCATCTTCATGATGTTATGAGGATTTGTGACAAACATTTAGAATATATATGAGC	2086
Db	605	CTTTCCATCTTCATGATGTTATGAGGATTTGTGACAAACATTTAGAATATATATGAGC	664
Qy	2087	TAATTGTGATTTCCCTCAAAATCAGATGCTCTAAGGACCTTCCCTGCTAGATATTTCTCG	2146
Db	665	TAATTGTGATTTCCCTCAAAATCAGATGCTCTAAGGACCTTCCCTGCTAGATATTTCTCG	724
Qy	2147	AAGGAGAAATACACATGTCATTTATCAACGTCCTTTAGAAAGATTTCTTCTAGAGAAA	2206
Db	725	AAGGAGAAATACACATGTCATTTATCAACGTCCTTTAGAAAGATTTCTTCTAGAGAAA	784
Qy	2207	AGGGATCTAGGAATGCTGAAAGATTAACCAACATAC	2242
Db	785	AGGGATCTAGGAATGCTGNAAGATTTACCCAAATAC	820
RESULT 14			
LOCUS	AW963657	716 bp	mRNA linear EST 01-JUN-2000
DEFINITION	EST375730	MAGE resequences, MAGH Homo sapiens CDNA, mRNA sequence.	
ACCESSION	AW963657		
VERSION	AW963657.1	GI:8153493	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 (bases 1 to 716)		
	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,		
	Holt,I.E., Speed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and		
	Quackenbush,J.		
TITLE	Assessment of gene expression patterns in a model of colon tumor		
	metastasis using a 19,200 element CDNA microarray		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: John Quackenbush		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 3528		
	Fax: 301 838 0208		
	Email: johnqu@tigr.org		
	Plate: 190		
	Seq primer: Reverse.		
FEATURES	Location/Qualifiers		
source	1..716		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone_lib="MAGE resequences, MAGH"		
	/note="Vector: pBluescriptSKm"		

QY	1290	CAGAGCCTTCCAAACGGTCTGAATTACAATGACTTGACTCCACGCTTCTCCTAGGAGTC	1349
Db	481	CAGAGCCTTCCAAACGGTCTGAATTACAATGACTTGACTCCACGCTTCTCCTAGGAGTC	540
QY	1350	AGGGTCTTTGGACTCTTCTCGTCATTTGGAGCTCAGTCCAGGACCAACACCAAGATGAG	1409
Db	541	AGGGTCTTTGGACTCTTCTCGTCATTTGGAGCTCAGTCCAGGACCAACACCAAGATGAG	600
QY	1410	AGGTCATCTAAGTAGCAGTGGAGCATTGCACGGAACAGATTCAGATGAGGATTTTCCTTAT	1469
Db	601	AGGTCATCTAAGTAGCAGTGGAGCATTGCACGGAACAGATTCAGATGAGGATTTTCCTTAT	660
QY	1470	ACAATACCAACCAACGACAAAGGATGTAAGCTGATTCATCTGTAAAA	1515
Db	661	CAATACCAACCAACGACAAAGGATGTAAGCTGATTCATCTGTAAAA	706
RESULT 13			
AL598458		820 bp	mRNA linear EST 04-SEP-2003
LOCUS	DKFP313H2320_r1_313 (synonym: hlcc2)	Homo sapiens	cdna clone
DEFINITION	DKFP313H2320 5', mRNA sequence.		
ACCESSION	AL598458		
VERSION	AL598458.1	GI:15161149	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 820)		
AUTHORS	Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.		
TITLE	EST (Duesterhoeft, et al.)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: MIPs		
	MIPs		
	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany		
	This is the 5' sequence of the clone insert		
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer		
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;		
	sequenced by Qiagen (Hilden/Germany) within the cdna sequencing		
	consortium of the German Genome Project.		
	No si sequence available.		
	This clone (DKFP313H2320) is available at the RZPD in Berlin.		
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059		
	Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.		
FEATURES	Location/Qualifiers		
source	1..820		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="DKFP313H2320"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/clone_lib="313 (synonym: hlcc2)"		
	/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;		
	cdna-collection"		
ORIGIN			
Query Match	27.8%;	Score 683.6;	DB 1; Length 820;
Best Local Similarity	98.6%;	Pred. No. 1.1e-168;	Gaps 0;
Matches 686;	Conservative	0; Mismatches 10;	Indels
QY	1547	AGGGAAGCAGGAGTCCAAATCTATTGTTGACACGAGCCTGTGGTGAAGGTTGGGA	1606
Db	125	AGCCAAAGCAGGAGTCCAAATCTATTGTTGACACGAGCCTGTGGTGAAGGTTGGGA	184
QY	1607	AAGGTGAGGTGAATATACCTAAACCTTTAATGTGGGATATTTTGTATCATGCTTTGAT	1666
Db	185	AAGGTGAGGTGAATATACCTAAACCTTTAATGTGGGATATTTTGTATCATGCTTTGAT	244
QY	1667	TCACAAATTTTCAAGAGGAAATGGAGTCTGTTTGTAAATTTTCTATGCAATCTCTGCAAC	1726

Wed May 11 07:24:22 2005

QY	2043	TGTTATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGATTTC	2102
Db	432	TGTTATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGATTTC	373
QY	2103	TCAAATCAGATGCTCTAAGGACTTTTCCTGCTAGATATTTCTGGAAGGAGAAATACAA	2162
Db	372	TCAAATCAGATGCTCTAAGGACTTTTCCTGCTAGATATTTCTGGAAGGAGAAATACAA	313
QY	2163	ATGTCATTTTATCAACGTCCTTAGAAAGAAATTTCTTAGAGAAAAGGGATCTAGGAATGC	2222
Db	312	ATGTCATTTTATCAACGTCCTTAGAAAGAAATTTCTTAGAGAAAAGGGATCTAGGAATGC	253
QY	2223	TGAAAGATTACCCCAACATACATTTATAGTCTCTTCTTCTGAGAAATGTGAACCCAGAA	2282
Db	252	TGAAAGATTACCCCAACATACATTTATAGTCTCTTCTTCTGAGAAATGTGAACCCAGAA	193
QY	2283	TTGCAGACTGGGTGGACTAGAAAGGAGATTAGATCAGTTTCTCTTAATATGTCAAGG	2342
Db	192	TTGCAGACTGGGTGGACTAGAAAGGAGATTAGATCAG--TTCTCTTAATATGTCAAGG	135
QY	2343	AAGGTAGCCGGGCATGGTGCAGGCACCTGTAGAAAATCCAGCAGGTGGAGGTGCAGT	2402
Db	134	AAGGTAGCCGGGCATGGTGCAGGCACCTGTAGAAAATCCAGCAGGTGGAGGTGCAGT	75
QY	2403	GAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGCGGGACTCCGTCTC	2458
Db	74	GAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGCGAGCAAGACTCCGTCTC	19

Search completed: May 6, 2005, 04:19:45
Job time : 7375 secs